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(57) Abstract

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID: 1) peptide corresponding to amino acids 638 to 673 of the HIV-1 LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

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METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a 5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

The present invention relates, first, to DP178 15 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1_{LAI} transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability, antiviral activity, such as the ability to inhibit HIV 20 transmission to uninfected CD-4+ cells, or an ability to modulate intracellular processes involving coiledcoil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178 25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids 30 558 to 595 of the HIV-1_{LAI} transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion 35 capability, antiviral activity, or the ability to

modulat intracellular processes inv lving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, noncytotoxic inhibitors of HIV-1 transfer to uninfected CD-4 cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

2. BACKGROUND OF THE INVENTION

2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

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Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell death.

2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of each of these types. Infection of human CD-4 Tlymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and

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replicate via a DNA int rmediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I,-II,-III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

HIV is targeted to CD-4⁺ cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalgleish, A. et al., 1984, Nature 312:763-767; Klatzmann et al., 1984, Nature 312:767-768; Maddon et al., 1986, Cell 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4⁺ receptor molecules (McDougal, J.S. et al., 1986, Science 231:382-385; Maddon, P.J. et al., 1986, Cell 47:333-348) and thus explains HIV's tropism for CD-4⁺ cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

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2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991, FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptasetargeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been developed which have been shown to been active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989, Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4⁺ T-cells by some HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,

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recombinant soluble CD-4 clinical trials have pr duced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

Attention is also being given to the development
of vaccines for the treatment of HIV infection. The
HIV-1 enveloped proteins (gp160, gp120, gp41) have
been shown to be the major antigens for anti-HIV
antibodies present in AIDS patients (Barin, et al.,
1985, Science 228:1094-1096). Thus far, therefore,
these proteins seem to be the most promising
candidates to act as antigens for anti-HIV vaccine
development. To this end, several groups have begun

as immunogenic targets for the host immune system.

See for example, Ivanoff, L. et al., U.S. Pat. No.

5,141,867; Saith, G. et al., WO 92/22,654; Shafferman,
A., WO 91/09,872; Formoso, C. et al., WO 90/07,119.

Clinical results concerning these candidate vaccines,
however, still remain far in the future.

to use various portions of gp160, gp120, and/or gp41

Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

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SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate 5 LAI (HIV-1_{LAI}), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1, but found in viruses and/or organisms other than HIV-1,A: Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 30 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1 LAI transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

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DP107 peptide sequence present within the gp41 pr tein of HIV-1_{LAI}, but found in viruses and organisms other than HIV-1_{LAI}. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for for example, enveloped viruses, such as retroviruses other than HIV-1_{LAI}, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

15 The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of 20 the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4+ cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory 25 activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-asociated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

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th peptid s of the invention may be used as modulators of intracellular events inv lving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

10 The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said 15 moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for 20 example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus 25 and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

Embodiments of the invention ar demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4⁺ cell-cell fusion (i.e., syncytial formation) and infection of CD-4⁺ cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

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3.1. <u>DEFINITIONS</u>

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as follows:

A (alanine) R (arginine) N (asparagine) D (aspartic acid) C (cysteine) 20 Q (glutamine) E (glutamic acid) G (glycine) H (histidine) I (isoleucine) L (leucine) K (lysine) M (methionine) 25 F (phenylalanine) P (proline) S (serine) T (threonine) W (tryptophan)

> Y (tyrosine) V (valine)

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BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV1A1; DP178 homologs derived from HIV-1sp (DP-185; SEQ ID:3), HIV-1_{RF} (SEQ ID:4), and HIV-1_{MN} (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2_{md} (SEQ ID:6) and HIV-2_{NDZ} (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which 10 inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. 15 Throughout the figures, the one letter amino acid code is used.

Inhibition of HIV-1 cell-free virus FIG. 2. infection by synthetic peptides. IC50 refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

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Inhibition of HIV-1 and HIV-2 cell-free FIG. 3. 25 virus infection by the synthetic peptide DP178 (SEQ ID:1). IC₅₀: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

4B: DP-180 (SEQ ID:2) represents a scrambl d c ntrol peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1_{SP2} isolate; Control, refers to the number of syncytial produced in the absence of peptide.

- FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.
- FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell proliferation data is shown.
 - FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM. The proteins are more fully described, below, in Section 8.1.1.
 - FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.
- FIG. 9. Abrogation of DP178 anti-HIV activity. Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41 Δ 178 or M41P Δ 178.
 - FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.
- FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common

f atures of both m dels include (1) the native stat is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally though gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended α-helix. This conformational change positions the fusion peptide for 20 interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

FIG. 20. Search results for HIV-1 (BRU 10 isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (*): PLZIP; Diamonds (*): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program 15 designed to search for such peptide regions). Asterisk (*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and 20 in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations are as in FIG. 20.

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FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data.
FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D:

Peptides derived from the F1 DP107-like region.

Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

"-", negative antiviral activity;

"+/-", antiviral activity at greater than
100μg/ml;

"+", antiviral activity at between 50-100µg/ml;
"++", antiviral activity at between 20-50µg/ml;
"+++", antiviral activity at between 1-20µg/ml;
"++++", antiviral activity at <1µg/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

"-", no helicity;

"+", 25-50% helicity;

30 "++", 50-75% helicity;

 ${\rm IC}_{50}$ refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures

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c ntaining no peptide. IC₅₀ values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC $_{50}$ are as in FIG. 27A-D. IC $_{50}$ values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3
F1 DP107-like region. Peptide antiviral and CD data.
Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.

27A-D. Purified peptides were used to obtain IC₅₀
values, except where the values are marked by an asterisk (*), in which cases, the IC₅₀ values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3
F1 DP178-like region. Peptide antiviral and CD data.
Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.
27A-D. Purified peptides were used to obtain IC₅₀
values, except where the values are marked by an
asterisk (*), in which cases, the IC₅₀ values were
obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dim rization domain, as defined

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by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for Pseudomonas aerginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human cfos proto-oncoprotein. Sequence search designations are as in FIG. 20.

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FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. IC_{50} values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

fig. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.q., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amidoand acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B:

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column to the immediate right of the test peptide name

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indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself. IC_{50} is as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC₅₀ was obtained using a crude peptide preparation. 15

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data. IC_{50} as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide.

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length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

5. <u>DETAILED DESCRIPTION OF THE INVENTION</u>

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1_{LAI} transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate

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intracellular pr cesses involving coil d-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, infra. HIV protein, gp41, DP178 corresponds to a putative α helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced 20 by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. is of interest that mutations in the C-terminal α helix motif of gp41 (i.e., the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is 30 involved in membrane fusion while the C-terminal α helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virusinduced membrane fusion.

On the basis f the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107

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can be considered.

peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178

domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

5.1. <u>DP178 AND DP178-LIKE PEPTIDES</u>

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1_{LAI} isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH2-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)

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In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below. 10 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH2) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not 15 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or 20 peptide group. Further, "2" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred 25 "X" or "Z" macromolecular group is a peptide group.

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TABLE I DP178 (SEO ID:1) CARBOXY TRUNCATIONS

X-YTS-Z X-YTSL-Z X-YTSLI-Z X-YTSLIH-Z X-YTSLIHS-Z X-YTSLIHSL-Z X-YTSLIHSLI-Z X-YTSLIHSLIE-Z X-YTSLIHSLIEE-Z X-YTSLIHSLIEES-Z X-YTSLIHSLIEESQ-Z X-YTSLIHSLIEESQN-Z X-YTSLIHSLIEESQNQ-Z X-YTSLIHSLIEESQNQQ-Z X-YTSLIHSLIEESQNQQE-Z X-YTSLIHSLIEESQNQQEK-Z X-YTSLIHSLIEESQNQQEKN-Z X-YTSLIHSLIEESQNQQEKNE-Z X-YTSLIHSLIEESQNQQEKNEQ-Z X-YTSLIHSLIEESQNQQEKNEQE-Z X-YTSLIHSLIEESQNQQEKNEQEL-Z X-YTSLIHSLIEESQNQQEKNEQELL-Z X-YTSLIHSLIEESQNQQEKNEQELLE-Z X-YTSLIHSLIEESQNQQEKNEQELLEL-Z X-YTSLIHSLIEESQNQQEKNEQELLELD-Z X-YTSLIHSLIEESQNQQEKNEQELLELDK-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKW-Z 20 X-YTSLIHSLIEESQNQQEKNEQELLELDKWA-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWAS-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASL-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWN-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNW-Z X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limit d to lipid-fatty acid 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE IA DP178 (SEO ID:1) AMINO TRUNCATIONS

```
X-NWF-Z
                                                    X-WNWF-Z
                                                   X-LWNWF-Z
                                                  X-SLWNWF-Z
                                                 X-ASLWNWF-Z
                                                X-WASLWNWF-Z
                                               X-KWASLWNWF-Z
                                              X-DKWASLWNWF-Z
                                             X-LDKWASLWNWF-Z
                                            X-ELDKWASLWNWF-Z
                                           X-LELDKWASLWNWF-Z
                                          X-LLELDKWASLWNWF-Z
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                                         X-ELLELDKWASLWNWF-Z
                                        X-QELLELDKWASLWNWF-Z
                                       X-EQELLELDKWASLWNWF-Z
                                      X-NEQELLELDKWASLWNWF-Z
                                     X-KNEQELLELDKWASLWNWF-Z
                                    X-EKNEQELLELDKWASLWNWF-Z
                                  X-QEKNEQELLELDKWASLWNWF-Z
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                                 X-QQEKNEQELLELDKWASLWNWF-Z
                                X-NQQEKNEQELLELDKWASLWNWF-Z
                               X-QNQQEKNEQELLELDKWASLWNWF-Z
                              X-SQNQQEKNEQELLELDKWASLWNWF-Z
                             X-ESQNQQEKNEQELLELDKWASLWNWF-Z
                            X-EESQNQQEKNEQELLELDKWASLWNWF-Z
                           X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
                          X-LIEESONOOEKNEOELLELDKWASLWNWF-Z
20 -
                         X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                        X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                       X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                      X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                     X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                    X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                   X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides f the inventi n als include DP178like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTIS, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

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HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amin acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The 10 insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that 15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to 25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178 region of the gp41 protein.

D letions of DP178 (SEQ ID:1) r DP178 truncations are also within the sc pe of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, 10 as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

5.2. <u>DP107 AND DP107-LIKE PEPTIDES</u>

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1_{LAI} transmembrane (TM) gp41 protein, as shown here:

NH2-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH (SEQ ID:25)

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In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

inv lving coiled-c il peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group $(-NH_2)$ and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE II DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

X-NNL-Z X-NNLL-Z X-NNLLR-Z X-NNLLRA-2 X-NNLLRAI-Z X-NNLLRAIE-Z X-NNLLRAIEA-2 X-NNLLRAIEAQ-Z X-NNLLRAIEAQQ-Z X-NNLLRAIEAOOH-Z X-NNLLRAIEAOOHL-Z X-NNLLRAIEACOHLL-Z X-NNLLRAIEAOOHLLO-Z X-NNLLRAIEAQQHLLQL-Z X-NNLLRAIEAQQHLLQLT-Z X-NNLLRAIEAQQHLLQLTV-Z X-NNLLRAIEAQQHLLQLTVW-Z X-NNLLRAIEAQQHLLQLTVWQ-Z X-NNLLRAIEAOOHLLOLTVWOI-Z X-NNLLRAIEAOOHLLOLTVWOIK-Z X-NNLLRAIEAQQHLLQLTVWQIKQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z 20 X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA DP178 (SEO ID:25) AMINO TRUNCATIONS

```
X-KDQ- Z
                                                    X-LKDQ- Z
                                                   X-YLKDQ- Z
 5
                                                  X-RYLKDO- Z
                                                 X-ERYLKDO- Z
                                                X-VERYLKDO- Z
                                               X-AVERYLKDO- Z
                                             X-LAVERYLKDO- Z
                                            X-ILAVERYLKDQ- Z
                                           X-RILAVERYLKDQ- Z
                                          X-ARILAVERYLKDO- Z
10
                                         X-QARILAVERYLKDQ- Z
                                        X-LQARILAVERYLKDQ- Z
                                       X-QLQARILAVERYLKDQ-.Z
                                      X-KQLQARILAVERYLKDQ- Z
                                     X-IKQLQARILAVERYLKDQ- Z
                                    X-QIKQLQARILAVERYLKDQ- Z
                                   X-WQIKQLQARILAVERYLKDQ- Z
15
                                  X-VWQIKQLQARILAVERYLKDQ- Z
                                 X-TVWQIKQLQARILAVERYLKDQ- Z
                                X-LTVWQIKQLQARILAVERYLKDQ- Z
                               X-QLTVWQIKQLQARILAVERYLKDQ- Z
                              X-LQLTVWQIKQLQARILAVERYLKDO- Z
                             X-LLQLTVWQIKQLQARILAVERYLKDQ- Z
                            X-HLLQLTVWQIKQLQARILAVERYLKDQ- Z
                          X-QHLLQLTVWQIKQLQARILAVERYLKDQ- Z
20
                         X-QQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                        X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                       X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                      X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                     X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                    X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                   X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
25
                  X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                 X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
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The one letter amino acid code is used.

Additionally,

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"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"2" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

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HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid 20 conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of the invention. Utilizing the DP107 and DP107 analog 25 sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid 30 substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) t aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The 10 insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107 20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107 region of the gp41 protein.

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Deletions of DP107 (SEQ ID:25) r DP178 truncations are als within the sc pe f the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

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DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1_{LAI} enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

ability t m dulate intracellular pr cesses involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (i.e., other than HIV-1_{LAI}) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates.

DP178 analogs derived from the corresponding gp41 peptide region of other (i.e., non HIV-1_{LAI}) HIV-1 isolates may include, for example, peptide sequences as shown below.

NH₂-YT<u>NT</u>IYTLLEESQNQQEKNEQELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH2-YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF-COOH (SEQ ID:4);

 NH_2 -YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1_{SF2}, HIV-1_{RF}, and HIV-1_{MN} isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding positi n in the DP178 (SEQ ID:1) peptide. One such

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DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV- $2_{\rm NHZ}$ isolate has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH,-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

of the HIV-2_{NHZ} DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH₂) and "Z" may represent a carboxyl (-COOH) group.

Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a

c valently attached macr molecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

TABLE III

HIV-2_{NDKZ} DP178 analog carboxy truncati ns.

X-LEA-Z X-LEAN-Z X-LEANI-Z X-LEANIS-Z 5 X-LEANISQ-Z X-LEANISOS-Z X-LEANISQSL-Z X-LEANISQSLE-Z X-LEANISQSLEQ-Z X-LEANISQSLEQA-Z X-LEANISQSLEQAQ-Z X-LEANISQSLEQAQI-Z 10 X-LEANISQSLEQAQIQ-Z X-LEANISQSLEQAQIQQ-Z X-LEANISQSLEQAQIQQE-Z X-LEANISQSLEQAQIQQEK-Z X-LEANISQSLEQAQIQQEKN-Z X-LEANISQSLEQAQIQQEKNM-Z X-LEANISQSLEQAQIQQEKNMY-Z 15 X-LEANISQSLEQAQIQQEKNMYE-Z X-LEANISQSLEQAQIQQEKNMYEL-Z X-LEANISQSLEQAQIQQEKNMYELQ-Z X-LEANISQSLEQAQIQQEKNMYELQK-Z X-LEANISQSLEQAQIQQEKNMYELQKL-Z X-LEANISQSLEQAQIQQEKNMYELQKLN-Z X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

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"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV HIV-2_{NDHZ} DP178 analog amin truncati ns.

```
X-NWL-Z
                                                    X-TNWL-Z
                                                   X-FTNWL-Z
                                                  X-VFTNWL-Z
                                                 X-DVFTNWL-Z
                                                X-WDVFTNWL-Z
                                               X-SWDVFTNWL-Z
                                              X-NSWDVFTNWL-Z
                                             X-LNSWDVFTNWL-Z
                                            X-KLNSWDVFTNWL-Z
                                           X-OKLNSWDVFTNWL-Z
                                          X-LQKLNSWDVFTNWL-Z
10
                                         X-ELQKLNSWDVFTNWL-Z
                                        X-YELQKLNSWDVFTNWL-Z
                                       X-MYELQKLNSWDVFTNWL-Z
                                     X-NMYELQKLNSWDVFTNWL-Z
                                     X-KNMYELQKLNSWDVFTNWL-Z
                                   X-EKNMYELQKLNSWDVFTNWL-Z
                                  X-QEKNMYELQKLNSWDVFTNWL-Z
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                                 X-QQEKNMYELQKLNSWDVFTNWL-Z
                                X-IQQEKNMYELQKLNSWDVFTNWL-Z
                               X-QIQQEKNMYELQKLNSWDVFTNWL-Z
                              X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
                             X-QAQIQQEKNMYELQKLNSWDVFTNWL-2
                            X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                           X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                          X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20
                         X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                        X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                       X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                      X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                     X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                    X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
                   X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
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```

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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> DP178 and DP107 analogs are recognized or identified, for example, by utilizing one r more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, 10 in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence 15 homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV).

Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or 25 otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et

35 al., 1991 Science 252:1162-1164) is inadequate for

identifying protein regions analog us to DP107 r DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

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The computer search strategy of the invention, as demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database package, preferably PC/Gene.

A series of search motifs, the 107x178x4,
ALLMOTI5 and PLZIP motifs, were designed and
engineered to range in stringency from strict to
broad, as discussed in this Section and in Section 9,
with 107x178x4 being preferred. The sequences

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> identified via such search motifs, such as thos listed in Tables V-XIV, below, p tentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed or braced amino acids is followed by a number in 20 parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

The ALLMOTI5 is written as follows: 25

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\{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-
\{CDGHP\} - \{CFP\} (2) - \{CDGHP\} - \{CFP\} (3) -
 \{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-
   \{CDGHP\} - \{CFP\} (2) - \{CDGHP\} - \{CFP\} (3) - \{CDGHP\} 
 \{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-
```

Translating this motif, it would read: "at the 30 first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except 3, F, or P is acceptable, at the fourth 35 heptad position (D), any amino acid residue except C,

D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTIS motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino a cid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

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The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is d signed to search for

four consecutive heptad repeats (thus the repeat of the first line four times), meaning that it search search for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in Table VII, below at the end of this Section, being preferred.

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The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.

19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. Fr example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lsts viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table XIV lists viral sequences identified via P23TLZIPC search motifs The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention.

The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

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The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178, above, in Section 5.1. For example, these peptides

may include any of the additional amin -terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section 5.2.

15 Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory 20 Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX presents Human Parainfluenza Virus 3 F1 region DP178 25 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped according to the specific virus which they inhibit, 35

including respiratory syncytial virus, human parainfluenza virus 3, simian immunodeficiency virus and measles virus.

TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

		All Virgan (ne beterlophe fri)	٦	7	T		75.24	48.54	1.18	1 V III V
PCCENE	ALLMOTTS		J	7	Y Y	Т	Ţ	:		
COLBANE	PROTEIN SOUTH STATE OF STATE O	TOBACCO RATTLE VIRUS (STRAIN PSG)	T	Ī	277 100	A14.A78	1045.1079	1135.1176	413:11	4.0.44
PLYCK TRVPS	POTENTIAL IN NO PROTECT		7	14:33	١					
PINK TAVIY	POTENTIAL IN ALTHOUGH	N UGANDA-1102)	2							:
PSSKD HSV6U	STARD ROLEIN	IEPATITIS DELTA VIRUS (ISOLATE AMERICAM)	1	2						:
PAANT HOVAL	DELTA ANTINCA	HEPATITIS DELTA VIRUS (ISOLATE DIM)		8	T					
אסאען אסאס)	DELIA ANTIGER	HEPATITIS DEL TA VIRUS (ISOLATE ITALIAN)		20.5					:	
PAANT HOVIT	DELTA ANTICEM (ALTHA ANTICEM)	HEPATHTIS DELTA YINUS (ISOLATE LERANON-I)	7							:
PAANT HOVE:	DELIA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE M·1)	148	8						: :
PAANT MOVAL	DELTA AMILIEM	HEPATITIS DELTA VIRUS (ISOLATE IAPANESE AI-3)	.4	8						:
PAAMT HOVAS	DELTA ANIMOEN	HEPATITIS DELTA VIRUS (ISOLATE MAURU)	3.48	100-144						
PANT MOVIA	DELTA ANTIGEN	IEPATITIS DEL TA VIRUS (ISOLATE JAPANESE S-I)	1-49	5 5						
PANT MOVS!	DELTA ANTICEM	INFRATITIS DELTA VIRUS (ISOLATE IAPANESE S-1)	1.49	100-144						:
אסאד אסאר	DELTA ANTIGEN	REPATITIS DEL TA VIRUS (ISOLATE WOODCINCK)	3.48	100.144						
PAAMT HEVWO	DELTA ANTIGEN	EOWN POX VIEUS (ISOLATE IP-438)	011-14							:
PATTH FOWTH	ANTITION DEPOSITION OF THE PROPERTY OF THE PRO	VACCIDITA VIBITS (STRAIN WR)	14-57	420.564	\$70-625					:::
PATH VACCV	94 KD A.TYPE DACLUSION FROTEIN	ANCHINA WALLE	425-525	\$31.565	\$71.628					
PATTI VARV	11 KD A.TYPE INCLUSION PROTEIN	TOTAL OF THE EVILLE (TVPE II	304.345							
PATTI HSVII	ALPHA TRANS-INDUCING FACTOR	MEMES SIMPLEA VINOS (1174.)	102.130	304.345						-
PATT2 HSVIP	ALPHA TILANS INDUCING FACTOR	REICES SECTER VIRGO (1975)	101.147	264.331						: : !_
PATT2 HSVED	ALPHA TRANS-INDUCING FACTOR	EQUINE FERVES VIRUS 1 TPE 1 (3) RAIN AGE()	30.134	19.761						-
PATT VACCE	PUTATIVE A-TYPE INCLUSION PROTEIN	VACCINIA VIRUS (STIAIN CUPENNAUEN)	10.							
PATTI VACEV	PUTATIVE A-TYPE INCLUSION PROTEIN	VACCIMA VIRUS		101.430						i I
	AT PHA TRANS-DIDUCING FACTOR	VANCELLA-ZOSTER VIRUS (STRAIN DURIAS)	Of -847							
200	PLITATIVE ALTITYE INCLUSION PROTEIN	VACCINIA VIRUS	31-93						-	
	AS PHA TRANSCHOCONO PROTEIN (VACWES)	HERPES SDALEX VIXUS (TYPE 2)	178-218	104-576						:
TALIN ROYS	AT BUY THE ANY DATHER PROTEIN (VACWES)	HENDES SIMPLEX VIRUS (TYPE 1)	177.772	124-381				1		!_
MAIN MAN	AT BANK DESILEDED PROTEIN	BOVINE HERPESVIRUS TYPE I	195.236				-			٠.
PATTIN HSVD	AT MAY THANK THE PROTECTION	EQUINE HEADESVIRUS TYPE I	241-289							:
PATTIN MSVE	AT BUS THE ANS THAT PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	206-252				000	971.		; ;
DAZA NILY	A TYPE DATI INTON PROTEIN	COWPOX VIRUS	14-57	\$2.26	332-366	27.2.4.75	Asc. for			:
A POST OF THE POST	PROTECTION BINES	EPSTEIN-BAALR VIRUS (STRATIV B95-8)	80-131							: : :
	THE MICHELLINGS ACTIVATOR BRLF!	EPSTEIN-BARK VIRUS (STRAIN D95-8)	130-187							:
Value Lav	COAT BROTERI VP	POLYOMAVIRUS BK	101.141							!
YOU IND	CONT. SECTION OF	POLYCHAYRUS BK	107.141							-1-
במעו במעו	CONTROL VAL	HAMSTER POLYONAVIRUS	189.195						İ	
TOAL SOLE	COAT PROTEIN VP	SINILAN YIRUS 40	33.15					-	!	
SCOA! BED	COAT PROTEIN VP3	BUDGERIGAR FLEDGLING DISEASE VIRUS	14:21					<u> </u>	-	
A POVEN	COAT PROTEIN VP2	POLYDMAYIRUS DK (STRAÍN AS)	14-64				 			<u>:</u>
PCOAT POVEK	COAT PROTEIN VP2	POLYOMAYIRUS BK	001							:
PCOA2 POVID	COAT PROTEIN VP3	BOVINE POLYONIAVIRUS					<u> </u>			<u>:</u>
PCOA1 POWIA	COAT PROTEIN VP2	HAMSTER POLYONIAVIRUS							<u> </u>	<u>:</u>
PCDA3 POVIC	COAT PROTEIN VP3	POLYOMAVIRUS IC		207-101						
PCOA POW Y	COAT PROTEIN VP3	LYAPHOTROPIC POLYONIAVIRUS	14.78	8						
0000	COAT PROTEIN VP1	MOUSE POLYONIAVIRUS (STRAIN))	2			1	1			ļ
77000	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS	2.5	137-113						-
300	COAT PROTEON VP3	MOUSE POLYOMANTRUS	2:32							-
200	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS	3.30	177.311						; ;
202	COAT PROTEIN VP2	SDAGAN VIRUS 40	3	23 P- 362	718-335					
200	COAT PROTEIN	ABUTILON MOSAIC VIRUS (ISOLATE WEST INDIA	180-214							: - - -
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	- COAT PROTEIN	APPLE CHA.OROTIC LEAF SPOT VIRUS	134-111				1			-
A PORT	COAT PROTEDI VPI	AEDES DENSONUCLEOSIS VIRUS	243.284							
	COAT PROTEIN	AATICHOKE MOTILED CRIMKLE VIRUS	200	B						
TON YOU	SOLVE BEATER	BEAN LEAFROLL VIRUS	127							
POAT BLAY	LOAI TROITE									

		All Virgies (no bacterlophoges)	1	ABEA 2	2000	ARIAN	7			1
PCCLVE	ALLMOIIS		£33	-	1				ľ	
TI.	ZAOTLIN	E MOSAJC VIRUS	163-197							Ĺ
l	COAT PROTEIN	AF VIRUS	141.107							Ĺ
POORT BYDY!	COAT PROTEIN			-						!
WONT BYDY	COAT PROTEIN			+						-
5000	COAT PROTEIN		1	+						1
70x	COAT PROTEIN	TRAIN	Ī	07.0						
OVI BIOLE	POTTER TOTAL			*77.4	1					-
2041 CAN			26.80	104-333	1					
OAT CAMP	National Property of the Prope	CAULIFLOWER MOSAIC VIAUS	8.3	10.333						
PCOAT CAMME	COALTROICE		53.41	187-224						_
DAT CALIVIN	COAT PROTEIN									!-
DAT CAMVS	COAT PROTEIN	CARNATION MOTTLE VIRUS								!
WAT CABLO	COAT PROTEIN	CONTRACTOR DESTRUCTION OF STREET					L			
	COAT PROTEIN	COWTEN CHLOSE BANG VIRUS	193.226		Ī				į	-
COA! COA!	SECOND TO COAT PROTECT	CARNATION ELEMENT AND STATE A VIRUS I	303-435	+						_
COAT CEAV	CANADA CARRIN PROTEIN	PARAMECTUR BURSAMA CITEDRE	167.231							
COAT CHAF	TOTAL STATE OF THE PARTY OF THE	CASSAVA LATEM VINUS	167.331	1						
COAT CLVK	CONTRACTOR	CASSAVA LATENT VIRUS	133-167							<u>.</u>
DAT CLVM	COATPROILIN	CUCUAMER MOSAIC WRUS	101.10						-	
PCOAT CHATC	COATPROTEIN	CUCLAMBER MOSAIC VIRUS	101							· <u>:</u> -
COAT CHAM	COAT PROTEIN	CILCIDIBER MOSAIC VIRUS							إ	;
PCOAT CANYS	COAT PROTEIN	CHILD THE MOSAIC VIRUS								-
Prost CAVO	COAT PROTEIN	CHOINGES ANGAIC VIRUS	137-187							: - ;
WW	COAT PROTEIN	STORY CARRY	153-117				ļ	-		_
	METURE PROTEIN	CUCUMBER BIOSAIL VIRGO	328-365				1			ļ -
COALCAV	September 1	CUCUMBER MECRUSIS VINOS	184-218					1		 -
COAT CAV	COAL FROID.	CHE ORIS STRUKTE MOSAIC, VIRUS	2.5				1			i T
PCOAT CSMV	COAT PRUIEM	CITAUS TRUSTEZA VIRUS	163.304						-	<u> </u>
COAT CTV36	COAT PROTEIN	CLOVER YELLOW MOSAIC VIRUS								1
COAT CYNIV	COATPROTEIN	ECOPLANT MOSAIC VIRUS	777	366.600						1
COAT EPMV	COATPROTEIN	FELINE CALICIVIAUS	95 600	266.400		L			1	+
COAT FCVC6	COAT PROTEIN	FELINE CALICIVIRUS		140.403		L		-		+
COAT FCVF4	COAT PROTEIN	FELINE CALICIVIRUS	80.	Τ	449-43)				1	+
PCOAT FCVF9	COAT PROTEIN	FIGWORT MOSAIC VIRUS		T						1
COAT PAND	PROBABLE COAT PROTEIN	FOXTAIL MOSAIC VIRUS	2							1
PCOAT FXOAV	COAT PROTEIN	TIME A BLIDESCENT VIRUS	ž.							-
COAT DAVI	CAPSID PROTEIN	STATE TO THE SCENT VIRUS	200					-		-
COAT BV22	CAPSID PROTEIN	CAR O RIPECTENT VIRUS				1	-	L		-
COAT BY6	CAPSID PROTEIN	LA V CYLOTOM ESS VIRUS	33.30	A		1	-			-
COAT LSV	COAT PROTEIN	MALT STREET CARLOS	3.4	121-121		1		-		+
VIST VSTV	COAT PROTEIN	MALE STREAM VIEWS	187-231			1	-	-	L	
NOVE TO SECOND	COAT PROTEIN	STRUCTURE STRUCT	167-231				-		-	
W. W.	COAT PROTEIN	MAKE STATES AND STATES	107-221				+	-	-	
COAL MAN	COAT PROTEIN	MAJZE STREAM VINOS	105.139				-	-	-	
NOV IND	COAT PROTEIN	ODDANIOULUSSUM MINOSTOT TIES	380-414	444-480			-	+		
PCOAT ONS	COAT PROTEIN VP2	BOVINE PARVOVINOS	165-265				$\frac{1}{1}$		-	i T
PCOAT PAVED	VOLUMENT NATIONAL VOLUMENT NAT	CANTINE PARTOVIRUS	3:11			 -	-	1	<u> </u>	-
COAT PAYC	COAT PROTEIN	PEA EALLY BROWNING VINUS	16.01				1	1	-	<u> </u>
PCOAT PLBY	NOT THE PARTY OF T	POPLAR MOSAIC VIRUS	104-138				+		-	<u> </u>
PCOAT POPMY	COAL PROTECT	PEPPER MILD MOTTLE VIRUS	18.31	151-292				1	 -	T
PCOAT PPACYS	COALTROLE	POTATO VIRUS	190-224	_				+	1	+
PCOAT PVSP	٦	POTATO YELLOW MOSAIC VIRUS	79	140.139					+	+
PCOAT PYMVV		RASPBERRY BUSHY DWARF VIRUS	333.306						1	+
PCOAT INDV	٠	RED CLOVER NECROTIC MOSAIC VIRUS		81.120	29.30					+
PCOAT RCPORY	COAT PROTEIN	NICE STRUE VIRUS							$\frac{1}{2}$	$\frac{1}{2}$
PCDAT RSV	l	STEEL SECTION AND STREET								
		THE PART OF THE PA				1				

	AT MOTH	The state of the s								
T.CLAIL	PROTEIN		81-3		١					
T SANGE TO SANGE	COAT PROTEIN	C VINCS	77.							
TO THE LABOR TO THE PARTY OF TH	COAT BEOTER									
COAL SOCAN	COAT PROTECT		2							
COAT SIRVI	COAT PROTEIN	SATELLITE TOBACCO NECROSIS VIRUS 1					-			
2001 TANS	CENOME FOR VPROTEIN	TAKABULO MOSAIC VIRUS								
COAT TAV	COAT PROTEIN	TOMATO ASPERMY VIRUS	Ţ	41.13						1
MODAT TRISVI	COAT PROTEIN	TOMATO BUSHY STURY VIKUS		80.00						: _1
PCDAT TRSVC	COAT PROTEIN	TOMATO BUSHY STUNT VIRUS	Ī							:
COAT TCV	COAT PROTEIN	TUNIP CAPALE VIRUS	186-220							:
COAT TGACV	COAT PROTEIN	TOMATO COLDEN NOSAIC VIRUS	101-101							i 1
COAT THOMY	COAT PROTEIN	TOBACCO MILD GREEN MUSAIL VIAUS	10)-137							j
COAT TAN	COAT PROTEIN	TOBACCO MOSAIC VIRUS	10.00							
COAT TANS	COAT PROTEIN	TOBACCO MOSAIC VTRUS	100							اٰ
COAT TANCO	COAT PROTEIN	TOBACCO MOSAIC VIRUS	101.101							
COAT TAMBA	COAT PROTEIN	TOBACCO MOSAIC VIRUS								
COAT TANKE	COATPROTEIN	TOBACCO MOSAIC VIRUS								
1	COAT PROTEIN	TOBACCO MOSAIC VIRUS	10.00							
COAT TAND	COATPROTEIN	TOBACCO MOSAIC VIRUS								
MOONT TANGE	COAT PROTEIN	TOBACCO MOSAIC VIRUS	101							
	COAT PROTEIN	TOBACCO MOSAIC VIRUS								L
TOVE TOUR	COAT PROTEIN	TOBACCO MATTLE VIRUS	813				 			! !
35.00	COAT PROTEIN	TOBACCO RATTLE VIAUS	00-107							
7/4/4	COAT PROTEIN	TOBACCO YELLOW DWARF VIRUS								1
200	COAT PROTEIN	TURNIP YELLOW MOSAIC VIRUS					 			<u></u>
COAL THE	COAT PROTEIN	TURNIP YELLOW MOSAIC VIRUS	41:75							-
TOUR TIME	COAT MOTERA	WHITE CLOVER MOSAIC VIRUS	183.197							i_
COAL WCHAP	COAL ANDREM	GROUND SQUIRREL INFRATITIS VIRUS	2.03							<u>;</u>
COM WAS	COME AVEICEN	HEPATITIS & VIRUS	\$			†				
1/200	CORP. AVTICEN	WOODCHUCK HEPATITIS VIRUS I	85.24			†				<u>:</u> _
TOTAL TRACES	CORP. ANTIGEN	WOODCHUCK HEPATHIS VIRUS 8	8	-						
ACTES ACTES	PROTEIN DISOR	AFRICAN SWINE PEVER VIAUS			-			:	:_	
POWER ADERS	FARLY ELA DNA-BINDING PROTEIN	HUMAN ADENOVIRUS TYPE 3	2						:	
POPUL AFERI	FABLY ELA DNA-BRYDING PROTEIN	HURIAN ADENOVIRUS TVPL 5	4		1001	10:1:104		!	:	<u>.</u> .
783 1870	MAJOR DNA-BRODRO PROTEIN	EPSTERY. DARR VIRUS						-		
AVACH IMONA	DALAICE DAYA-BRADING PROTEIN	HOMAN CYTONEGALOVIRUS		007 003	100.04	1070.1140	1- 	i 	:	
PONTE HEVIL	MAJOR DNA-BINDING PROTEIN	HERPES SCALLEX VANUS	100	1	164-661	1079-1140			!	
PENNI HSVIP	NAJOR DNA-BRODRG PROTER	HERPES SINGLEX VIRUS	101	04.00	749.101	1079-1140	- 			•
POPOSI MSVIK	MAJOR DNA-BINDING PROTEIN	HEAPES SIMPLEX VIRUS	101	114.001	1040.11		 			
FONDI HISVOR	MAJOR DNA-BINDING PROTEIN	BOUTH IERPESTIRUS TYPE 2							:	
PONDI HSVEI	MAJOR DNA-BINDING PROTEIN	EQUINE HERPESVIRUS TYPE		1107.1149		 	-			- ;
POWEL HIS VER	MAJOR DNA-BINDING PROTEIN	EQUINE INTERVIEWS TYPE. I	333 350	. 41	100.00	102.03		<u> </u> -	<u>i</u> _	:
MSVXA HSVXA	MAJOR DWA-BINDING PROTEIN	HERPESVIRUS SAIMIRI	446-437	35.11.00						• ·-
SVACM INCOM	MAJOR DNA-BINDING PROTEIN	MURINE CYTONEGALOVIRUS	30.00				i			
POINT POWE	MAJOR DWA-BINDING PROTEIN	SDIIAN CYTOMEGALOVIRUS	202-202	12.		†] 			
QAZA ISAQA	MAJOR DNA-BINDING PROTEIN	VALICELLA-20STER VIRUS	000			1				:
DOSA LANCE	DNA LIGASE	AFAICAN SWINE FEVER VIRUS	3							:
AVC.	DNA LIGASE	VACCINDA VIRUS	103-416			1				<u>:</u> -
2000	DNA LIDASE	VACCIMIA VIRUS	193.436				T			:
2000	DNALIGASE	VALIDLA VIRUS	195-416							-
100	DNA POLYNGRASE	MINIAN ADENOVIRUS TYPE 2	667.743							ļ_
10.00	DNA POLYMENASE	HUNLAN ADENOVIRUS TYPE S	107.763							-

			ALC:	444	ANTA	1				
				•				1		
			Ì						-	:
			23-64	:03::40		1			-	
		ENIONOLOGY THE	343.284							
									1	
		CHIORELLA VIRUS I	Ī		19.55				-	
			7							
			183.787	1033-1074		-				
		US (STICKIN ALLEN)	1.10				j		j	
		(STRAIN CHINA)				-			1	
		IAI DUCK ISOLATE ST	5.30	1		!				
			291.325							:
				134.361	137.595					
			2.7					_		:
		200	201-105							
	1		201.319		_	-				: ;
П									Ì	1
			311:334			-				:
		IEDUES SIMILE CONTROL OF A NOTELOTTI	\$11-559			1			_	
1			\$11.559			4				!_
1			611.610		_					i_
DECL HISVIK DNA PO		GEBBER SALPLEX VIRUS (TYPE I / STRAIN SCIB)								نـ
Γ		PERSON CALIFOR VIRUS (TYPE 2/ STRAIN 186)	313-380		1	-				:
T		ELCES SUPERIOR COME A COME A PRAPE	194.528		-		13			_
T		EQUINE HELDES VIRUS 111E 1 (311CH)	13-67	110.166	401.435	100-100				· - -
POPOL HISVED UNA PU		т	700							į.
POPOL HSVII DNA PO		S	2			-	_			
Ī,		ACTION OF THE ABLICOPENIAGEN	627-613	7.0-01.2		-		L		_
T		ACCINIA VIXUS (3) PARIF CO	(7)-40)	136E	828-162			1		i L
		VACCIDIA VIRUS (STRAIN WR)	100	760.817	127-161					<u>:</u>
PDPOL VACCY DNA PC		VARIOUA VIRUS								į
Γ	DNA POLYMERASE	SCHOOL & PACTER VIRIIS (STRAIN DUMAS)	473-533		-	-	-	ļ.		
Ī		VAUCELANGUE CONTRACTOR	205-336			1	1	-		
T		WOODCHUCK NEFATITIS VINGS	160-331				1			
٦		WOODCHUCK HEPATITIS VIRUS 29	111.000		_					<u>:</u>
		WOODCHUCK JEPATITIS MRUS 7	000		L	_				; ;
		WOODCHUCK HEPATITIS VIRUS B		-		-	-			i
POPOL WHYS DNA P		WOODCHINE HEPATITIS VIRUS & (INFECTIOUS CLONE)	6	1	+					
Γ	DNA POLYMERASE	THE PARTY OF THE ANALYSE AND	201-233			1	-	-	-	_
T		HEFALLIND VINCE COMP. 1 STRAIN ABAD	135-169			1	+			 -
1	THINK THE MUCLED TIDORIY	EQUINE HENDESVINUS LYTE I ISTRAM ALT	139.223		_					:
POUT HISVED DEUX	TIDOHY	HERPESVIRUS SAIMIN (STRAIN !!)	17.141							:
	LIVIE INCESSION	HIMAN ADENDVIRUS TYPE 41	10	1	-	-		<u> </u>		-
	BARLY BIA 37 KD PROTEIN	A APPRIATE TYPE 40	102-166			1	-	L	_	
Ī	END DECITED I ARGE T.ANTIGEN	HUNAN ALCINOTING	103-137			1	-			:-
1	CONTROL CALALL T. ANTIGEN	HONCAN ADENOVIRUS 1 TPE 4	103.137		-		 		1	-
	KOIEN, SMALL TANKER	HIDWAN ADENOVIRUS TYPE S		-	-	-				ļ
	EIB PROTEIN, SMALL I-ANTIOC	HIDAAN ADENOVIRUS TYPE 12	2	+		-				
	EIB PROTEIN, SMALL T. ANTIGEN	TANAN AMENOVIRUS TYPE 40	8		-		-		_	_i
Ī	FIR PROTEIN SHALL T-ANTIGEN	TOTAL STRUCTURE TVPE A1	180-134		1	1	+	-	-	_
T	EIN MOTERN SMALL T.AMTIGEN	HUMAN ADEAU VIEWS	116.133			-	+		-	
1	TANTICEN	MOUSE ADENOVIRUS 1 TTE 1	. i		L					-
	KUIER, Small	HOMAN ADENOVIRUS TYPE ?			-				1	-
	EALY EIB 14 KD PRUIEW	INDIAN ADENOVIRUS TYPE)		1	-	-	L			1
	EALLY ED 15.3 KD PROTEIN	AND ADDROVED STYPE S	2		+	+				
Ī	FARLY ES 14 5 KD PROTEIN	TOTAL STATE OF THE TABLE TO THE	77			+		-	-	L
T	EAST VENTS 1 KD PROTEIN	HUMAN ALEROVINOS COMO	70-107				+	+		-
1	STATE OF THE PARTY	HOMAN ADENOVIRUS 1 TPE 33	123.169			-	1			-
1	SALES OF VOOROUTEN	HUMAN ADENOVINUS 1 TVE 22	10.44					1	-	ļ
PESSI ADESS EAST	LY ED AVENUE AND THE PARTY OF T	HIDAAN ADENOVIRUS TYPE 2	3	-	-					1
PE411 ADE01 PRO	PROBABLE EALT OF 11 P.	HUMAN ADENOVIRUS TYPE S		+		-				1
	PROBABLE EAST Y EA II KU PROTEST	EPSTEIN-BARR VIRUS (STRAIN B95-8)		+		-	-			-
	EARLY ANTIGEN PROTEIN R	CALLED DATE WELK (CTLAIN 1995.5)	487-521	$\frac{1}{2}$	1	+	-			
I	FRANA A NORTH EAR PROTEIN	EVIEW FACE VIEW	11:11	307.341						
VEBY EBV	HAUBUS CITION TO TO SUBLIMINE	VALIDLA VIRUS								

THE NAME	A LEAST TO THE PARTY OF THE PAR						7			
VI 00 1/0/20			4	7000			Г			
	ENY POLYPROTEIN PRECURSOR	FAIEND SPLEEN FOCUS-FORMING VINUS	11.							
TOTAL CANADA	BANY POLYPROTEIN PRECURSOR									
TENAY THE	SALES VIENTED	SVIRUS	77.07.0							! !
PENY AVIDE	The Part of the Control of the Contr		426-47							! !
PEAV AVISIN	STATE OF STA	BABOON ENDOCENOUS VIRUS (STRAIN MIT)	٠		1	014.01	414.401			i <u>!</u>
PERV BAEVI	ENV POLITICISE	BOVINE INDIGINODEFICIENCY VIRUS (ISOLATE 106)		T		35.55		1999		! -i-
PENV BIVOR	ENT COLUMN TO CO	BOVING INDIGINADEFICIENCY VIRUS (ISOLATE 117)	10.44	18:522	134-157	1				; !
PEN BINT	ENV POLITICISM PROCESSOR	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE FLK)	ğ. 38							: !-
PENV BLVA	ENV POLITICAL	BOVING LEUKEMIA VIAUS (AUSTAALIAN ISOLATE)	106.379			1	T			; :
PENY BLVAU	ENV POLITICAL SERVICES	BOVING LEUKEMIA VIRUS (AMERICAN ISOLATE VIDA)	104-179							<u>;</u> _
PENV BLVAV	ENV POLITICOLES	BOVINE LEUKEARA VIAUS MELGIUMI ISOLATE LA285)	304.379							:
PENV BLVB2	EN FOLTROIEM	MOVING LEUKEMIA VIRUS (DELGIUM ISOLATE LBS9)	304-379	-						: : :
PENV BLVBS	ENV POLYTROTEUN	HOVING LEUKEMIA VIRUS (IAPANESE ISOLATE NI.V-1)	304.379				<u> </u>	j		. <u>.</u>
PENV BLVJ	ENV POLYMOIEIN	CAPAINE ARTHRITIS ENCEPTIALITIS YIRUS (STRAIN CORK)	137-196	615-730	231-365	20.15				:
PENY CAEVC	ENV POLITICAL PROPERTY OF	CAPRINE ARTIDUTIS ENCEPHALITIS VIAUS (STRAIN GA))	134.193	911.318	916.783	643.543				: i
NEW CAR	THE SALES SECTIONS	EQUINE INTECTIOUS ANEMIA VIRUS (CLONE P) 1-1)	19.76	416-525	339.393	100				<u>.</u>
PENV EIAVI	PAN TOLITANIEM PRODUCTION	EQUINE INTECTIOUS ANEMIA VIRUS (CLONE P3 3-3)	19.76	\$ P. 22	550.593	264-869				: - : -
PENV ELAVZ	ENV PALITACIEM PRECORDE	EQUINE INFECTIOUS ANEALIA VIRUS (CLONE P) 3-3)	39.74	19.53	550-593	638-716				: - -
PENV EIAVI	ENV POLITICIEM PRECORDOR	FOILME DIFFECTIOUS ANEAUA VIRUS (CLONE P) 2-3)	38.76	433-526	300.34	659-603				
PEN EIAVS	ENV PULTIFICIEN PRECUMEN	FOUNDE INFECTIOUS ANEAUS VIRUS (CLONE 1369)	19.76	436-525	550.50)	631.716			j	· :
PENV EIAW	ENV POLITICIA PRECURSOR	FORING INTECTIOUS ANTAINA VIRUS (CLONE CL22)	19.76	436.529	559.50)	658.716				:
PENV ELAVC	DAY POLYFOLDIN FALLURSON	FOURTE INTECTIOUS ANEMIA VIRUS (STRAIN WSUS)	39-76	436-535	159-501	656.71A				
PENV ELAW	ENV POL TYRU ELIN PACCURSON	FOURT DEFECTIOUS ANEALLA VIRUS (150LATE WYOMING)	39.76	436-525	159.303	658-716				: -
PENV ELAYY	ENV POLYTHOLE IN PRECUASOR	FEI INE EMPOCEMONS VIRUS ECE!	503-555	\$67.604						- - -
ושע עשו	DAY FOLLYFIOTEIN FRECURSON	FEI DE DAG DOOFFICIENCY VIRUS (ISOLATE PETALUMA)	610-690	318.756						! _
PENV FIVE	ENVELOPE FOL TPROTEIN PRECUREDA	SEI DAR MARINDOEFICIENCY VIRUS (ISOLATE SAN DIEGO)	177-109	113.754						-
PEN FINED	DAVE OF FOLITICIES PRECURSOR	SET THE TAMENODEFICIENCY VIRUS (ISOLATE TAIS)	171-00	629-609	714-735					<u>:</u> +
VENV TIVES	DIVELOPE POLITICAL PRECINCAL	FELINE LEUKENBA PROVIRUS (CLONE CFE-4)	497.549	\$61.598						-
אם אוואס	ENV POLITICO INITIA PACCOLOGIA	FELINE LEUKEMIA VIRUS (STRAIN A/GLASGOW-1)	478-530	\$42.578						ļ
PENV PLVAL	EAV PALITION PROTEIN PROTEINS	FELINE LEUKENIIA VIRUS (STRAIN LAMBDA-BI)	498-550	262.596						-
PEW ILVE	CAN THE STREET PROPERTY.	FELINE LEUKEMIA VIRUS (STRAIN SARMIA)	475-527	536.533						-
AN HAY	DAY BOX VALOTEDA	HODAN SPUMARETROVIRUS	7	134-205	<u>=</u>	263.683	86.80			
A LOVAL	EAN PAY VAROTE IN PRECIDENCE	FELDIE SARCOMA VIRUS (STRAIN GAADNER-AUNSTEIN)	498-530	262.58						! ‡
ADAK FRACE	DAV PAY VPROTED PRECURSOR	FELINE SARCOMA VIRUS (STRAIN GA)	476-530	\$43.576						1
TOTAL STATE	BAY FOR YPROTEDY PRECURSOR	FELINE SARCOMA VIRUS (STIVIN SM)	681.534	\$65.579						-
PERO SEVET	ENV POLYPROTEIN PRECURSOR	PTLINE SARCOMA VIRUS (STRAIN SWIDER-THEREN)	20 E			1				1
PEN OALY	ENV FOL YPROTEIN PRECURSOR	GIBBON APE LEUKENDA VIRUS	200.00	170-146		-				
PENY HTLIA	ENV POLYTROTEIN	HIDRAN T-CELL LEUKENIA VIRUS I VPE I (STRAIN ATR) (331-34)	741.30							
PENY HILIC	ENV POLYPROTEIN	HUMAN T-CELL LEUX EMIA VIRUS I TPE I (CAMBBEAN I SOCATE	100							
PEN HILIM	ENV POLYTROTEIN	MUMAN I CELL LEUREMIA VINOS I PECTUSOCALE TITAL	113.133							
PEN HILY	ENV POLYPROTEIN PRECURSOR	HEMAN BOATHODEFICIENCY VIRUS TYPE I (ARV2/5/2 ISOLATE		111.211	764-845		Ц			
PEN HVIAS	ENVELOPE FOL TPROTEIN OF 180 PACK OR AND	HEDLAN DANINODEFICIENCY VIRUS TYPE I (BHIG ISOLATE)		610-713	167-843					
PERV HVIBI	ENVELORE FOL TYROLEIN OF 180 PARCHOASON	HINZAN DARINODEFICIENCY VIRUS TYPE I (BHI ISOLATE)	500-519	£0; 70)	762-838					
PENV HVIBS	ENVELOPE POLYPROTEIN GFISO PARECURSON	٠.	331-365	% .io .io	801-609	763-831				
PENV HVIBN	ENVELOPE FOL TEXO I EIN OF 180 PARCONSON (CO.)	_	510-599	615.313	773-841					
PENV HVIBR	ENVELOPE POLYTRO I EIN GFIBD PACCURSON	KIDAAN DOMUNODEFICIENCY VIRUS TYPE I (CDC-45) ISOLATE)		310-606	626-724	779-855				
PENV HVICE	DAVELOPE FOLTTROIEIN OFIN PRECINCOL	HEMAN BANDNODEFICIENCY VIRUS TYPE 1 (ELI ISOLATE)		502-591	607-709	768-829				-
PEN HOLE	ENVELORE POLITING CONTROL OF THE CON	HUMAN INDAUNODEFICIENCY VIRUS TYPE I (HXB) ISOLATE)	205-594	\$10-313	767-836					1
PERV HVIR	ENVELOPE DE YPROTEIN GP160 PRECURSOR	HUMAN DOAUNODEFICIENCY VIRUS TYPE I (HXD) ISOLATE)	203-304 203-304	610-712	263-43		-			+
200	SAVET ARE POLYPROTEIN OF 140 PRECURSOR	HOMAN DOWNODEFICIENCY VIRUS TYPE I (IN) ISOLATE)	12	517-405	623-733	775-603				\downarrow
TENA BATT	SAME ONE BOX VPROTEIN CPIES PRECURSOR	HUMAN DOMUNDOEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	129-363	197-586	403-704	759-835				

			ĺ					1	Į	
	TATINOTIS		Ţ	145	505-115	Ī	110-911	911.119	172-648	
PCCENE	PROTEIN	Ē	Ţ	T	Γ	170-825				
TILK DATE	ENVELOPE POLYPROTEIN GP150 PRECURSOR	_	T	Τ	T					
PERV MVINE	ENVELOPE POLYPROTECN GPI60 PRECURSOR	٦	1	T	T	734.841				
PERV RVIDA	CONF. OPE POLYPROTEON GP 140 PRECURSOR	٦	1	T	T					
PENV HVING	PENYEL OPE POLYPROTEIN GPISS PRECURSOR	징	1	T		343.034				
PENV HVIMO	ENVELOPE POLYPROTEIN GPI60 PRECURSOR		T	Т	21.00	766-143				
	ELACEL COPE POLYPROTEIN CIPIED PRECURSOR		٦	T						
PENV INTRO	ENAST OF POLYPROTEIN GPI66 PRECURSOR	,	٦	T	101.00	174.00				
PERV HVIOI	COST ONE BOX VPROTEIN GP160 PRECURSOR	(3)	344.378	٦	77.410					
PER HVIPV	ENVELORE OF VARIOTEIN CPIEG PRECURSOR	Г	496-585	601-109	158-830					
PEN HVIRH	ENVELORE POLITICAL COLOR PRECIDESOR		111.166	494-590	607.708	763-837				L
PENV HVISI	ENVELOPE POLITICAL COLOR COLOR	Т	Γ	498-864	216-119	747-134				
PEN HVIS	ENELOPE POLYTROI EIN OF THE STATE	٦,	Ī	Γ	611-312	767.636				
PENV HVISC	ENVELOPE POLYPROTEIN GF 180 FACULTURE	2	T	Γ	603-303	758-827				
PENY HVIWI	ENVELOPE POLYPROTEIN GFIRM PACCONSON	MANAN DOLUMODEFICIENCY VIRUS TYPE I (WAUT ISOLATE)	T	Ţ	610-709	764-831				
ENIVE WIND	ENVELOPE POLYPROTEIN GPIAO PRECURSOR	₹1	T	T						
27170	ENVELOPE POLYPROTEIN GP140 PRECURSOR	TOWNS TO STATE OF THE PERSON OF THE 1 (ZAINE 3 ISOLATE)	1	T	111. 947	764.840				
	ENVELOPE FOR YPROTEIN OPISO PRECURSOR	TE)	٦	I			174.611			
	ENVELOPE POLYPROTEIN GPI60 PRECURSOR			T	614-110					
ENV KVICE	CANAL CAR BOY VAROTEIN GP160 PRECURSOR	9	\$22-594		675-7112					
PENV HVIZE	THE CONTROL OF THE CURSOR	Γ	447-481		617-610					
PEN HVIZH	ENVELOR COLOR COLOR PRECURSOR	Τ	\$12.597	619.109						 -
FEAV HV28E	ENVELOPE POLYTROLEGA COLOR SOFT IN COR	Ţ	T	169-609						1
PENY HYJCA	ENVELOPE POLYTRUIEIN GFINA FACCINGO	T		(4)	609-609					1
ENV HYZDI	ENVELOPE POLYPROTEIN GF 180 PACE UND	[]		99			-			1
IDAY HYZGI	ENVELOPE POLYPROTEIN OF INCHES	LAPATA BARANDOEFICIENCY VIRUS TYPE 3 (ISOLATE MIN-2)								
ENV HYZNZ	ENVELOPE POLYTROTEIN GP160 PALLURSON	UNDALAN MARINDDEFICIENCY VIRUS TYPE 2 (ISOLATE ROD)		3	419.707	-	L			
ENV INVEO	ENVELOPE POLYPROTEIN GP160 PRECURSOR	ARAIAN MARINDEFICIENCY VIRUS TYPE 2 (ISOLATE STALIC)		203-506				L		
ENV HOTES	ENVELOPE POLYPROTEIN CP160 PILECURSOIL	STATES THE SECTION OF THE STATE SECTION		30.	.00	-	-	_		
ESTATE AND IN	ENVELOPE POLYPROTEIN CP160 PRECURSOR	HAVIN MANINODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	442-476	303-390		+				_
10000	ENVELOPE POLYPROTEIN GP140 PRECURSOR	TOPICAL PROPERTY AND	167-411	463-327		1	ļ Į	_		
ENV NV.	SAV BOY YOU DE TO PRECUESOR	MOUSE INTENDED STATES AND A TOTAL OF THE STATES	403-455	\$71-60\$		1	1			L
ENA LIMAGE	STATE OF VEROTEIN PRECURSOR	SHEEP PULMURANT ADELYCHISTOSIS ETIMERALA VIRUS	473-525	117.571		-	1	1	-	_
PENV JSKV		MINK CELL FOCUS-FORMING FICHER EI RESAILA VIRUS (150LA		538-572		-	1			-
ENV MOT	ENV POLITICAL PROTECTION COAT POLYPROTE	THINK CETT FOCUS-FORMING MUNING LEGISLE		167-601						-
ENV MOTE	ENV POLITICISM STATEMENT	AK V MUMUR LEUKEMIA VIRUS		562.596						 -
PENV MALVAV	ENV POLYTROIEN FACTORIOS	CAS-BR-E MURINE LEUKENIIA VIRUS	777 92.	174.610						 -
PENY MALVOR	ENV POLYPROTEIN PRELUASOR	FAIEND MUNDE LEUKENIA VIRUS (ISOLATE ST)	200	174.410					1	+
PERV MAYES	ENV POLYPROTEIN PRECURSOR	FRIEND MURINE LEUKEMIA VIRUS (1SOLATE FB39)	2000	917.7		-	L			1
PENV MANTE	ENV FOR YPROTEIN PRECURSOR	PATEND MUTUNE LEUKENITA VITUS (ISOLATE PVC-311)	38.30	200.00			L	_		; -
PENV LA VIP	ENV POLYPROTEIN PRECUISOR	LANGE VARINE LEUKEANA VIRUS	364.33	20.00		-		L		_
PORV NO VIRO	ENV POLYPROTEIN PRECURSOR	CHARLES AND THE LEUKENIA VIRUS	26-05	104-136			-			_
NO NO VICE	ENV POLYPROTEIN	AND PARENTAL FURENIA VIRUS	\$0.534	200		-			-	_
98 87 889	ENV POLYPROTEIN PRECURSOR	TOTAL TOTAL STRENGY VIEWS	407-549	261.393			-	-	ļ -	
	SAV POLYPROTEIN PRECURSOR	MANA TICK FIRE TO VIRUS (STRAIN KAPLAN)	497.540	561-595				-	_	<u> </u>
	DAY POL YPROTEDY PRECURSOR	MADIATION NUMBER CONTRACTOR (CTRAIN BR6)	417-534	936-612			-	-		i 1-
A A A A A A A A A A A A A A A A A A A	ENV POLYMOTER	MOUSE MAKINIARY TURIOR TIROS (STRAIN GR.)	477-530	156-612			-	+	1	i-
PENV MORTVE	T	MOUSE MANNIART TUNIOR TITLE	408.474	L		4	+	-	-	: - !
PEN POUT	T	SOUTH MASON-PRIZER VIRUS	5	101.161			1	+	<u> </u> -	- -
אניי אפויל	ENV POLITICAL DE LA COMPANIA DEL COMPANIA DEL COMPANIA DE LA COMPA	FBI MURINE OSTEOSARCONIA VINUS	25	113.233	664.746	780-016				.: i
ENV MSVFB	ENV POLICE DE COMPANION DE COMP	OVINE LENTIVIRUS (STRAIN SA-ONINV)	444.528	\$40.574					1	
PEN ORONS	ENV POLYMOIEN PRECINCOL	RAUSCHER MINK CELL FOCUS-INDUCING VIRUS	147.176		-					: ĭ
ADM MOA	DIV POLITICOLE IN THE COMPANY	RAUSCHER SPLEEN FOCUS-FORNING VIRUS		101-100	154.205	131.353	363-651	(V) 1-64)	-	i-
PEN MSTEV	ENVIOLENTIAL SECTION AND AND AND AND AND AND AND AND AND AN	SOMAN FOAMY VIRUS (TYPE !)		50.30	319-357	\$60-706	161.001			- -
PEN STVI	EN POLYFIOTELIA	SDAILAN FOLMY VIRUS (TYPE 1 / STRAFN LK1)		1	(4)(49)	-			-	-
15.00	PAN POLYMONTH	CONTRACTOR (ACMINE ACMINE)	704.							
TALE AND		TOWARD NAMED OF PARTY OF THE PA								

		All Viruses (no bacteriophages)	П						П	100
PCGENE.	PROTEIN		Ţ	7	74100	4		Ţ		į
SENV SIVAGE	PAVEL OPE POLYPROTEIN GP160 PRECURSOR	AN INDAMMODEFICIENCY VIRUS (AGM) ISOLATE)	T	4		737.57	079.600		-	į
SENV CIVAL	FAVEL COR POLYPROTEIN GP160 PRECURSOR	CLONE GR	1	336-370		200			+	:
PENV CIVAT	ENVELOPE POLYPROTEIN GP160 PRECURSOR	STATION IN THE MODE FICIENCY VIRUS (TYO-1 ISOLATE)		70.65		101	601.017		<u> </u> 	
PENV SIVEZ	ENVELOPE POLYPROTEIN GP140 PRECURSOR	CHINGPANZEE INMUNODEFICIENCY VIRUS (SIV(CPZ))		Carter	316:38				İ	
PENV SIVOR	ENVELOPE POLYPROTEIN GP140 PRECURSOR	SINITAN INDIUNODEFICIENCY VIRUS (ISOLATE GRI)	300-03	9		110	200.00		! - 	:
PENV SIVAL	ENVELOPE POLYPROTEIN GP140 PRECURSOR	SIMIAN INDIONOCEFICIENCY VIRUS (AMILA)-13 ISOLATE)	16.5	000				<u> </u> 	<u>:</u> –	:
PENV STAND	ENVELOPE POLYPROTEIN GRISS PRECURSOR	STATAN TANGNODEFICIENCY VIRUS (PARTS) ISOLATE)						-	i i	
PENV SIMAR	ENVELOPE POLYPROTEIN GP140 PRECURSOR	SIMIAN INDRINOPEFICIENTY VIRUS (KAW ISOLATE)						!	 !	
PENV SIMA	ENVELOPE POLYPROTEIN OP140 PRECURSOR	SIMIAM INDRINODICFICIENCY VIRUS (K71 ISOLATE)	200.000		21.5	113.811	<u> </u>		 !	
PENV SIVSA	ENVELOPE POLYPROTEIN CPIES PRECURSOR	SPANN BOAMODEFICIENCY VIRUS (F1)6/5/APP ISOLATE)	200				-	<u> </u> - 	:	
PEN SINSP	ENVELOPE POLYPROTEIN GPISS PRECURSOR	SDAAN DORNODEFICIENCY VIRUS (PRINCLI) ISOLATE)	110.01	270-176			_	 - 	:	
PEN BOW	ENV POLYPROTEIN PRECURSOR	SOUTHREL MONKEY RETROVIRUS (SMRV-H)	410-400				+		: ·	
MAN CRVI	ENV POLYPROTED ^N	SINIAN RETROVIRUS SAV-I	409.473				-		i	
A 20 A 40 A	PAY POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 1514)	79-12	184.22	637.740	773-80-	-		-	
IV IV VICE	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN ISIA/CLONE LVI-IKSI)	7	2	97.178	100.00	-		i	
CA 10. 20.	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN 1914/CLONE LVI-IKSZ)	27-72	<u> </u>	10.72			1	 i	
PSERA AVIER	EABA ONCOCENE PROTEIN	AVIAN ERYTIMOBLASTOSIS VIRUS (STRAIN ES4)	09-140				1	<u> </u>		
PETEL FOWDI	EABLY TRANSCRIPTION FACTOR TO KE SUBUNIT	FOWELOOK VIRUS (STRAIN FP.1)	7.7.7	25.50				<u> </u>	- 	
PETEL CEVEA	SABLY TRANSCRIPTION FACTOR TO KD SUBURIT	SHOPE FIBROSIA VIRUS (STRAIN KASZA)	17.71	267. 267.	3:0:36			-	<u>.</u>	:
	EAST V THANKERIPTION FACTOR 70 KD SUBUNIT	VACCIMIA MRUS (STRAIN COPENIAGEN)	13-71	101.34				<u> </u>	: -	
2000	FARE Y TRANSCRIPTION FACTOR TO KD SUBUNIT	VACCINIA VIRUS (STRAIN W.R.)	13.71	107-34					: 	:
מינוני מינוני	FARLY TRANSCRIPTION FACTOR 82 KD SUBUNIT	VACCINIA VIRUS (STRAIN COPENHAGEN)	\$2.03	72.7G					+	;
מבוני הערה	RABLY TRANSCRIPTION FACTOR 82 KD SUBUNIT	VARIOLA VIRUS	\$1.07	174.208			-			!
4/0/07/	AT R AT DAR BY COMBICT FASE	HUMAN CYTOREGALOVIRUS (STRAIN AD169)	10-114				1		i	: :
TANKS PORTER	AT WAT THE EXPREISH FASE	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP)	19:141				+		<u>:</u> 	:
STATE OF STA	ALMAN THE EXONORICE FASE	PSEUDORABLES VIRUS (STRAIN NIA-1)	13.130					1	:	:
SALA MANAGE	AT KAI INE EXONACT PASE	VANCELLA-ZOSTER VIRUS (STRAIN DURIAS)	109-157	142.383					<u> </u>	. ::
PENON VEVE	AT A RO STREET PROTEON	HUNKAN ADEMOVIRUS TYPE 40	162-237			1	1		-	
PERS ADEAL	ALAKO FIRER PROTEIN	HUMAN ADENOVIAUS TYPE 41	112-223				1]	+	:
1030V	SINCE PROTEIN	HURAN ADENOVIRUS TYPE 3	156-194				1	1	+	!::
PERP ADEOU	FIRES PROTEIN	HIDMAN ADEMOVIRUS TYPE 7	176-210					-	Ť	; ;
PERP ADEAD	FIBER PROTEIN	HENGAN ADENOVIRUS TYPE 40	30.15				+		İ	-
PETRO ADEA!	FINER PROTEDN	HUMAN ADENOVIRUS TYPE 41	320-366						+	i
PETRO ADERI	FINER PROTEIN	BOVINE ADENOVIAUS TYPE 1	101-215	929-536			1		i	:
PEOSX MSVFB	V-FOS-FOX TRANSFORMING PROTEIN	FBR ARMINE OSTEOSARCOMA VIRUS	131-169					1	1	!
PEOS AVDOC	PSS-V-FOS TRANSFORKING PROTEIN	AVIAN RETROVIRUS NX24	28-120				 	<u> </u> -	-	1
PTOS MSVTB	PSS-V-FOS TRANSFORMING PROTEIN	FBJ MUNINE OSTEOSARCONIA VIRUS	3				+	-		
POAGC AVISC	PATIGAGCER() PROTEIN	AVIAN SARCOMA VIRUS (STRAIN CT10)	27.10			1	 	<u> </u>	<u>!</u> -	:::
POAG AVEVI	DAG POLYPROTEIN	AVIAN ENDOGENOUS VIRUS EV.1	K.				1			:
POAG AVEV2	DAG POLYPROTEIN	AVIAN ENDOGENOUS ROUS-ASSOCIATED VIRUS-9	6.0					-	<u>:</u> 	:
POAG AVDAC	GAG POLYPROTEIN	AVIAN MYELOCYTONIATUSIS VIKUS MCZY	20.10						Ť	i
PGAQ AVD-CD	GAG POLYPROTEIN	AVIAN MTELOCT IONIA 10313 VIRUS TEI	2				+		<u> </u>	
POAG AVISU	CORE PROTEIN PIG	AVIAN SAUCONIA VIRUS (STRAIM URZ)	4				+		j	Ī
POAO AVISY	GAG POLYPROTEIN	AVIAN SARCONIA VIRUS (STRAIM Y 7.1)					1		-	Ì
POAG BIVOS	GAG POLYPROTEIN (P33)	BOVING DATUNODEFICIENCY VIXUS (150LATE 100)				\downarrow	-		\dagger	ĺ
POAG ELAVY	QAG POLYPROTEDN	EQUINE INFECTIOUS ANEMIA VIAUS (CLONE CLAS)					+		l	Ī
PGAG FIVE	GAG POLYPROTEIN	FELINE DAMINODEFICENCY VIRUS (ISOLATE PETALUAIA)	26.10			1			+	
POAG FIVSD	GAO POLYPROTEIN	FELTINE DIGHTUNODEFICIENCY VIRUS (ISOLATE SAN DIELO)	76-110				-		+	
POAD FIVE	GAG POLYPROTEIN	FELINE DOWNODEFICIENCY VIRUS (ISOLATE TAU)	26-110						$\frac{1}{1}$	
POAG_FLV	DAG POLYPROTEIN	FELINE LEUKEANA VIRUS	100	367	97.00	103.601			\dagger	
POAG FOALTV	GAG POLYPROTEIN	MUMAN SPURIABLE TROVINGS	1				1	-	H	İ
POAD PSVND	OAG POLYPROTEIN	FELINE SARCOMA VIRUS (3) FRAIM PICUUMUUM)								

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		0 10 10 10 10 10 10 10 10 10 10 10 10 10		72-326 71-326 71-326 91-336	 		+	+		
		10 0 10 10 10 10 10 10 10 10 10 10 10 10		71-326 71-326 71-326 92-336					-	
	PROTEIN FROTEIN	TO TO THE PARTY OF		71.326 71.336 92.336	1	-				•
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	PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	130 (E) 130 (TE) 130 (TE)		92.336	İ				-: 	
	PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN			25.370	1				- i	i
	PROTEIN TROTEIN	1150L 1150L 1150L 1150L 1150L			†	+				1
	PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	2 S		707-326	1	+	-			
	TROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	E) 150L NATE)		357:326	1	+	-		 	
	PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	हि जि		292-326						i i
	PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	N S S				+			Ì	
	TADIEN TROTEN TROTEN TROTEN TROTEN TROTEN	NAN ES NA		205.320		-	1	-	İ	i
	PROTEIN FROTEIN PROTEIN PROTEIN PROTEIN PROTEIN	O LE SAN E		202.326				1	1	1
	TROTEN TROTEN TROTEN TROTEN TROTEN TROTEN TROTEN	S X	Ш	210.323				1	1	
	TROTEIN TROTEIN TROTEIN TROTEIN TROTEIN	Q N	П	303-126				1	Ì	1
	TROTEN TROTEN TROTEN TROTEN	N N N	T	10.10					Ì	:
	PROTEIN PROTEIN PROTEIN	G Z		7,110					Ì	i
	YPROTEIN YPROTEIN YPROTEIN	HUMAN BATUNODE FICIENCY VIRUS TYPE I (STRAIN UGANDAN ET	Ţ	-					1	İ
	YPROTEIN	A CONTRACTOR OF THE CONTRACTOR	12.13	+						
	YPROTEIN	UNDALAN MARINODEFICIENCY VIRUS TYPE I (WAUZISOCATE)	207-126							١
		3	2012							1
	YPROTEIN	TOTAL TANDENDEFICIENCY VIRUS TYPE 2 (ISOCATE SOLISY) 2	Ţ	+						1
\prod	YPAOTEIN			130.75		-				
\prod_{\cdot}	RETROVIAUS RELATED GAG POLYPROTEIN		67.103							
	RETROVINUS RELATED GAG POLYPROTEIN		3	77.17						
	RETROVINUS AELATED GAG POLYPROTEIN	INUS	470-504							ļ
	GAO POLYPROTEIN	IR6)	<u>= = = = = = = = = = = = = = = = = = = </u>	20-160			-			i
5	GAG POLYPROTEIN		13-131	B						1
T	GAG POLYPROTEIN		117-360							١
Τ	GAO POLYPROTERI		13.04							į
T	CALO POLYPROTEIN	(CV-L-A)	102-134	1				-		
T	MANOR COAT PROTEIN		131-133	٦	283-434					
	DAD POLYPROTEIN	(CEACHLE)	113.407	415-572	201-012		-			
T	AAD POLYPROTEIN	(SOLATE)	107-136			†			İ	:
	DAD FOL YPROTEIN		106-340							
T	DAD BOLYPROTEIN	CLONE GR	112-217	473-507			-			:
T	OAG POLYPROTED	_	303-336				+			_
T	OAD POR YPROTEDY		301-338							!
CAC SIVA	GAG POLYPROTEIN		163-204	113-267	20.2				İ	
T	GAG POLYPROTEIN		167-161							
T	GAG POLYPROTEIN	TYPE 1 / STRAIN 17)	17.706	169-820						
Ī	PROBABLE WELICASE	(2)	461-502	T						
	PLOBABLE HELICASE		2 2	1		†				
	PROBABLE HELICASE	+ DUMAS)	445.517	201						
	PROBABLE HELICASE		208-242	1						
	HEMACOLUTINON-ESTERASE PRECURSOR	36)	200.742	1						·
>	HEMAGGLUTIMIN-ESTERASE PRECUESOR	BOYANE CORONA VIRUS (STRAIN MEBUS)	20.70	1						
Τ	HEMACOLUTIVINI-ESTERASE PRECUISOR	BOUTH CORDINAVARIES (STRAIN OUTBEC).	ž Ž	1						_
T	HEMAGGLUTININ-ESTERASE PRECURSOR	INTALA CORDINA VIRUS (STRAIN OC43)	204-22	1						Ц
l	DOLUTDIN ESTERASE PRECURSOR	PART I IFAZA A YIRUS (STRAIN A/AICHIZAGI)	207	1			-			
1	HENAGGLUTOW PRECURSOR	THE TENTA A VILLE (STRAIN ABANGKOKUM)	34.45	1			-			
L	HEMADGLUTTION PRECURSOR	INCIDENT A VILLE (STRAIN ABUDGERICARMOKKAIDOVIAT) 178-454	2							ĺ

-				ABEA 2 1AF	ARLAS	AND AND	10.10		ĺ	
1000	PROTEIN	I		Γ	Γ					:
MENA MENA	HEMAGGLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN ACHICAETACALANOMAS)	101.102	335-475	104-528					:
MIENA IACKO	HEMAGGE UTININ PRECURSOR		T	11.513		- -				:
MENA IACKE	NEMACCE UTININ PRECURSOR		Τ	487.312						
MENA IACKO	HEMAGGLUTOWN PRECURSOR		Τ	\$64.540		-				ļ
HEMA IACKS	HENACCLUTININ PRECURSOR	INFLUENZA A VIRUS (STRAIM ACHICA EMACONICALIA)	Ι	337-469						
HEMA IACKY	HENCAGGLUTINGN PRECURSOR		Γ	-	-					
HEMA IADAI	HEMACOLUTION PRECURSOR	INFLUENZA A VIRUS (3 INCHIA ANDICEXIAL BENTAMO76)	Γ	405-547				İ		
HENLA IADAS	HEMAGGLUTININ PRECURSOR	INTUENCA A VINUE GENERAL ACIDICAL BERTACHOS	180-453					1		
HENCE INDA!	HEMAGOLUTHON PRECURSOR		179.478	306-348						
HEMA MOA	HEMADGLUTBIN PRECURSOR	18/56)	Г				1	1		
HEMA INDCZ	HEMAGGLUTININ PRECURSOR	Π		111-111		1	1	1		
PHEMA IADE!	HEMAGGLUTININ PRECURSOR	THE LIEUZA A VIRIS (STRAIN ADUCKAIOKKAIDOSAI)	264.440							
PHEMA LADHI	HENLAGGLUTDEN PRECURSOR	INTEREST A VISIS (STRAIN ADDICKARDONA)	364-440							
MEMA INDRO	HENAGGUTININ PRECURSOR	THE LIENZA A VIRUS (STRAIN ADUCK/HOKKAIDO/13/10)	364-440			+	1			
HEMA IADHU	HEMACOLULININ PRECUASOR	REFLIENCE A VIRUS (STRAIN ADUCK/HOKKAIDO/1/82)	364-440		1			†		
HEMA IADHA	HEMAGGLUING PRECURSOR	INSTITEMENT A VIRUS (STRAIN ADUCKARDKKAIDOZIAZ)	364.440						1	
HEMA IADRO	HEMACOLUMN PRECIENCE		164-440			†	1			
HEMA IAUM	TEMPOREDINAL PROPERTY OF THE COR	,	164.440			†				
HENG AUR	ACAMOON INTO PRECIDENT	INFLUENZA A VIRUS (STRAIN ANDICKIREL ANDVI 13/13)	179-471	306-331		\dagger	T			
MENA IAUK	TO BE TOWN TOWN THE TOWN	INFLUENZA A VIRUS (STRAIN A/DUCK/A/EA/PHIS/346/16	21-55			1				
HENCY INDMI	HERACOLO LINA PRECIMENT	INFLUENZA A VIRUS (STRAIN A/DUCK/A/EMPHIS/938/74)	380-456	-						L
MEMA IADRO	TENANCIA INTENANCIA DE CONTRACTOR	INTLUENZA A VIRUS (STRAIN A/DUCK/NEW YORK/11/78)	21-55			†				
TENA MONT	HENNAGE ITTOWN PRECIBION	INFLUENZA A VIRUS (STRAIN A/DUCK/NEW ZEALAND/31/76)	178-454		+	1				
PEMA MURE	LIEVACCE ITTEM PRECINSOR	INFLUENZA A VIAUS (STRAIN A/DUCK/UKRAINE/1/60)	<u></u>		1	1		1		
THE MAY LANGE	VENANCE LITTING PRECUESOR	INTLUENZA A VIRUS (STRAIN A/DUCK/UKRAINE/1/83)	180-456		+					
THE PARTY OF THE P	MEMACIA UTDOM PRECURSOR	INFLUENZA A VIRUS (STRAIN A/ENGLANDA) 21/77	380-456		+					
THE PARTY	HEMAGOR UTDAIN PRECURSOR	INFLUENZA A VIXUS (STRAIN AFOWL PLAGUE VIXUS/ROSTOCK) 177-477	111-477	1	+	\dagger				
HEMA LAGRE	HEMAOCK UTINON PRECURSOR	INFLUENZA A VIRUS (STRAM AGREY TEAUAUSTRALIAZAM)								
PIENA IAGUS	HEMAGGLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN ANGLEMAN TLANDON !!)		†		 				
PIEMA IAGUA	NEMANOGLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN AGULL/ASTRAKHANGIITA)	207 04.1	†	+	\dagger				
PHENA LAHAL	HEMAOGLUTINGN PRECURSOR	INTLUENZA A VIRUS (STRAIN AEQUINEALUIZAS/1)	9	360-414	\$03-537					
PHENA INKO	HEMAOGLUTININ PRECURSOR	INTLUENCA A VIAUS (STANIN ACCUMENTANDES AND STANING (STANING S	91-21	Г	503-537					
THEMA INHC?	HEMADOLUTININ PRECURSOR	INTLUENTA A VIBILE (CTBAIN AFOLINGE)	160-484	503-537	-					
MEMA WHICD	HEMAGGLUTINGN PRECURSOR	INTLIENZA A VIRUS (STRAIN ACQUINE/DETROIT/1/44)	760.414	501-537						
PIEMA IANDE	HEMACACOLINING FACE CASON	INTLUENCA A VIRUS (STRAIN AEQUINE/FONTAINEBLEAU/14)	179.455			1				
MEMA IANGO	HEMACOLITHMA PRECINSOR	INFLUENZA A VIRUS (STRAIN ACQUINEMENTUCKYOM)	139-435			+				
PHENA IAMET	HEMAGGLUTIND PRECURSOR	INFLUENZA A VIRUS (STRAIN AEQUINERENTUCKY/1/87)	34455	Ī		T	1			
PHEMA IAIG.E	HEMAGGLUTION PLECURSOR	DYFLIENZA A VIRUS (STRAIN AEQUINEA EXINGTON/M6)	112.166	1000	10.10	†	T			
PHEMA WHEO	HEMAGGLUTDAN PRECURSOR	DIFLUENZA A VIRUS (STRAIN ARGUINEA CHODONI (1677))	112-140	Т		1				
PHEMA IMPO	HEMAGGLUTININ PRECURSOR	INFLUENCA A VIAUS (STRAIN ARQUINGALIAND 193)	130.455							
PHEMA IMPON	HEMAGGLUTERN PRECURSOR	INTELLENZA A VIRUS (STRAIN ACQUINEMENTEN ACCURATE 1779)	112.146	160-414	503-537					
PHEMA IANDON	HEMAGGLUTDAN PRECURSOR	INCLUENCE A VIACO (STRAIN ACCORDICE MICCALLINATION OF THE PROPERTY OF THE PROP	112.146	Τ	503-537					
PHEMA WHOR	HEMACOLUTININ PRECUISOR	INCLUENZA A VINIS (STRAIN AFOLINEMONAMATO)	378-455	Τ						
PHENA INFRO	HEMAGGLUTIMIN PRECURSOR	INSTITUTE A VIBILS (STRAIN AEQUINE/SANTIAGO/(A))	179-455							j
PIEDA LAHSA	HEMAGGLUTININ PRECURSOR	CALLENZA A VIETO (STEATH AFOUND SAO PAULO (76)	11.146	Γ	501-517					 -
PHENA MISP	HEMAGGLUTININ PILECUROR	RELUENZA A VIRUS (STRATA AEQUINE/SWITZERLAND/137/2)	113.146	П	501-117					j
PHEDICA TAHSW	HEMAGGLUTIMIN PRECUASOR	INFLIEDZA A VIRUS (STRAIN AEQUINE/TEMESSEE/5/16)	379.455			1				-
PHENA WHILE	PERADGLUINIM PRECURSOR	DATUENZA A VIRUS (STRAIN ARQUINETOKYOTI)	179-455			-				
PER WITO	HENCE OF THE COMMON	THE PERSON NAMED IN COLUMN NAM	1100 400							

10000			Ī	ĺ		7 4 5 5 1				
		All Varesse (no betteriophogus)	AREAL	TVIEV	7887	4	797		1	
1	ALLMOITS	VIRUS	7	25.50						
TANK	PROTEIN THAM PRECINGOR			26-34						
MEAN MAN	PENALOUINI PERCHASA	INTLUENZA A VIRUS (STRAIN MARIE VILLA	376-476	\$06.548						
HENLY LAKES	HEMACOLULININ FRECHECIE		337.453				1			
HEN INTEN	HEMACOLUL IMIN THE CONTROL	W114 MOS 1/821	382-458							
PHENCE INMAN	HEMAGOLUI IMM THE CORD		110.456							
PHEMA INMAR	HEMAGGLUTININ PRECURSOR	INTLUENZA A VIRUS (STRAIN AMIAL LAUDINEW TORING	180.456							
PHEMA IAMAO	HEMACGLUTININ PRECURSOR	PALLENZA A VIRUS (STRADY ARIENDILISMA)	777							
HEMA IAME!	HEMAGGI, UTTIMIN PRECURSOR	THE INTERNAL A VIRUS (STRAIN AMENINIS/102/72)	2000			L				i
1000	HEMAGGLUTIMIN PRECURSOR	INTEREST A CHAIR (STRAIN ANEAINISTEND)	264.440						j	
PHENA INCH	HEMACCLUTININ PRECURSOR	INCLUENCE A VIEW (STRAIN AAIINK/SWEDENIA)	108-143	13.473						
PHENA LAME	SECURSOR	DOLUENZA A VIRUS (STRAIL)	180-456							_
PHENA LAMIN	TOTAL STREET BOOK IN THE STREET	INGLUENZA A VIRUS (STIANIM ANTINOSSI)	378.477	696-534						<u>.</u>
PHEMA LANTS	HEMACGLUININ TACO	INTLUENZA A VIRUS (STRAIN APILO) WILLENZA A	176-478	SOE-348						
PHEEMA_LAPPIL	HEMAGGLUTININ PRECUPACIO	INFLUENZA A VIRUS (STRAIN APUERTO RICORDA)								!
PHEMA IAPUE	IEMAGGIUTININ PRECUASON	INTELLENZA A VIRUS (STRAIN ARUDDY TURNSTUNG PERS	-							:
PHEMA IARUD	HEMACGLUTING PRECURSOR	THE LENTA A VIRUS (STRAIN ASEALAIASSACHUSETTSI) AND	-							<u>:</u>
PATELIA TASEZ	HEMA OCLUTIVAN PRECURSOR	AND THE LITE A VIBIG (STRAIN ASHEARWATER AUSTRALIANS)	7	200			_			:
170.00	HEMAGGLUTTIMIN PRECURSOR	INTUCACTORIS (CTBAIN ASTARL INCAMICTORIANS) SATS)	113-146	377.40						
PIERA IASTA	NEWACCE UTININ PRECURSOR	INTLUENZA A VINCE (STELLAND ATTIME EYARELAND) 1941)	379-471	:06.551		-	-			
PHEMA IASIA	VENA COLUMNIA PRECUESOR	INTELENZA A VIAUS ISTRACTION EVALUATES SOT AND AND	378-454				1			_
PIESAN IATRA	STATE OF STREET PARTIES OF	DOLUENZA A VIRUS (STANIS ALICENZA ALICATIONE)	192-470	504.548				1		!
PHENA IATEM	TOTAL SECTION	DOLUENZA A VIRUS (STIMIN ALICANE CONTRACTOR	178-454	64).540						: -
HEMA IATRO	HEMACALUININ PRECOME	INFLUENZA A VIRUS (STRAIN ACTURKE TOOLI AKICATION	19.01	174.474			j		-	· -
MEMA LATE	HEMAGGLUTBRIN PRECORSON	DAYLUENZA A VIRUS (STRAIN A/TURKE YOREGONI)		207.519			-			·
PHENA LATER	HEMAOGLUTININ PRECURSOR	DOLUENZA A VIRUS (STRAIN A/TURKEY/W:SCOMSINI/00)								: -
PARTA LATKW	HENAGGLUTORIN PILECURSOR	THE TENZA A VIRUS (STRAIN AMERINAUSTRALIAGIOCAS)	2							!
SIGNA IATRA	MENAGOLUTIYAN PRECURSOR	THE SECULA A VARIES (STRAIN ANDORNISORIES)	367.456				<u> </u>			:
100	HEMAGGLUTININ PRECURSOR	TANALOGY A MARIE CETAIN AUSSEMON?	176-478	506-348		1	 -			
1	HEMAGGLUTTHEN PRECUISOR	INTLUENCE A STATE OF THE ANICTORANDS)	381-457				 -			
	HEMAGGE UTTIVITY PRECURSOR	INTEREST STATE STRAIN ANNI SON SAILTION	115-417	\$09-547			1	-		_
5	MENACOL UTININ PLECURSOR	INTLUENCA A VINCE (STEAM AND AND AND AND AND AND AND AND AND AND	380-456			+		-		
1	THE CONTRACT OF THE CURSOR	DATUE A VIROS (SINCE)	364.440				i		_	<u></u>
MENT MACO	THE THE PRECURSOR	INTLUENZA A VIRUS (STRAIN WATHINGTON OF DINGLISER)	364-440	ļ_		-			-	:
MENA INZIN	TO SECTION OF THE PARTY AND TH	INTLUENZA A VIRUS (STRAIN ASWINGLION CONTRACTOR	139.478	\$5.98	L					: -
PHEDA'A LAZHO	MENTACOLULININ PACCOSCO	DELUENZA A VIRUS (STRATA ASWINDINDAMPA) (2000)	110.67	\$06-543					1	:
PIEDAD IAZIN	NEWACCLUTININ PRECUESOR	INTLUENZA A VIRUS (STRAIN ASWINEMEN IERSETTITIO)	444							i
PHEDAN IAZNI	NEWAGGLUI INDIN PRECURSOR	INTLUENZA A VIRUS (STRAIN ASWINEAURKELJIM)		1		-				!
PHENCA LAZUK	HEMAGGLUTININ PRECURSOR	DATE LIENZA B VIRUS (STRAIN BINEITING IA)		+		-				-
PIEDA PABE	MENAGOL UTINAN PRECURSOR	INFLUENZA B VIRUS (STRAIN INDONN443)	378-403		-		_			1
PHEDAA BABBO		INFLUENZA B VIRUS (STRATIN D/ENGLAND/32/82)		-		-				1
PIEDA INEDA	Г	INTLIENZA B VIRUS (STRAIN BHONG KONGANS)		-						1
PHENA DIBHE	Ī	INFI LIFINZA B VIRUS (STRAIN BAEE/40)	7	1	-	-				1
PLEDA POLE	Γ	INCT LENZA B VIRUS (STRAIN BALARYLAND'S9)	771-407	-						\ -
PAGA DOM	Γ	THE LIENZA B VIRUS (STRAIN BACENDHIS MACA)	101	+	1		-			4
PHEMA DIBING	Ī	DATI (ENZA B VIRUS (STRAIN BOREGON/STO)	116.471	$\frac{1}{4}$	1	+				4
PHENA DODOR	F	INCH I FENZA B VIRUS (STRAIN BASINGAPORE/12/79)	780-01		1	-	 -	L		-
MENA DOS	Γ	DATE LIENZA B VIRUS (STRAIN BASSIVICAN)	379-464		\downarrow	1	 -			-
STEET DOLLS		CAST (SELVE & UTBIIS (STRAIN BANCTORIA)	311-460		1	-	 -	-		_
NOW YOUR	T	ANTI GENT A B VIRGIS (STRAIN BAYICTON ANAT)	368-473	1	\downarrow	1				
100 A 100 A	T	INTOCKEN TO CHEATH CICALIFORNIATE	483.571		-					
1	T	INTLUENCA L. VINOS (STRAIN CAFACLANDASVE)	471-559			1		\ +		
1	T	INTLUENCA C VINUS (STRAIN CIGREAT LAKES/1167/54)	471.559			+	-	1		
	T	INTLUENCA C VINIS (STRAIN CATYOGOLIA))	470-558		1	1	+			
1	Ţ	THE STATE OF VIRIS (STRAD) CHOKANNESBURG(186)	484-572		+	$\frac{1}{1}$	+			
No.	T	INTERPLET CORTS (STRAIN CK YOTOVINZ)	470-558	_	4	$\frac{1}{1}$				
1	T	INTUENZA C VINUS (STEERING			٠					
PHENA INCK	٦									

JA JOSEPH	ALLMOTIS	Att Virence (no bacteriophages)	1,120	ABEA 3 AREAS	AREA	AREAS AREA 6	16 ABEA1	AUAL	IJ
FIT P HAME	PROTEIN		Γ	Γ					
DOM ALCOHOL	HEMAGGLUTININ PRECIASOR	1020)	***					-	
PLETA PACKA	HEMAGGLUTININ							-	<u> </u>
PHEMA DACPI	HEMAGGLUTIMIN PRECURSOR	INFLUENZA C VIRUS (STRAIN CPIGMELLING/1971)	466-174						ĺ
PHEMA DACES	HEMAOGLUTIMIN PRECURSOR	INFLUENZA C VIRUS (STRAIN CPIC/BELIING/115/41)	46.17		-			L	
HEMA INCPO	MEASLES VIRUS (STRAIN HALLE)	INFLUENZA C VIRUS (STRAÍN CPÍGNEUINGA) WAL		1					
PIEMA INCTA	HEMACGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN C/TAYLOR/12) 1/47							
PHEMA INCYA	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CYANIAGATA/10/11)							
PIEMA MEASE	HEMAGGLUTPIN-NEURAMINIDASE	MEASLES VIRUS (STRAIN EDAIONSTON)	26.0						
PHEMA MEASH	HEMAGGLUTIPM-HEURAAMMDASE	MEASLES VIRUS (STRAIN HALLE)	24-00					 -	<u> </u>
HEMA MEASI	HEMAGGLUTININ-NEURAMINIDASE	MEASLES VIRUS (STRAIN IP.).CA)						<u> </u>	!
PHEMA MEASY	HEMACCI UTDINAMEURANIMIDASE	MEASLES VIRUS (STRAIN YANIAGATA-1)	46-87				-	+	<u> </u>
102.01	HEMACK LITHEN NELBANDASE	LIDAOS VIRUS (STRAIN SBL-1	34.99						
THE PARTY OF THE P	MENANCE ITTEMS MEI BANDATDASE	MUDICES VIRUS (STRAIN MIYAHARA VACCINE)	34.99		+			+	Ī
THE MAN WASH	HENA CCI TTEMNINETE AND THE	MUNUS VIRUS (STRAIN RW)	34-98		+			<u> </u>	Ī
THE PERSON NAMED IN	HEWACO I TRANSMITTEN	MUNCHS VIRUS (STRAIN SBL)	34.99			1	ļ	+	į
THE PERSON NAMED IN	LIEVA COST TENNAMENTE IN AMORIDA SE	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORUA/)?)		477.539		1	1		:
	VENA COLUMNIA METRIA ANTONIO A SE	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)			1		- 	1	i
PHEMA NOVE	ACCOUNT OF THE PARTY OF THE PAR	NEWCASTLE DISEASE VIRUS (STRAIN D2676)	1.52					1	Ī
PHENA MOVE	REMANDED INTERPREDICTION OF THE PARTY OF THE	NEWCASTI & DISEASE VIRUS (STRAIN MIYADERA/SI)	1.52				1	1	İ
PHENA MOVA	HEMACOLULININ-REUMANINIMASE	NEWCASTI E DISEASE VIRUS (STRAIN QUEENSLAND/66)	1.52					-	1
PHEMA MOVQ	HEMACOLU IMIN-NEUROMINIUMSIE	AFWCASTI E DISEASE VIRUS (STRAIN TEXAS G B./45)	67					1	1
PENA MOVTO	PEMAGGLUTININ-PEUIDAMINIDAM	NEW CAST E DICE ACE VIRES (STRAIN IN STER6)	1.53						
MENA NOVO	HEMACCLUTININ REURANINIDASE	MANCONE DISTRIBLE VIRIS	19-73						
PHENA PHODY	HENAGGE UTTRIN-MEUTAMINIDASE	SECOND STATE OF THE STATE OF TH	04-110		-		_		
PIEMA PITHW	HEMAGGLUTING-NEURAMINIDASE	TOWARD A DELIENTA 3 VIBILE							
PIENCA PIEM	HEMACCI UTIMIN-YEUTAMINIDASE	CONTACT DESCRIPTION OF STREET TOTALDAY	247-281						
PHEMA PIZHT	HEMAGGLUTDIN-NEURANDINE	MUMAN FAMAINT LUCKEA & VINOS (STRAIN TOSTION)	11.93						
PHEDAN PISB	HEMACCLUTININ-NEUBAMINIDASE	BOVING FAMILY COCKES STATES	13-110	394.428					
PIEMA PUH	HEMAGGLUTIMIN-MEURANDHIDANE	SECTION OF SECTION ASSESSMENT OF SECTION ASSESSMENT	20-110	36-428					
PHEMA_PISHA	HEMAGGLUTININ-NEURAMINIDASE	HUMAN PARAINFLUENCA I VIRUS (STRAIN TEXISASTO)	01:0	394-428	-				
PHEMA PISHT	HEMADGLUTININ-NEURAMINIDASE	SALAN AND AND THE NAME OF THE PARTY OF THE P	13-110	25-420					
PHEMA PUHU	HEMAGGLUTININ-NEURAAMNIDASE	ROMAN TALANTICALA STATES (STRAIN TEXTS (STRA	13-110	364.428					
MENA PDHY	HEMAGGLUTININ-NEURAMIRIDASE	THOMAS AND A THE NAME AND A STREET OF THE ABOVE ASSESSED.	13.110	394-428					
PHEDAL PIDHW	HEMACCLUTININ-MEURAMINIDASE	CHARLE STANDARD TENZA I VIETE (STRAIN WASIVISHO)	01-0	394.428					
PIENA PISIC	MEMAGGLUT IMIN-MEURAMINIAN SE	LUDAAN BABARTI (FNZA A VIRUS (STRAPA TOSHIDA)	24.88					-	
PICMA PWHA	HEMACOLU ININ-NEUVONAMINAS	RACCOON POXVIRUS	166-214	236-390				-	İ
PHEMA INCM	PENALUGUATION NOTE AND THAT	ANDEAPEST VIRUS (STRAIN KARETE O)	19-97						Ì
PHENA KINDA	AND A COLUMNIA TO THE AND THE	RINDERPEST VIRUS (STRAIN L.)	19-93	191-225			1	1	Î
THEMA MINUT	SENACO INDIANAMENTALIMATERA	SENDAI VIRUS (STRAIN Z / HOST MUTANTS)	57-110					1	1
STATE OF THE PERSON NAMED IN COLUMN 1	HENACCI LITRON NELDANDIDASE	SENDAI VIRUS (STRAIN FUSIIINII)	57.110					$\frac{1}{1}$	İ
THE PERSON	LEVACCE LITTOM-NEURAL MINDASE	SENDAI VIRUS (STRAIN HARRUS)	53.110					1	Ī
THE STATE OF THE S	HENA COLL LITTERIA NELBANINIDAS E	SENDAI VIRUS (STRAIN HVI)	23.10					1	i
TOTAL COMM	HEMACAL LITHON-NEURAMINIDASE	SENDAI VIRUS (STRAIN Z)	27-110		1		+	1	i
THESE STATES	SCHARCE IFFOR NEITHANDINDASE	SDGAN VIRUS 41	18-52	307-421				1	1
200	MENANCE INTRINSECTION DASE	SPECH VRUS I (STRAPH WI)	17.61				1	1	1
PHENA CVEN	HEMAGGLUTININ-YEURANDHOASE	SDOAN VOUS S (ISOLATE HUMANAM)	3.63			1	1	+	
200	HEMACOLLITINAN PRECURSOR	VANOLA VIRUS	137.211					1	ļ
THE A VAN	PERIPENTONAL HEXON-ASSOCIATED PROTEIN	HUMAN ADEMOVIRUS TYPE 2	80.D4					1	
TOTAL ANEWS	PERIPENTONAL HEXON ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE S	8-134 134				+	1	Ī
PACE X A DECT	HEXINA ASSOCIATED PROTEIN	HUMAN ADENOVIAUS TYPE 2	5 D			1	1	+	Ī
BUT WE AREON	HEXON-ASSOCIATED PROTEDY	HIDAAN ADENOVIRUS TYPE S	20.5			1	1	$\frac{1}{1}$	Ī
STATE OF THE PARTY	MEYON, ASSOCIATED PROTEIN	HUMAN ADENOVIRUS TYPE 1, AND IRUMAN ADENOVIRUS TYPE	93-138			-		$\frac{1}{1}$	7
THEAT ADEN									

ALLEGOISTIC AUGUSTA	11 12 12 13 14 15 15 15 15 15 15 15											
MERCHASSOCATED FROTTEN TANAMA ADEROVATES TYPE 1 11-10	COLUME DIGITAL MALAN ADDOOMIG 1705 13 14 14 14 14 14 14 14				П		777	1	TOTAL OF			
ACCOUNTS SECONTROL PROTECTION TALANA MACROMINISTY THE STATE	The coloniary of the			13000	Ē							
RESONATION TO THE PROTEIN FIGURAL ADERSONIUS TYPE 1 11:101	CANDER ADEROVILIS 1778 11:101 11:				7.126							L
RECONSTRUCTION PROTECT RECURSION PROTECT RECU	CALIFFORM INCOMESTIVE 111-101	_			91.6							
RECORA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENA ASSOCIATED PROTEIN FREENAN PROTEIN FREENAN PROT	Tippal Adeisovinis Tyre Tippal Adeisovinis Tyre Tippal Adeisovinis Tyre Tippal Adeisovinis Tyre Tippal Adeisovinis Tyre Tippal Adeisovinis Tyre Tippal Adeisovinis Tyre Tippal Adeisovinis Tyre Tippal Type Ti	Ī			1.100							
	HOLDER HOLDER ADEROVIUS TYPE 10-219 10-2	Г				133-467	583-624					
RECORD HOUTEN HOLAN ADERIONALY TITE 4 1911-144	HOLIAN ADEROVINIS 1776 1 101-101	Г			Τ							
REXON HOTTEN REXON HOTTEN ROLLING FOTEN		Γ			T	401.449	553-587					
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1 TROSING PROTEIN RUASE TRANSFORMOR PROT ABELSON MURDE LEUKEMAN NASS TYROSING PROTEIN RUASE TRANSFORMOR PROT FELINE SAKOOMA VIRUS (STRAIN GALDNER-ARNSTERN) TYROSING-ROTEIN KINASE TRANSFORMOR PROT FELINE SAKOOMA VIRUS (STRAIN GALDNER-ASSEED) TYROSING-ROTEIN KINASE TRANSFORMOR PROT FELINE SAKOOMA VIRUS (STRAIN MADONOUCH) FINASTRANSFORMS KINASE TRANSFORMOR PROTEIN FELINE SAKOOMA VIRUS (STRAIN MADONOUCH) FINASTRANSFORMS KINASE TRANSFORMOR PROTEIN FELINE SAKOOMA VIRUS (STRAIN MADONOUCH) FINASTRANSFORMS KINASE TRANSFORMOR PROTEIN FELINE SAKOOMA VIRUS (STRAIN MADONOUCH) FINASTRANSFORMS KINASE TRANSFORMOR PROTEIN FELINE SAKOOMA VIRUS (STRAIN MADONOUCH) SAFAN	NO PROT ABELSON MURRILE EUREAGA VRIUS 113-127 143-150 AKT I MUNDEL EUREAGA VRIUS 113-144 104-173 104-173 NO PROT [FELDE E ARCOMA VRIUS (STRAIN GARDNER-AKSTERN) 211-244 104-173 NO PROT [FELDE E ARCOMA VRIUS (STRAIN GARDNER-LASTERED) 211-243 511-243 NO PROT [FELDE E ARCOMA VRIUS (STRAIN MCDONOUGH) 111-243 511-543 NOTERY FELDE SARCOMA VRUUS (STRAIN MCDI) 55-79 55-79	PRIZ HOAVA	THE OFFICE PROTEIN KINASE TRANSFORMING PRO		11.33	L				1	+	\mid
AKT KRASE TAANSFORMING PROTEIN AKT MINDE LEUCHAIA VIRUS AKT KRASE TAANSFORMING PROT FELINE SARCOMA VIRUS (STIVAN GARDNER-ARDSFEED) 116-133 TYRIOSINE-ROTEIN KINASE TRANSFORMING PROT FELINE SARCOMA VIRUS (STIVAN MICHORITE SARCOMA BY TRANSFORMING PROT FELINE SARCOMA VIRUS (STIVAN MICHORITE RANSFORMING PROTEIN FELINE SARCOMA VIRUS (STIVAN MICHORITE TRANSFORMING PROTEI	ARTS MANDE LEUCEAN VIOLS ARIO PROT FELINE SARCOMA VIOLS ARIO PROT FELINE SARCOMA VIOLS (STRAIN GARDNER-AASHEED) ARIO PROT FELINE SARCOMA VIOLS (STRAIN GARDNER-AASHEED) ARIO PROT FELINE SARCOMA VIOLS (STRAIN MCDONOUGH) ARIO PROT AYTAN SARCOMA VIRUS (STRAIN PRCII) ARIO PROT AYTAN SARCOMA VIRUS (STRAIN PRCII)	PKABL FSVHT	THE OFFICE PROTEIN KINASE TRANSFORMING PRO		13.227	263-304		-	1	+	1	+
TYTOSINE-PROTEIN KINASE TRANSFORMING PROT FELINE SARCOMA VIRUS (STRAIN GARDNER-LASHEED) 316-353 ITAGOSINE-PROTEIN KINASE TRANSFORMING PROT FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) 1313-343 PAG TYROSINE ROMASE TRANSFORMING PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) 51-79 FAG TYROSINE KINASE TRANSFORMING PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) 51-79 FAG TYROSINE ROMASE TRANSFORMING PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) 51-79 FAG TYROSINE ROMASE TRANSFORMING PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE ROMASE TRANSFORMING PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE ROMASE TRANSFORMING PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE ROMASE TRANSFORMING PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR TYROSINE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR THE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR THE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR THE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR THE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR THE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH) FOR THE PROTEIN FOR THE PROTEIN FELINE SARCOMA VIRUS (STRAIN MCDONOUCH)	AIRNO PROT FELINE SARCOMA VINUS (STRAIN GARDNER-LASHEED) JIETS SARCOMA VINUS (STRAIN GARDNER-LASHEED) JIETS SARCOMA VINUS (STRAIN INCOMOUGH) JIETS SARCOMA VINUS (STRAIN PICCI) JURG PROT AVIAN SARCOMA VINUS (STRAIN PICCI)	PKABL MLVAS	ANT PRAKE THANSFORMMYO PROTEIN		36	10-17		-	1		-	+
THEOSDIC-PROTEIN KINASE TRANSFORMING PROTEENING SACCOLA VIRGO (STRAIN MCDONOUGH) 311-343 PAS TYROSDIC KINASE TRANSFORMING PROTEIN FEING SACCOLA VIRGO (STRAIN MCDONOUGH) (S1-99)	FELNE SACCHAY VRUS (STRAN MCDONOUGH) 111-142 618-479 FELNE SACCHAY VRUS (STRAN MCD) 65-79 AYAN SACCHAY VRUS (STRAN MCD)	WAKT MEVA	TYTOSINE-PROTEIN KINASE TRANSFORMING PRO	IT FELINE SARCOMA VIXUS (STRAIN GAMONER, RASHEED)	318-352			+	-	+	+	-
PASS TYROSING KINASB TRANSFORMING PROTEIN FELING SALCOMA VIRUS (STRAIN PACII)	FELINE SACCOMA VIRUS (STRAIN PICII)	PRES PSYCA	TYROSDAR PROTEDI KINASE TRANSFORMING PRO	IT FELLING SARCOMA VINOS (STINAIN CONTINUED OF STATE AND LACTONICION)	313-362	638-679	\$ 2 2 3	1	-	1	+	
	ITYDSDB- MOTEN KINASE TRANSFORMEND ROOT ANALOMA VIKUM CATTON TRANSFORMEN TRANS	PKECH PSVCK	FAR TYROSDIE KINASE TRANSFORMINO PROTEIN	FELING SALCOMA VIALDS (STRAIN MELANICONS)	66-59		H	$\frac{1}{1}$		$\frac{1}{1}$	-	
TANSFORM KINASE TRANSFORM		PKENG FSWED	THE STATE PROTEIN KINASE TRANSFORMING PRO	OF AVIAN SARCOMA VIRUS (STRAIN PACE)								

PECENT PRINT AND PRINT AN	ALLAOTIS PROTEIN PROTEIN PROTEIN KINASE TRANSFORAING PROT PHYMIDINE KINASE	YORUS FUTHALAIS SARCORIA YIRUS	65.89	152-251 348-348	677				. !
LE NANT. KETH ALGEV KETH ALGEV KETH CAVK KETH EBV KETH HSVII KETH HSVII KETH HSVII KETH HSVII KETH HSVII KETH HSVII KETH HSVII	r NOT	POXVIRUS						-	:
KITH AMEDY KITH AMEDY KITH AMEDY KITH HAVII KITH HAVII KITH HAVII	\prod					_			ļ
KITH AMENY KITH CANK KITH EBV KITH HSVII KITH HSVII KITH HSVIE KITH HSVIE		A MINOR LINE CONTROL OF THE PARTY OF THE PAR			1				ļ
KITH CAPVE KITH EBV KITH HSVIC KITH HSVIE KITH HSVIE KITH HSVIE		CAPRIDOXVIRUS (STRAIN KS-I	1						
KITH EBV KITH HSVII KITH HSVIE KITH HSVIE		PPSTEIN-BARR VIRUS (STRAIN 895-1)		431:472					:
KITH HSVIC KITH HSVIC KITH HSVIE KITH HSVIE	THYMODINE KIMASE	JERPES SOUPLEX VIRUS (TYPE 1/STRAIN 17)	8 22						
KITH HSVIC KITH HSVIE KITH HSVIE	THYMDRE KRASE	HERPES SUPLEX VIRUS (TYPE 1/STRAIN CLIOI)	% 	1		1			
KITH HSVIE	THYMODING KINASE	GRAPES SOUTHEX VIRUS (TYPE 1/STRAIN HFEA!)	8		+	1			
KITH HSVIK	THYMODUE KOWASE	PERPES SOUPLEX CIRUS (TYPE I / STRAIN KOS)	80-124		+	-			!
WITH HSVIS	THYNODRIE KINASE	STRAFE CAMPIEX VIRILS (TYPE ! / STRAIN SC16)	% 134		-	-			
	THYNODE KINASE	Property of the Control (TVPE 2 / STRAIN 33)	91-129		-				:
PKITH HSV23	THYMIDING KINASE	HERCES SIMPLEX VIACOLITIES (1900)	\$99-919						:
PKITH HSVBM	THYMIDINE KINASE	BOVING PORTUGE STATE 2 (STEAT)	Γ	915-811		-			:
PKITH HSVE4	THYNIDDG KINASE	EQUINE REPESVIRUS LITE 4 (3) PAIN ABAPA	Ī	(78-330					:
PETTH MSVER	THYMIDDÆ KRASE	EQUINE SERPESVINUS TYTE (13 INA) AND S	180.214						:
PKITII HSVP	THYMDONE KINASE	FELINE HEAVES VIAUS (PELIN HILLINGS VINCS VI	2.5						:
MAY WITH	THYMIDDAE KDVASE	MARANOSET HERPESVIRUS	11.11						!
A MANA	THYMIDDE KONSE	HERPESVIRUS SAINURI (STRAIN 11)		-					_;
PRILITY NO VOICE	THOUSE KINASE	PSEUDORABIES VIRUS (STRAIN KIA-3)	7,17.10		-				
TRIIN TRIIN	ME CERMETHREDWINE PROTEIN KINASE TRANSF	AVIAN RETROVIRUS KIIT	21.5						_i _i
TAMIL AVING	CENT 15 PROTECUL KINASE	ICTALUNIO HERPESVIRUS 1				 -			
PKAIS HSVII	CENE IS PASSIBLE OF THE PROTECT KINASE	HERPES STIPLEX VIRUS (TYPE 1/STRAIN 17)	T		+				_
PKR2 HSVII	TOTAL SERVICE	ICTALUMD HERPESVIRUS I		397-631					
PKR74 HSVII	GDG 14 PROTEIN KINASE		?		-				<u> </u>
PKILAT MSV36		VACCINIA VIRUS (STRAIN COPENIAGEN)	137-168						
PKRBI VACCC	10 KD PROTEIN KINASE HUNIULIA	VACCIONA VIBINS (STRAIN WR)	137-168						[_
PKRBI VACCV	10 KD PROTEIN KINASE HONIOLOG	VARIOUA VIRUS	133-131						!
PICIES VARV	10 KD PROTEIN KINASE HOMULUO	VACCINIA VIBIN (STRAIN COPENIAGEN)	147-181		-		-		: !_
PKILBY VACCC	POSSIBLE PROTEIN KINASE BIZ	VACCINIA VIBING (STRAIN WR)	147.181		1		1		! -
PKEBS VACCV	POSSIBLE PROTEIN KINASE BIZ	VACCIONA VIRUS (STRAIN COPENIAGEN)	169-203		1				\ \ \
PKRF1_VACCC	POSSIBLE PROTEIN RIMASE 7 10	VACCINIA VARUS (STRAIN L.IVP)	136-170		+		-		<u>:</u>
PICULI, VACO	POSSIBLE PROTEIN KINASE FID	VICENT ANDIO	169.303		-				
PICULI VARV	POSSIBLE PROTEIN KINASE FIG	ASSAULT OF THE STRAIN URD	111-145		$\left \right $				1
PKROS AVISU	ROS TYROSINE KINASE TRANSFORMING PROTEIN	AVIAN BETBOOKERS BELSO	13-66						
PKKYK AVDU	TYROSING-PROTEIN KINASE TRANSFORMING PROT		133-169						Ì
PKTHY VACCV	THYMOTHATE KONASE		114-211						j
PKYES AVISY	NASE IKANSFORMI	INDIAN ADENOVIRUS TYPE 3	441-475		+	+			İ
PLIDO ADEGS	LATE 100 KD PROTEIN	MAKAN ADENOVISUS TYPE 5	223-264			 			1
PL 100 ADE05	LATE 100 KD PROTEIN	LUDAAN ADENOVIRUS TYPE 40	191-332	408-442	-				
PL 100 ADE40	LATE 100 KD PROTEIN	MANAN ADENOVIRUS TYPE 41	П			1	$\frac{1}{4}$		
7 180 ADE41	LATE 100 KD PROTEIN	HOMAN ADENOVIRUS TYPE 2	٦	101.349		+			
PLS2 ADEAS	LAIR LIST NO PROTECT	HUMAN ADENOVIRUS TYPE S	T	301.349	+	-	 		
PLS2 ADE05	LATE LIST AND TANKER	EPSTEIN-BALA VIRUS (STRAIN 895-8)		244-338		-	-		
PLOT EBV	CENE TEMMINAL PROTEIN	SHOPE FIBROMA VIRUS (STRAIN KASZA)	2	623-656	+	+	-		
PMCEL SPVKA	Court Cobstruction	VACCIMIA VIRUS (STRAIN COPENHAGEN)		653-657	1	+			
PACEL VACE	MUN CATANACTA THE	VACCINIA VIRUS (STRAIN WR)		633-633		+			
PMCEL VACCV	MUNA CATTON EACH INC.	VANOLA VIRUS	٦	623-437	-	+			
PACEL VARY	MUNA CATURUS ENT. I PRE	VACCINIA VIRUS (STRAIN COPENHAGEN)		243-206			-		L
PMCES VACCO	MUNA CAPTURE ENERGY	VACCINIA VIRUS (STRAIN WR)	T	245-216					<u> </u>
PMCES VACCV	MOUTA CAPTING ENGINEER	VARIOLA VIRUS	٦	1	+	-	-		
PACES VARV	MOUNT CATHING ENG 1 PAGE	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	_	275-317 (11.471					
PMCE ASPB7	MOUNT CAPPING ENTINE	ODDAYTOGLOSSUM RINGSPOT VIRUS	53-90		+	1			
PAOVP ORSV	┪	PEPER MILD MOTTLE VIRUS (STRAIN SPAIN)	3		+				
PACOVE PPACVS	MOVEMENT PROTEIN	TOBACCO AM D GREEN MOSAIC VIRUS (TMY STRAIN U.)	39-66	-	$\frac{1}{2}$				

4.						П	П	Ιī	Т	
PCCFWE	ALLAROTIS	All Victors (no bottertophe Mil	AREAL	AREAI	CREAZ	98544	4854	DELAC.	707	
PILE NAME	PROTEIN	SEALCED MOTALE VIRILE (STRAIN TONIATOL)	33-66				+			i
PHOVE THINTO	MOVEMENT PROTEIN	SALLED MODELL WEIR (CTRADILIA)	13-10							
PHOVE TOMVA	MOVEMENT PROTECT	SALL TO AND LIFT VIBILE (CTIAN) LIII	33-60							
PHOVE TOWN	MOVEMENT PROTEIN	ICAM I CANDARY WAS IN	332-356							
PATCI CHAMI	MODIFICATION METHYLASE CYTH	CHUCKLIA CINOS POR CIO ORELLA VIXUS	116-164							
ויייים סאייו	MODIFICATION METHYLASE CYIASI	PACAGE COM BOARDON CIT COM	329-266	175-410						
PHYC AVDG	MYC TRANSFORMEN PROTEIN	A VIAM PITCLO. I LOW LOSS VIBIGACTO	330.367	176-410						
PACY AVOAC	MYC TRANSFORKING PROTEIN	AWAN MYELOCTIONALISM	Γ	176-420						
PLAYE AVBAD	LAYC TRANSFOREMA PROTEIN	AVIAN MYELOCTIONALIOSIS VINOS III	117-111							
PARY AVIAGE	MYC TRANSFORMING PROTEIN	AVIAN RETROVIRUS MILLELI		370-414						
MAY AVIOR	LAYC TRANSFORLENG PROTEIN	AVIAN RETROVIAUS OK 10	T							į
V 12 - 10 - 10 - 10 - 10 - 10 - 10 - 10 -	LAYE TRANSFOREMO PROTEDI	FELINE LEUX EAILA VIRUS								
1000	LAY TRANSFORMING PROTEIN	FELINE LEUKEMIA PROVINUS FTT								
1000	MANY ECCAPCIO PROTEDI	ARJUNE COROMAVIRUS ARIV (STRAIN ASS)	•							
THE ALL LANGE	TOTAL SOCIETY OF THE PROPERTY	AINO VIRUS								!
PHCAP AIROV	MULTICON STREET	BEANE VIRUS	3	22-156						
PNCAP BEV	MUCL EOCAVSID PROTEIN	SOUTH BESPIRATORY STREYTIAL VIRUS (STRAIN AS1904)		163-200	348.303	10.50	Ì			
PNCAP BRSVA	NUCLEOCAPSID PROTEIN	PERSONAL CERTAINSTON	136-220							
PHCAP BUNGE	NUCLEOCAPSID PROTEIN	ALEXA AMERICA A CONCER	176-279							
PNCAP BUNGC	NUCLEOCAPSID PROTEIN	BUNTAVIAGE LA CROSSE	176.219							
PNCAP BUNSH	NUCLEOCAPSID PROTEIN	BUNTAVIRUS SHOWSHOE HANG	135.220							
PHCAP BURTW	NUCL EOCAPSID PROTEIN	BUNY ANWERS VIALS	Γ	427.461						
VOCA COSV	MUCLEOCAPSID PROTEIN	CAMEAN-CONCO REMORNAGIC PEVER VIRUS (ISCLATE COM	Τ	110.313	114.402					1
COVO.	NACL EOCAPSID PROTEIN	CANINE DISTEMPER VIRUS (STRAIN ONDERSTENDAR)	ī							
200	MICL FOCAPSID PROTEIN	CHANDIFURA VIRUS (STRAIN 1651514)	Ţ,							
200	MICH EDCAPSID PROTEIN	BOVINE COROMAVIRUS (STRAIN F15)	101.401							
700	MICH EOCAPSID PROTEIN	BOVINE CORONAVIRUS (STRAIN MEBUS)								
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MAICH EOCAPEID PROTEIN	CANINE ENTERIC CORONAVIRUS (STRAIN K 178)								
2000	MICH EDCAPSID PROTEDY	HUMAN CORONAVIRUS (STRAIN OC+1)								! !
2000	MAIN FOCAPSID PROTED	AUTUME COROMAVIRUS MITIV (STRAIN HIN)							:	:
100 CALL	MAIN BOCAPSID PROTEIN	PORCINE TRANSAUSSIBLE GASTAGENTERITIS CORGNAVIRUS (S	149.700							-
3	NAITH FOCAPSID PROTEIN	PORCING TRANSMISSIBLE GASTROENTERITIS COLCRAVIAUS (S								
200	MAICH EDCAPSID PROTEIN	PORCINE RESPIRATORY CORONAVIRUS (STRAIN BATENDO / BALL								:
7187	MAICH EOCANSID PROTEIN	PORCINE RESPIRATORY CORONAVIRUS (STRAIN RAIN)								
CS CAN AND AND AND AND AND AND AND AND AND A	NAICH EDCAPSID PROTEIN	RAT CORONAVIRUS (STRAIN 481)								
TALL CALLE	MAICH EOCAPSID PROTEIN	TURKEY ENTERIC CORONAVIRUS								
VECTAR DATES	NAICH EOCAPSID PROTEIN	DUCEE VIRUS	2							
PACAP TRV	NAZCI EOCAPSTO PROTEDI	FELINE INFECTIOUS PERITONITIS VIRUS (STRAIN 79-11%)	******	1	111.111					
PHEAP HANTY	NUCL EOCAPSID PROTEIN		18							
PHEAP HAZVI	NUCL ECCAPSID PROTEIN	HAZARA VTRUS (1SOLATE JC210)	T	141.300	240.103	343.180				
IN UT ON JAN	NAJOL EDCAPSID PROTEIN	2	Ţ		101 101	141.100				
ANS AN ANA	MAICH EDCAPSID PROTEIN	HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN AZ)	T	3			-			İ
PACAP DVG	MUCI EOCAPSID PROTEIN	AVIAN DRECTIOUS BRONCILLIS VIRUS (STRAIN CRAT)	À							
PACA PACE	MAIN EDCAPSID PROTEIN	AVIAN INTECTIOUS BRONCHIES VIRUS (STRAIN RBISSS)	0//-							
200	MARTI FOCAPSIO PROTEIN		Ī				+		 	
The Party of the P	MAIN FOCAPUM PROTEIN		1						-	
200	Name of APACE PROFESS			2	20.75					i -
	AND TOCABLE PROTEON		Ì					İ	<u>-</u> -	
100 P	COLVESTION OF THE PROPERTY OF	STRON		٦			+	 	: 	:
שכיים דוניא	SALE COLARGE SALES	LYMPHOCYTIC CHORIOMENINGITIS VIRUS (STRARY WE)		9.113	460.477			İ		:
	A COANTE PROTECT	PLACUAL VIRUS	٦						1	-
200	CAN TO A PROTECTION	AREASLES VIRUS (STRAIN EDMONSTOM)	٦	2					T	i
Service Service	ALCO ROC ABOUT DE CATE DE	MEASLES VIRUS (STRAIN HALLE)	1	20.25			 -			i
THEAT MEASH	MACAGO AVID PROTEIN	AREASLES VIAUS (STRAIN IP-1-CA)	189.326 3	161-411			1	1		
PACAP MEAN	MULTION AT SIN TRUST SIN		İ							

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PCCENE	ALLAIOTIS		TVJEV	4854	4854	MEA	2000	2000	Τ	
THERANG	PROTEIN	ES VIRUS (STRAIN YANIAGATA-1)	٦	=						
PHCAP MEASY	MOCI EOCAPSID PROTEIN		901-69	471-505						:
PHCAP MOPE!	MUCL ECCAPSID PROTEIN	COTO ALEX COL. A)	214-235	500-534						i
PHCAP MARDI	MUCLEOCAPSIO PROTEIN	IARA VACCINE)	314.355							
PHCAP MARON	MICH EOCAPSID PROTEIN		1-35	AO. 74	113.101					
PHCAP PIN	MUCLEOCAPSID PROTEIN	ZA I VIBUS (STRAÍN C39)	111-111	141.310						;
PNCAP MIHC	MUCL EOCAPSID PROTEIN	HINGTOWISS?	111.111	441-510						
PHCAP HIMM	NUCL EOCAPSIO PROTEIN		314.346	14.11				1		;
PHCAP MINT	MUCLEOCAPSID PROTEIN		100-001	146.470			 			
PICA MIS	MUCLEOCAFSID PROTEIN	CETRAIN MIL 476155	0.03	208-366	144.401	440.491				
PHCAP PISH	MUCLEOCAPSID PROTEIN		30.0	191-267					_ 	
PHCAP PIANA	MUCLEOCAPSIO PROTEIN	Ī	3.5	191-367						
PNCAL PICKE	MUCLEOCAPSID PROTEIN									
PHCAP PHARY	MUCLEOCAPSID PROTEIN		Ī	125.150						
PHCAP PIRTY	PRUCLEOCAPSID PROTEIN		T	46.75	133.30					
PHCAP PURSH	MUCLEOCAPSID PROTEIN	MUNIALA VIRUS (STRAIN INALERANTE)		\$6.33	111.111					
PHCAD PUBMS	MUCL EOCAPSID PROTEIN			246.303	14:11					٠
PACA PAR	MUCL EOCAPSID PROTEIN		1.						<u> </u>	
PHEAP BABVA	NUCLEOCAPSID PROTEIN		T				İ		: -	
PACAP SENDS	NUCLEOCATSID PROTEIN	ARUTANTS)	Ī							
SOCAP SENDS	MUCL EOCAPSID PROTEIN	DEAS	T	200						
PACAS COMP	MAICL EDCAPSID PROTEIN		<u> </u>	103:00						:
PACAS CENTR	NAMES OF A PROPERTY	RAIN SR-11)	T	0.74	117-181					.
200	MAICH EOCAPHID PROTEIN		٦	172.406	416.486					: :
200	Language Description	IN MET VIRUS	112-164							1
THE STRV	MOCESCA SECTION			210.264						
PHCAL IALV	Potte Control of the Control		215.249							
PNCAL TOSV	NUCLEOCAS SILVANOTES	D WILT VIRUS (BRAZILIAN ISOLATE CPMINAR	29-120							-
PACA TSWY	NUCLEOCATION PROTEIN		79-470							
THE A TSWAM	NOCTED AND PROTEIN		79.130				- - -			
PICA TSWA	NUCLEUCATION PROTEIN		\$11.102							
אכאי המצ	MULTEUC ASSISTANCE OF THE PROTECT	GIC SEPTICEMIA VIRUS (STRAIN 01-71)	249-325							!
PACAP WHSW	NUCLEUCASIU PROTEIN			249-325						
PHCA WHSWA	MULTEUCASSIO PROTEIN	VESICIA AR STORIATITIS VIRUS (SEROTYPE INDIANA / STRAIN C	43-108							
PACAP VSVID	AUCTEUM PROTEIN	VESICULAR STOMATITIS YARUS (SEROTYPE NEW JERSEY / STRA	63-115							-
מיירי הייירי	MICH SOCKAPSID PROTEIN		42-115							-
THE PARTY	NEGATIVE FACTOR	٦	=							
PARF HV2DI	NEGATIVE FACTOR	7	Ţ							
PNEJ HVJRO	NEGATIVE FACTOR	_	3							
PAGE HYSS	NEGATIVE FACTOR	È	061.00							!
PINES HV7ST	NEGATIVE FACTOR		101.00							:
PHEF SIVAL	MEGATIVE FACTOR	SINIAM INDICADE PICIENCY VIRUS (ISOLATE AUTOLICE ON THE		311.343						1
PNES SIVSA	NEGATIVE FACTOR	7620								
PREAM, WADA	NEURAL MIDASE	IN LUENZA A VINUS (STRAIN MOLACE DUCINOCIONALISMOS	11.74							
PHRAM IACAO	NEURAMMIDASE	T	10.01							
PRIMAM IACHE	PRUTAMENTOASE	SANCYI VANDA/1130/	19:10							
PARAM IACKO	NEURANDMIDASE		146,181							
PRILAM LACKE	NEURANDMASE		7							
PIRAM IADGE	NEURANDASE	SWEYBRID	Γ	194-179						
PHRAM LATPW	NEUTANDADASE	THE COURT A MALIE (STATE AND A PORTING FOR A		193-327						
PHALM LAHOO	NEURANDAIDAIG	VIAII		361-402						
PRAM WAT	NEURAMBUDASE									_
PARAM IAKTE	NEURANDASE									

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		see (no hacteriopheges)	ABEAL	AREAL	ABEAJ	MEAL	A STATE	1		
PCCVC			2.5							
CILL HAME		ENZA A VIRUS (STRAM ANEMINOMONAL)	10.00							
NAME IALEM	NEURAMINIDASE	Vacin							-	
PRAMI INCEI	MEURANDRIDASE									
PARAM IARUE	KEURAMBUDASE								-	-
NEAM 1ASH?	NEUTAMBRIDASE	┰								-
PARAMI IATER	NEURAMONIDASE	ŝ								
AND AND SATEA	NEUTAMBRIDASE		5							-
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	NET THE ANDROASE	DALCENZA A UNO LE SE DACIONOLI MA	3.46	141-313						
MAN LAWIN	ACT OF A LEGISLA	DALUENZA R VIRUS (SIRAIN DELLINICATION	5.46	149-311						!
אסשע שטער	MEDICAMINATION	DOLUENZA B VIRUS (STRAIN BINCHO ROMONA)	17	149.383						
PACAM DRINK	NEURANDASE									: :
NAME OF LE	NEURANDASE	I (STRAIN DA								<u> </u>
MAKE BOLK	MEURALEMEDASE	STEELE A VISITE (STRAD) BAIARYLANDYS)	2							
9190	MEURAMORDASE	CANADA CATALON BACENCHUS/ME)	5-46	701						
THE PARTY OF THE P	VERMANDEDASE	INCLUENZA B VINDS (STRAIN DORFOLDS)	27.5	19:11						
PIGAN LABOR	Section Authority A Cili	DATUENTA BYTHUS (SITANITA COLONIA)	5.39	149-313						
WEAL DOOR	A CONCENTRATION OF THE PARTY OF	INTLUENZA B VIAUS (STRAIN BAUMUANAMATA	. 10	100.00						i
PHEAST INIBS!	NEURAMINIDASE	INTLUENZA B VIRUS (STRADI BAUSSWICOAT)		100						
PARAM INBUS	NEURAMINIDASE	MEI IENZA B VIRUS (STRAIN BAVICTORÍA)/85	2							
PHRAM DOBYL		ACTION OF MICHEUSIS VIRUS	71.04							-
PACE CITIEN	PROBABLE STRUCTURAL PROTEIN PRECURSOR	STATE SECTION (POT VIRUS (STRAFN ML-07)	95.139	2						
70.000	NOW STRUCTURAL PROTEIN	MUALIERS RECEDED AN T VIETE MAAZILIAN ISOLATE CPINISM	1.1							
200	NAME STRUCTURAL PROTEIN	TONIALO SPOTICED AND STATEMENT (CTRAIN L.)	1:33							
	CONTRACTOR PROTECT	TOMATO SPOTTED WILL VINCE (1995)	19-61	110-144						
PRSS 13WVL	AND SOUTH TRIPHOSPHATASE	AMSACTA MODREL EMILIANOTOM INC.	133-169	613-449	114-115					
PHEN AMEN	TOTAL SECTION TO THE PROPERTY OF THE PROPERTY	CHOMSTONEURA DIENNIS EN UNDIONOTOR CIRCO	26.80	341.20	948-888					
PHTP1 CBEPV	MULEUMON I MONOCONTINUE I	VACCINGA VIAUS (STRAIN COPENIAGEN)	16.90	146-219	946-986					
PATPI VACCC	POCCEDING THE BUTCHATASE	VACCINIA VIAUS (STRAIN WIT)	114.191	133-505						-
PINTP1 VACCV	MULEUSING TERMINOPHIATASE 1	VARIOLA VIRUS	119.323	609.735						1
MATE! VALIV	THE STATE OF STRUCTURAL PROTEIN	HENDES SIMPLEX VIRUS (1 TTE 0 / 3 INC.) CONTINUED	131-180							
PP100 HSV6U	MADOR ANTINCHASE CATAL YTIC SUBUNIT	VACCINIA VIRUS (STRAÍN COFEMINORM)	931.169							!
PALL VACCC	POLICATION TO THE ASS. PATAL YTIC SUBURIT	VACCIMIA VIRING ISTRAIN WRI	131.180							
PAPI VACCV	POLY(A) POLY(A) SE CATALYTIC SUBUNIT	VARIOLA VIRUS	113.146							1
PPAPI VARV	POLY(A) POLYTHE MASE COLOR ATORY SUBURGE	CAPRIPOXVIRUS (STRATM KS-1)								1
PAN CANK	POLY(A) POLYMBIASE MEDICAL STORY CIRCIDAL	FOWL POX VIRUS								:
PPAP2 FOWPV	POLY(A) POLYNERASE REGULATORY SUBMIT	VACCINIA VIRUS (STRAIN COPEMINGEM)	20.							:
PALT VACCC	POLY(A) POLYNERASE REGULATORY SOUCH	VACCINIA VIRUS (STRAIN WR)	101.104							i
PPAPT VACCV	POLY(A) POLYMERASE REGULATORY SUBDRIT	STREET A VIBIL	203-249			-				_
POAP2 VARV	POLY(A) POLYMERASE REGULATORY SUBUNIT	STATES APHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	13.56	8			1	-		
PPS13 NEVAC	13.1 KD PROTEIN IN PE STECTION	CONTA PERIFYCERITATA AND FICAPSID POLYICOROSIS VIRUS	11.98							
PPELL NOVOP	11.5 KD PROTEIN IN P26 STECION	ATTOCK A MIN CAL ISORNICA MUCLEAR POLYMEDROSIS VIAUS	16.33	200						į
PPETE NOVAC	MAJOR DOIEDIATE EARLY PROTEIN	APCHA PERIMOTSUGATA MILITEAPSID FOL MIEDROSIS VIRUS	100.340			1			L	
40x64 11366	ľ	CHANTIA CALIFORNICA MUCLEAR FOLYIEDAOSIS VIRUS	6-43	=				-		
PPGAL NPVAC		ACCION DEFINITION TO MIR. TICAPSID FOL VITEDROSIS VIRUS	63-63	5.13						
ADVON SARA	43 3 KD PROTEIN IN PE.P36 INTERGENIC REGION	CACALLA ADENOVALIA TYPE 3	414.448							
ANIVO ADEDI	MATURATION PROTEIN	HUMAN ABENDARIE IVER	11.11							L
Serve Appens	PROTEIN VI PRECURSOR	HUNAN ALENOTHERS TOPE A	17.71				77.	100.315	2368-200	
10,000	PROTEIN VI PRECUASOR	HUNDAN ADENOVINOS 1112 /	134.163	141.77	957-741	183-173		1	3167.3350	1366.240
	GENOVE POLYMOTED I	BALLET TELLOW FROM CONTROL (140ANE CE STRADA -1)	139.363	11.70	141.111	237.88				
2	CENOME POLYPROTEIN I	BARLEY YELLOW MOSAL VIKAS (200 MILES	130-161	912-591	230-373	111-413		-	1904.1941	
A PART OF THE PART	THAT POLYTROTEM	HUNDALIAN GLAZEVINE CHACKE FROSTI	170-313	410-010	6)6.63					
	ENAL POLYPROTED	CRAPEVINE PARLEAU VINUS	223-270	619-619						
200	RMA! POLYPROTEIN	TOMATO BLACK FLOW VINOS (STEWN)	161-206							
TOTAL TOTAL	Т	TOWATO RUNGSPOT VIRUA (190CATE PART SECTION 100LATE)	340-381	111.699	139-173	107-170				
PPOLI TROVA	Т	BAJLEY YELLOW MOSAIC VIRUS (DENSIAN SOLS LE)								
PPOL2 BAYMU	٦									

		All Viruses (no bacteriophages)		П	П	П	П	П	П	
T. CLAL	PROTEIN	YIMUS	I		7	77.00	7	2 OFFICE	1	
Part Sand	GENOLOGY PROTEIN 2	EY YELLOW MOSAIC VIRUS (IAPANESE STRAIN II-1)	1	1	787-628					
7 157 1 200	PNA 2 POL VPROTEDA		ş	\$43-602				1	T	
SALE FOR	RNA 2 POL YPROTEIN	TOWATO BLACK RING VIRUS (STRAIN S)	٦							
PPOL 2 TREVE	RNAJ POLYPROTED	TOWATO RINGSPOT VIRUS (ISOLATE RASPBERLY)	٦	134-361						
VAVOR O BOVEV	GENOME POLYPROTEIN	BOVINE ENTEROVIAUS (STRAIN VG-5-27)	٦	901-1001	1382-1416	100			0.0.	2374.2340
PPOLO BYDYN	GENOME POLYPROTEIN	BOVING VIRAL DIAJUNICA VIRUS (ISOLATE NADL)	Т		1000	101-101			1370.1870	114.21.70
PPOLG BVDVS	CENDAGE POLYPROTEDA	BOVINE VIRAL DIARRIEA VIRUS (STRAIN SD-1)	I	440-491	679-678	1017-101		200.766		
PPOLO BYDAY	GENOME POLYPROTEIN	BEAN YELLOW MOSAIC VIRUS	8						ntar teat	10.00 mg
PPOLO COXA2	GENOME POLYPROTEIN	COXSACKIEVIRUS A21 (STRAIN COE)	Ş	562-596	664-608	1043-1100	402-1346	1907:1041	1803-1837	
Pacific Coxes	CENOME POLYPROTEIN	COXSACKIEVIRUS AP (STRAIN GRIGGS)	15-49	1040-1014	1895-1940					
1000	SENONG BY ASSOCIATION	COXSACKIEVIRUS BI	13-49	1021-1067	1876-1928					
	CENOME POLYBOTED	COXSACKIEVIAUS DI	61-61	1024-1070	1879-1924					
roce coxes	CENCHE FOLLTROITER	COXSACRIEVIRUS B4	87-51	642-641	1901-2201	1877-1922				
rono come	GENOME POLITICISM	COVEACHIENDINE	15.49	1034-1070	1879-1924					į
Prote coxes	GENOME POLITING	CONTROL OF VIEW VIEWS	120-154							
PPOLO CYVV	GENOMIE POLYTRUIEIN	APPLY IN THE PARTY OF THE PARTY	74-101							
PPOLG DENIS	GENOME POLYPROTEIN	DENOUE VIEWS 1 176 1 (01000 VIEW)	74.10							
PPOLG DENIA	GENOME POLYPROTEIN	DENGUE VIRUS 1 TYPE 1 (3) RAIN AND 41-80)	27.15							
PPOLO DENIC	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIM CVISSE//)	8 2		100 070	173.1130	1166.1470	1614.1448	2518.2554	2946-3016
PPOLG DENIS	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN SINGAPORE SZ7590)	50.4		100	9				
PPOLO DENIW	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN WESTERN PACIFIC)	100	2	2					
PPOLG DENTI	GENOME POLYPROTEIN		26.7.07							
POLO DENZ	GENOME POLYPROTEIN	AYSIA M2)	567-75				0000 775	.,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1416.1440	1417,3441
POLO DE026	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN 1661)	74-108	728-777	561-662	041-401	0071-0071	7691-010	400.5101	
PPOLO DENZ?	GENOMOR POLYPROTED	DENGUE VIRUS TYPE 2 (STRAIN 1664)-PDK53)	74-108	778-777	C44-104	2	2007	7601-0101	400	
PPOLO DENZO	CENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (STRAIN D2-04)	721-771							
POLO DENTH	CENOME POLYPROTEIN	DENGUE VIXUS TYPE 2 (STRAIN TH-36)	497-546						9771 3171	1300
POLO DERU	GENOME POLYPROTEIN		2	778-777	8	2	087 L-092	76 14 15	1013:101	
POLO DEDEN	GENOME POLYPROTEIN	EAC)	313-24)	388-432			900	000. 776.	237. 017.	1415.1640
PROLO DENTE	CENOME FOLYPROTEIN	DENGUE VIXUS TYPE 2 (STRAIN PRISMSI)	74-108	728-777	27.675	201-10		0071-071	9651-0101	
PPOLO DENTI	GENOME FOLYTROTEIN	970)	441-497	35.38	22.12	200-200		4791.6091		
PPOLG DENZU	GENOME POLYPROTEIN	(STRAIN PUO-218)	614-663				1636 0476	1114 1110	30.00.000	1010
POLO DENO	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 1	830-872	939-993	1313-1419	2220-222	767-0007	100.000	2/47-0443	
PROLG DENA	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 4	957-90)	1260-1414	2514-2555	2701-2735	241-242	107.70		
PPOLO_EC11G	GENOME POLYPROTEIN	ECHOVINUS II (STRAIN GREGORY)	213-632		W. 51. 51.51	1446 1986	1789.1831			
PPOLG_EMCV	GENOME POLYPROTEIN	ENCEPHALGAPOCALDITIS VIRUS	176.1113	6161-7151	1014.1530	104.167	1447.170			
PPOLO EMCVB	GENOME POLYPROTEIN	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-8 NONDAME) 145-179	44.170	1076-117	1474.1570	1524-1577	1667.1708			
PPOLO EMEVO	GENOME POLITIKO JEUN	MONCO ENCENDATION OF CONTINUE (STRAIN 17A)	145-179							
PPOLO ENAGE	GENOME FOLTPROTEIN	MENCO ENCEDIAL OMYOCARDITIS VIRUS								
PPOLG ENAIGO	GENOME FOR THROTEIN	FOOT. AND MORTH DISEASE VIRUS (STRAIN A10-61)	231-355	194.338	578-612	1103-1153	1493-1528	2165-2200		
POLO PROVI	CENTRAL POLITICAL	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12)	220-254	193-337	1119415	1103-1164	1493-1528	2164-2199		
THE PARTY	CENTAL POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIDES)	221-255	1103-1153	1493-1528	3164-3199				
	CENTRE POLYBRUTEN	FOOT. AND MOUTH DISEASE VIRUS (STRAIN CI-SANTA PAU (C-S	07-128	693-728						
TOLO POS	CONTRACTOR OF VEROTERA	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CI)	221-255	20.313	119-45					
1000	CENOVE POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE I)	364-398							
1000		HOG CHOLERA VIRUS (STRAIN ALFORD)	640-693	979-979	682-369	1033-1070	1190-1235	1307-1343	1779-1820	2136-2170
POLG HCVA	GENOME FOLTPROTEIN		3466-3500	2315-2155	1667-2700	3057-3098	1152-3193	3406-3440		
	Carolina Santa	HOG CHOLERA VIRUS (STRAIN BRESCIA)	460-493	626-660	603-720	1033-1070	1173-1235	1779-1820	3136-2170	2311-2436
POLO HCV	GENORE FOLTER		2466-2500	2525-2559	1647.1708	3057.3098	3183-3195	3404-3440	1521-3562	
POLO HCVBK		INEPATITIE CVIBLIS/ICOLATE DK)	187.388	3310-3365						
POLO HCVEO	GENOME POLYTROTEIN	INCOMING CONTROL OF THE BOOK	68.00							
POLO HCWH	GENOME FOLVFROTEIN	META HILL C VINUS HISUCALE EVING								

	1000	All Virace (no bacteriophoges)	ABEAL	ARFA 2	AREAS	AREA 4	AREAS A	AREAS	AREA?	AREA I
	A CONTRACTOR OF THE PARTY OF TH	VIRUS	T	Γ	Γ					
7	PAUL LA CONTROL	HEPATITIS C VIRUS (ISOLATE H)			T					
	DENOME POLITICAL	HEPATITIS C VIRUS (ISOLATE HCV-476)	26.39							
	GENOME FOLYTROIEUN	JEBATITIS C VIRIS (ISOLATE HCT27)	216-270							
	DENOME POLYPROTED	LEBY TITLE C VIBILS (ISOLATE HCT18)	248-282				+	1		
PPOLO_HCVIRK	GENOME POLYPROTEIN	THE MAN CONTRACT OF THE MCV-KF)	157-398			1				
	GENOME POLYPROTEIN	ALCALILIS CAINCE ASCA ME UP 13)	357-398				1			
Γ	GENOME POLYMOTEIN	MEANING CALABOTA CONTRACTOR	364-398							
PPOLO HCVM	GENOME POLYPROTEIN	MEPATTIS C VIKUS (ISOLATIE INC.)	Γ	1716-1750	2042-2116					
Ī	CENTRATE POLYPROTEDY	MEPATITIS C VIRUS (1501.A LE MC-16)	T							
Ī	OSNOAGE BOX YPROTEDA	HEPATITIS C VIRUS (ISOLATE HC-JT)	1	31.	3003.3116	2468-2502	2538-2572			
T		HEPATITIS C VIXUS (ISOLATE HC:18)	1	200	Т	Т				
	GENOME FOLVING	HEPATITIS C VIRUS (ISOLATE JAPANESE)	7	2331-2369						
PPOLO HCVIT	GENOME POLYPROTEIN	SEES THE C VISITE (150) ATE HC-IT)	357.391	2331-2365						
PPOLG HCVTW	GENOME POLYPROTEIN	TECNISIS CHECK TO THE TENTON	157.198	1326-2369	1444-190)	٦	╗			
PPOLO HPAYS	GENOME POLYPROTEIN	PEPATITIS C VINUS (ISOLATE INITIAL)	Γ	\$61-101	703-237			117:13		
PROFIT HOLYA	GENOME POLYPROTEIN	HEPATITIS A VIKUS (STRAIN 24A)		101-135	203-237	170-904	1021-1055	1117-1151		
20.00	CENOAGE POLYPROTEIN	HEPATITIS A VIRUS (STRAIN 43C)		101-101	101.237	100.00	1021-1055	1117-1151		
TOLO PAY	Section of the section	HEPATITIS A VIAUS (STRAIN 118)				T	Т			
PIOLO HPAVC	CENCIAL POLITICAL	HEPATITIS A VIRUS (STRAIN CRUZE)		101:133	107-107					
PPOLG HPAVG	CENCRE FOR THEOREM	INEPATITIE A VIRUS (STRAIN GA76)	80-114	183-216			Т	1011		
PPOLO HOAVH	GENOME POLYPROTEIN	THE CALL OF THE LEGISLAND AND AND AND AND AND AND AND AND AND	143	101-135	203-237	10.90	Т	101-101		
PPOLO HPAVIL	GENOME FOL YPROTEIN	INCALLIS A VINOS (SINGING)	2	101.135	101-137	10.00		1103-1131		
PPOR O HOAVA	GENOME FOL YPROTEIN	HEPATITIS A VIRUS (STRAIN LA)	1	301.101	203-233	10.904	1021-1055	1103.1158		
20,000	GENOME POLYPROTEDI	HEPATITIS A VIRUS (STRAIN MBB)		101	207.241	86.69	1025-1059	1113-1155	1158-1198	
1	COLOR DE VOEDTEDE	SDGIAN IEPATITIS A VIRUS (STRAIN AGN-27)								
POLO POAVE	CENTRAL POR CORPUSA	SINGAN IEPATITIS A VIRUS (STRAFIN CY-143)	25			0.01				
POLO HOVIE	CENCER TOLITAGE	HUMAN RUINOVIRUS 14 (HRV-14)	1020-1034	183-1427	1					
PPOLO HOVIA	CENTRAL POLITICAL	INDIAN BINOVIRUS IA (PRV-1A)	362-396							
PPOLO IQVIB	GENOME POLITICAL	HIDAAN RIGNOVIRUS 18 (ARV-18)	387-421	163.804						
PPOLO HOY?	GENOME FOLTEROIEM	HERAAN REMOVIRUS 2 (PRV-2)	156-297	\$ 2	1332-1383					
PPOLO HAVIS	GENOME POLYPROJEM	INDIAN EHMOVINUS 69 (P.Q.V-89)	1366-1607							
PPOLO HUEVI	GENOME FOLYPROTEIN	MALAN ENTEROVINUS 70 (STRADY 161071)	359.397	176-917	1033-1088	1403-1441	1830-1974			
PPOLO INDVO	GENOME POLYPROTEIN	TOTAL STREET STREET STREET STREET STREET	134-168	180-291	475-524					
PPOLO IAEVI	STRUCTURAL POLYPROTEIN	AVIAN IN ECTIOUS BURSAL DISEASE VINES (STEEL)	I	211.35	339-576	940-1014	1409-1450	2461-2497	2719-2777	1762-2823
PROLE IAEVI	GENOME POLYPROTEIN	IAPANESE ENCEPHALITIS VIRUS (STRAIN SATE)	200	1007-000						
					410.014	980-1014	1409-1450	2463.2493	2719-2779	1782-1873
17341	CENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA(V))	77				Т			
1000			1112-3119		1	1010	1404.14%	2463-2497	1719-2777	2781-2823
	CENONIE BOT VPROTEDN	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAOARS912)	74-128	27.	are are		Т			
1			200		25.57	908.943	1337-1378			
MAIN O WAS	CENOAGE POLYPROTEDY	JAPANESE ENCEPHALITIS VIRUS (STRAIN MAKATAMA)			367.138	2464.2480	Г	2740-2778	1325-3359	3319-3423
200	CENCALE NOT VPROTEIN	KUNUN VIRUS (STRAIN MINKEIC)	14-100				Т	3536.2501	2947.3001	1003-1017
	COLORS TO VERTER	LANGAT WRUS (STRAIN TP21)	69-102	ŝ			Т			
PROLO LANY	OENOME PORTING		3102-3145							
	CENONS BOY VEROTEIN	LANGAT VIRUS (STRAIN YELANTSEV)	69-103	9						
מומו	CENOME POR VPROTEIN	רסתשיאפ נדר אוויחז (בין)	64-123	7	2					
POLO LIVE	CENTAGE POLYPROTEIN	LOUPING ILL VIRUS (STRAIN SB 536)	131-103		1000	3610 3686	1014-1005	1750-3341		
	CONONE DO VEDITEDA	MOSQUITO CELL FUSING AGENT (CFA FLAVIVIAUS)	2	7	2000		Т			
Proto Myry	CERCAMI POLITICAL	MUDICAY VALLEY ENCEPHALITIS VIRUS	67-115		197-181	101-41				
ALONG CHA	CENTRAL POLYMENT	DENITHODAL UM MOSAIC VIRUS	481-513		0012-1100		Τ		101.101	1147-1201
THOU THE	NATIONAL PROPERTY.	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	35-100	201-24	377.4	10		0104 1004	7101.1001	
PPOCO POCIN	UENOME POLITICALES		1488-1929		1948-1987	177-7017	Т	1607.1847		
	METOTA SA VALOTEN	POLIOVIRUS TYPE I (STRAIN MAHONEY)	Ī	046.10	10101	981-0051	Т	1610.161	1101.1M2	1904-1949
Proce Poets	ACTION OF VOROTEDA	POLIOVIRUS TYPE I (STRAIN SABIN)	3	6	1007-1102	200	Т	14.0	106-1140	1902-1947
MOLO 701.21	GENOME FOLITACIEM	POLIOVIRUS TYPE 2 (STRAIN LANSING)	843	10.00	1045-1100	1413-1447	٦.	1000		
PPOLO POLIW	GENOME FOLTFRUIER									

THE RAME PROLE PROTECTION PROLE PIVEA PROL			48.54.1	AREA 1	AREAZ	AREA 4	AREA 3	П	AREA ?	1803-1801
		POLIOVIRUS TYPE 2 (STRAIN W-2)	Ī						200	- X
		The state of the s		162-161	85138			Т		
			9.43	94-930	1044-1098	1412-1446	1498-1346	1607-1648	1803-1634	1001-1040
		POLIOVIRUS TYPE I (STRAINS PIALEONI)? AND PIALEON IZA[1]B)	176	196-930	1044-1099	1612-1646	1498-1546	1607.1648	1805-1839	1901-1946
		PLUM POX POTYVIRUS (STRAIN D)	164-208	441.503	721-769	115-867	921-955	1741-1782		
		PLUM POX POTYVIRUS (STIAIN EL ANAR)	116-157	784.01	1146-1197					
		PLUM POX POTYVIRUS (ISOLATE NAT)	164-308	403-433	440-503	727-768	814-873	T	1740-1781	
				403-437	440-502	727.768	914-666	26-026	1340-1381	Į
				134-468						
		PAPAYA RINGSPOT VIRUS (STRAIN P / MUTANT HA 5-1)	325-359							
		PAPAYA RINGSPOT VIRUS (STRAIN W)	125-359							
		PEA SEED-BORNE MOSAIC, AND (STRAIN DPD!)	253-315	355.389	539-519	318-818	101-786	1040-1177	1301-1627	1808-1860
			1971-2015	2379-2413	2712-2746	1870-2907				
		POTATO VIRUS Y (STRAIN C)	13:196	201-735	950-000					
		POTATO VIRUS Y (STRAIN HUNGARIAN)	144-181	21.735	101-163	94-106	1401-1441	1492-1526	1726-1772	1777-1818
			2272-2306							
		POTATO VIRUS Y (STANKIN)	140-196	211-245	261-101	103-103	1401-1441	1492-1526	1728-1772	1777-1818
			1929-1970							
		POTATO VIRUS Y (STILAIN O)	140-196	311-345	701-735	803-836				
		PASSIONFRUIT WOODINESS VIRUS (STRAIN SEVERE)	203-237							
		PASSIONFRUIT WOODINESS VIRUS (STRAIN TIP BRIGHT)	103-237							
		PARSAIP YELLOW FLECK VIRUS (ISOLATE P-121)	20-328	2411-1111	1379-1413	1836-1699	1661-0661	11703-1777		
			106-143	673.707	719-773	975.1009	1404-1438			
		76)	13-49	1024-1070	1779-1813	1890-1924				
		SWINE VESICULAL DISEASE VIRUS (STRAIN UKGA1771)	13-49	1024-1070	1390-1924					
		TICK-BORNE ENCEPHALITIS VIRUS (STRAIN SOFIIN)	69-140	221.172	431-465	1158-1192	1431-1433	1929-1966	3183-2216	1515-2590
			8	1051-3093	3100-3143					
		TICK-BORNE ENCEPHALITIS VIRUS (WESTERN SUBTYPE)	091-99	22:102	431-465	1156-1192	1431-1492	1913-1966	1836-2591	1967-3001
			1001-1001	3053-3094	3102-3145					
	PHALOMPELTTIS VIRUS (S	TOBACCO ETCH VIRUS	73-124	164-232	540-584	720-782	128-925	1148-1192	09117111	1494-1535
				1343-1381	1792-1826	2395-2434	2787-2821			
		12		1161-181	1601-1635					
		THEILER'S MUNIDE ENCEPHALOMYELITIS VIAUS (STRAIN DA)	1304-1336	1411-1316	1599-1643					
		THERE EXIS MUNICHE ENCEPHAL CONTELTTIS VINUS (STIVAIN GOVIL) 1366-1340	1306-1340	1413-1518	1601-1633					
			216-259	314-362	494-528	768-439	1403-1477			
		TOBACCO VEIN MOTTLING VIRUS	7	408-449	20.704	22	\$7.50 \$2.50	969-1017	1011-1072	1643-1677
			1686-1735	2316-2374	2701-2749	2814-2848				
		WATERMELON MOSAIC VIRUS II	64 -105	202-236				┪		
		WEST MILE VIRUS	╗	207-251	187-881	73.i80	1413-1449	2461.2495	333.336	=======================================
П			1110-1111	3115-3436		7		Т		
			418-452	523-563	720-768	7	2211-2276	7	2938-3996	1097-3143
		A 17D-204)		335.563	728-768	138-1444	111:1136	2477-2565	79.10.78	303.75
٦			75-116	410-453	\$25-563	71-74		╗		
PPOLIN EEVYT GENOME POLYPROTEIN		POLIOVIRUS TYPE I (STRAIN MAHONEY)		1047-1103	1415-1469	1501-1349	1610-1651	100-1042	1904-1949	
	PROTEIN	IUS (STRAIN TRINIDAD		191-932	1945-1979					ļ
	PROTED	V61 FIV)	10.544							
	PROTEIN	FELDAR CALICIVATUS (STRAIN F9)	50-0	369-410	916-1020	1937-1061				
Γ	PROTEDI		971-179	1136-1177						
Ī	PROTEDI		330.379							
Γ	PROTEIN	HEPATITIS E VIRUS (STRAIN MYANGAR)		1139-1184						
Т	PROTEIN	HEPATITIS E VIRUS (STRAIN PAKISTAN)	117.370	1136-1176						
PPOLY ONDIVIO MONSTRUCTURAL POLYPROTEIN	PROTEIN		119-514							

		Att Virgos (no becteriophs (**)	Γ	Γ	A A S A	ABEA 4	AREA :	ABLA		
PCCENE	ALLMOTIS]	7010	344.3502				2 2 2	
TILEMAKE	PROTEIN AT BOX VISUTEDA	MO-NYONG VIRUS (STIVAIN GULU)	1		237-007	1657-1716				
POLN RODY	NONSTRUCTURAL FOR LYNDIES		Ť							L
POLN RRVN	NON-STRUCTURAL POLITICIES		626-63	728-1967	20197					
POLN RRVT	NONSTRUCTURAL POLITICAL		397-631	601-001	1361 0161	201.000				
POLN RUBY	MONSTRUCTURAL TOURISMENTEN	£	Т							
POLN SFV	NONSTRUCTURAL POLYPROTEIN	T		1401-162	1961.1996	2444-2478				
POCH SOCIO	MONSTANCE IN ALL BOLLYBOTEN	E OCKELBO / STRADI EDSBYN 82-3)		1046-1064	2403.2476	-				
POLN SPOY	NOTES INC. 1 DOL VPROTEDI	T	2761-164	1						
HOLL ENV	MONSTANCE CONTRACTOR		EA-A33							
POLS EEEV	MA REPLICASE POLITROLES	ALITIS VIRUS	37.40	16-316				_		
PPOLS EEEVI	STRUCTURAL FOL TRADIEN	(STRAIN VAJ)(TEN BRO	79-67	26-616		-				
PPOLS EEVVI	STRUCTURAL POLYPROTEIN	VENEZIJEJ AN EQUINE ENCEPHALITIS VIRUS (STRAIN TC-41)	1216-1250					-		
PPOLI EEVVT	STRUCTURAL POLYPROTEIN	DVD	1216-1250			1				
PPOLS BDVS	STRUCTURAL POLYPROTEIN	A MAN THE CTIONS BURSAL DISEASE VIRUS (STRAIN 12/70)	134-161	21.28	436-520					
PPOLS INDVA	STRUCTURAL POLYPROTEIN	A VIAN INSECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRAL 134-168	134-168	231-226	3					L
PPOLS IBDVC	STRUCTURAL POLYPROTEIN	AND THE POST OF STREET OF STRAIN CU-1)	134-161	231.216	470-523				-	
PPOLS BIDVE	STRUCTURAL POLYPROTEIN	A COAN DESCRIPTIONS BITTE AL DISEASE VIRUS (STRAIN E)	134-161	311-286	20.78					ļ
PPOLS DIDVP	NOWSTRUCTURAL PROTEIN VP4	A CAN PRECITIONS BURKAL DISEASE VIRUS (STLAIN PBG-94)	115149	200	431-504					
PPOLS IBDVS	STRUCTURAL POLYPROTEIN	AVIAN MECTICALS BURSAL DISEASE VIRUS (STRAIN STC)	174-168	249-283	48.53					1
PPOLS DWV	STRUCTURAL POLYPROTEIN	INTERTRICK PANCE ATIC NECROSIS VIXUS (SENOTYPE JASPER)		23-715						
PROLS DWW	STRUCTURAL POLYPROTEIN	IN ECHIODS (STAIN NI)	316-786					1		1
PPOLS CHONG	STRUCTURAL POLYPROTEIN	TARELLIDOS FONDES (STRANGELD)	1204-1238							1
PPOLS RAYS	STRUCTURAL POLYPROTEIN	CONTONO VIDER (STRAIN 211970)	35.68							1
POLS REVN	STRUCTURAL POLYPROTEIN	ACCS ALVEN VIEW (CTE ATM NESSO2)	369-403	939-973						+
PPOLS RAYT	STRUCTURAL POLYPROTEIN	KOSS (LYEN VINCE) STORY (1997)	619-973							+
PPOLS BURNH	STRUCTURAL POLYPROTEIN	LOSS BUYER VIRUS (STINAIN 199)	969-1036						1	+
PPOLS RUBYR	STRUCTURAL POLYPROTEIN	RUBELLA VICUS (VACCINE SINGLE) IN 1973	900.006							\downarrow
PPOLS RUBYT	STRUCTURAL POLYPROTED	RUBELLA VIACA (*ACLINE SINGERIA	900.006						1	+
PPOLS STATEO	STRUCTURAL POLYPROTEIN	CANNELLY VICE (CITATOR OCKEL NO / STRAIN EDSBYN 02-5)	362-396							+
PPOLS SINDV	STRUCTURAL POLYPROTEIN	Commercial (STEAMS HOSP AND HOLP)	362-396					+	1	+
PPOLS SINDW	STRUCTURAL POLYPROTEIN	Shanne walls own D TYPE SR DERLYED FROM STRAIN AU19)	34-68							+
PPOLS WEEV	STRUCTURAL POLYPROTEIN	WESTERN SOUTH ENTERHALTIS VIRUS	913-947							1
PPOL BAEVM	STRUCTURAL POLYPROTEIN	BAROON ENDOCENDES VIRUS (STRAIN M7)	43-80	676-743	704-832	1001-1042		+		+
PPOL_BLVAU	POL POLYPROTEIN	ROVINE I ELIKEMA VILUS (AUSTRALIAN ISOLATE)	625-673					1	1	+
PPOL_BLVJ	POL POLYPROTEIN	BOVING LEUKELIA VINUS (IAPANESE ISOLATE BLV-1)	635-473			1	$\frac{1}{1}$	-	1	ŀ
PPOL_CAEVC	POL POLYPROTEIN	CAPEDIG ARTHURIS ENCEPHALITIS VIRUS (STRADY CORK)	179-934			-	\downarrow	1		ŀ
TOL CAND	POL POLYRUIGAN	CAIL BLOWER MOSAIC VIRUS (STRAIN DAY)	1			76.5	90,400	1310-1351	-	-
Prof. COYN.	ENZTHALIK FOLITROLEM	CONDITION YELLOW MOTTLE VIRUS		107-767						-
Prof. EAV	TOTALING PARTIES.	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE 1969)	8	1017-103	\downarrow	+	-			H
PPOL EIAVC	TOT TOT TOT TOT TOT	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL22)	30.76	201-701	1	-	-			L
POL ELAVI	TOUR TOUR VANCOUR IN	EQUINE DIFFICTIOUS AMENDA VIRUS (ISOLATE WYOMING)		CGI-IZOI	18	+	-			H
POC. PENV	TOT TOTAL THE PARTY OF THE PART	FELINE ENDOGENOUS VIRUS ECE!	8	400		-	-			
POL PINTE	TOTAL POLICE OF THE PARTY OF TH	FEI DE DOMINODEPICIENCY VIRUS (1SOLATE PETALUMA)			1	1	1	-		
TOTAL PARTY	Current and and and and and and and and and and	FELINE DOALMODEFICIENCY VIRUS (ISOLATE SAN DIEGO)	428-4/3			+	-			H
POL HATE	POLINE VAROTEN	FELING INAUNODEFICIENCY VIRUS (ISOLATE TMZ)		78		\downarrow	1			-
	SATISFIED OF VALOREDA	FIGWORT MOSAIC VIRUS (STRAIN DXS)			711		-			L
ALC: LOVE	AND AND AND AND AND AND AND AND AND AND	HUNGAN SPUMARETROVIRUS (FOAMY VIRUS)		87-1-1		-	-		-	L
אסר פאר	POL POR VERGITERA	GIBBON APE LEUKEMIA VIRUS	2			-	-			
TOL RILLY	POLYBOTEN	HUMAN T-CELL LEUKEMAN VIRUS TYPE I (STNAIN ATK)	200	\downarrow	-	1				
מורוני בייניייייייייייייייייייייייייייייייי	POS POS VPROTEDN	HUDAN T-CELL LEUKENDA VIRUS TYPE I (CALIBBEAN ISOLATE	E 976-711	777	$\frac{1}{1}$	1	-	-		-
2	NO POLICED	HUMAN DOMINODEFICIENCY VIRUS TYPE I (ARVZ/SPZ ISOILATELXI)			1	+	+	-		H
						•				

	A C C A CONTRA	All Vocace (ne beclerhabeter)	•							
PH P HAMP	PROTEIN		AREAL	AREAL	AREA?	AREA 4	AREA 5	ANEA	AREA?	AREAI
PPOL HVIBR	POL POLYPROTEIN	MINGAMODEFICIENCY VALUS TYPE I (BHS ISOLATE)	\$13.549	969-319						
PPOL HVIEL	POL POLYPROTEIN		313-549	918-676						
PPOL HVIID	POL POLYPROTEIN	HUBGAN DIDMUNDDEFICIENCY VIRUS TYPE I (ELI ISOLATE)	500-536	626-663						
PPOL HVID	POL POLYPROTEIN	7	20.537	199-909						
PPOL HIVING	POL POLYPROTEDY		\$65.541	99-019						
PPOL HVINON	POL POLYPROTEIN	٦	476-536	()						
PPOL HIVINS	POL POLYPROTEIN		340	100-606						
PPOL HVIND	POL POLYPROTEIN	링	Т	****						
MOL HVIOY	POL POLYPROTEIN	HUMAN BOUNDERICENCY VINUS TITE I (NOK ISOLATE)		777 707						
POL HVIPV	POL POLYPROTEIN	T.	10.10	200						
POL HVIDA	POL POLYROTEIN	Té	717-005	177.47						
MAC HAID	FOL POLITIKUIEIN	75	Т	177						
TOT HAIE	POL POLITIKO I EIN		Τ	197 957						
FOL. HYZBE	POL POLYPROTEIN	5	Ī	00-070						
PPOL HYZCA	POL POLYPROTEIN	Т	Т	Т	100					
POC, HAZDI	POL POLYPROTEIN	HUMAN DANUMODE FICIENCY VIRUS 17PE 2 (150LATE CANZ)	BC-XC	T	977-909					
PPOL_HY2D2	POL POLYPROTEIN	П	203-400	671-705						
PPOL, HYZO!	POL POLYPROTEIN		376-410	414.526	338-377	033-487				
PPOL, HYZNZ	POL POLYPROTEIN	31	464-562	613-667						
PPOL_HYZRO	POL POLYPROTEIN		46.78		464-529	63,667				
PPOL_HV75B	POL POLYPROTEM		_		634.468					
PPOK, HV2ST	POL POLYPROTEDM	S.			633-667					
POL DHA	POL POLYPROTEIN	E 2 (ISOLATE ST)		522-577	653-487					
PPOL_ISRV	PUTATIVE FOL POLYPROTEIN	HAMSTER INTRACISTERMAL A-PARTICLE	462-503							
PPOL_MALVAK	POL POLYPROTEIN	SHEEP PULMONARY ADENOMATOSIS VIRUS	190-231							
PPOL MALVAV	POL POLYPROTEDI		325-392							
POL MENTS	POL POLYPROTEIN		677-764							
PPOL MALVIF	POL POLYPROTEIN		682.749							
PPOL MA.VIP	POL POLYPROTEIN		662.749							
PPOL NA. VA4O	POL POLYTROTEIN	FILEND MONTHE LEUKENIA VIRUS (ISOLATE PVC-211)	47.70							
PPOL NA VIED	POL POLYPROTEIN		677.746							
POL MENTE	POL POLYTHOIR IN	Ī								
ALC: PORS	POL POLYPROTEIN	A VIRUS (STRAIN KAPLAN)	62.139							
POL ORAN	POL POLYFROTEIN		9	272						
Prof. RSV9	POL POLYPROTEIN		470-505	155.910						
PPOL RTBV	POLYPROTEIN	ROUS SARCORA VIRUS (STRAIN PRACUE C)		2 6	101	1	.,,		9401 9001	9071 3071
FOLKIBVE	POLITICOLEM	CONTRACTOR OF THE STATE OF THE		T	101.133	76.94	136.363	207.07	101.00	1401.1410
17.0	POL POLYPROTEIN	T	=	,	404-535					
PPOL SIVAI	POL POLYPROTEIN		Π		494-530					
PPOL SIVAS	POL POLYPROTEIN		31:36	637-678	111-111	938-979				
PPOL SIVAG	POL POLYPROTEIN	E	45.24							
PPOL_SIVAL	POL POLYPROTEDM	SDAAN DOADNODEFICIENCY VIRUS (AGAS) ISOLATE)			143-783					
PPOL SIVAT	POL POLYPROTEIN	CLONE GR		476-515	641-700	943-983	1020-1054			
PPOL SIVEZ	POL POLYTROTEIN			157.781						
PPOL_SIVGD	POL POLYPROTEIN	•	\$27.561	119-979						
PPOL_SIVAI	POL POLYPROTEIN		9-33	446-483	629-673	103-127	912-946			
PPOL, SIVACK	POL POLYPROTEIN	ATE)	485-519	654-688						
PPOL SIVS4	POL POLYPROTERY	SPICAN DIPAUNODEFICIENCY VIRUS (KOW ISOLATE)		119-059						
PPOL SIVSP	POL POLYPROTEIN	3		617-651						
TOL SOCIAL	POL POLYPROTEIN	BI/BCI I ISOLATE)	٦	620-654						
PPOL SRV1	ENZYMATIC POLYPROTEIN	SOVBEAN CHOOKOTIC MOTTLE VIRUS	23-23	373-416						

THE NAME FROL, VILV FROL, VILV FROL, VILV FROL, VILV FROL, VILV FRATA, MACTO FR	ROTH	VIRUS	747							
Z Q Q Q Q Z	CALL COMPANY IN			578-613				1		
Z Q Q Q Q Z	ALL MALLY BOX	SOUTH RETROTING OFF	420-524	174-929						
Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z	POLICE PO		760 637	174.070						
Z Q Q Q Q Z	TOUR CONTRACTOR		200.00							
	CLICATION CO.	VISNA LENTIVIRUS (STRAIN 1514/CLONE LVI-1KSZ)	276-403							
	TOLITACIES. TICOSTANDONE DO 100	HIDIAN CYTOMEGALOVIRUS (STRAIN AD169)	201-201							
ATT MATTYO ATT MATTYO ATT MATTYO ATT MATTYO		MOLISE MANDALARY TUMOR VIRUS (STRAIN BR6)	133.200							
AT MATVO AT MATVO AT MATVO	PROTEIN PR73	MACHINE MANDRARY TUMBR VIRUS (STRAIN CHI)	20.73							
ATL BOTTYO ATL BOTTYO PYIO CEVEM	PROTEDN PR73	LOUIS MANAGEY TIMOR VIRUS (STRAIN GR)	54-19	143-301						
ATA MATTYO	PROTEIN PRTS	CONTRET LANDALARY TIMOR VIRIS (STRAIN GR.)	145-204	270-311						
WO GW	PROTEDY PAT)	MOUSE PARAMENT TOTAL CONTRACTOR (CTEAN) CR.	141.200	266-307						
2000	PROTEIN PRT3	MOUSE MANAGEMENT TOWNS VINCE (1100)	500							
	POLYNEDAIN PRECURSOR	BOARRYX MOIL CYTUTLASMIC FULTIMEDADES	2							
PPYTED NOVAS	POLYHEDRIN	AUTOGRAPHA CALIFORNICA PUCLEAR POL HEBROSIS	3							
WAYAN MAYAN	POLYIEDRIN	AGROTIS SEGETUM NUCLEAR PALTICUMOSIS VINOS	27.6							
PEND NEVBS	POLYNEDADA	BOMBYX MONI NUCLEAR POLYMEDROSIS VINUS				_				
PEND MAY D	POLYNEDRIN	BUZURA SUPPLESSAUA NUCLEAR PULTHEDRUSIS VINUS								
2000	POLYMETRIN	LYMANTHUA DISPAR MULTICATSID MULLEAR FOLTHERMOSIS								
TALL STATE	POLYMEDIUM	MANGSTRA BRASSICAE NUCLEAR POLYMEDROSIS VIRUS								
TOTAL COLUMN	Nacional Control	ORGYIA PSEUDOTSUCATA MALTICAPSID POLYHEDIUSIS VIKUNI 1947								
PYTO PETOS	TOTAL STATE OF THE PARTY OF THE	ORGYTA PSEUDOTSUGATA SINGLE CAPSID MUCLEAR POLYNED				-				L
PYND REVER	POLITICIAN.	PANOLIS FLANDÆA MULTIPLE NUCLEOCAPSID POLYHEDROSIS	7							L
PYND NEVSE	POLTHEUM.	SPODOPTERA EXIGUA NUCLEAR POLYHEDROSIS VIRUS (STRAIN 14-48	14.6							L
PAND WASE	POLYNELIA	SPODOPTERA FRUGIPERDA NUCLEAR POLYHEDROSIS VIRUS	14.6				1			
PYND NOVSIL	POLYHEDIUM	SPODOPTERA LITTORALIS MUCLEAR POLYMEDROSIS VIRUS	17-51			-	-	1		
PRASK MSVKI	POLYPRING	KIRSTEN MUNDNE SARCOMA VIRUS	143-176					-		L
PREV BIVIT	TRANSFORMING TROTTERS AT	BOVINE DAMINODEFICIENCY VIRUS (ISOLATE 127)	3:			1	1	-		L
PREV ELAVO	MEV PROTEIN	FOURIE DIFECTIOUS ANEMIA VIRUS (CLONE 1169)	21-89					1		L
PREV, ELAVC	REV PROTEIN	EQUINE INFECTIOUS ANEARA VIRUS (CLONE CL22)	5					-		ļ
REV ELAVY	REV PROTEIN	EQUINE INFECTIOUS ANEAUA VIRUS (ISOLATE WYOMING)	91119							ļ
PREV HVII2	REV PROTEIN	HUMAN IMMUNODEFICIENCY VIRUS TYPE I (CLONE 12)				+	+	+		L
MEV HVIA	NEV PROTEIN	HUMAN INDIAMODEFICIENCY VIRUS TYPE I (ARVZISTI ISOLATE				1		-		L
PREV HVIBI	NEV PROTEIN	HUBLAN DOLUNODEFICIENCY VIRUS TYPE I (BIIIO ISOLATE)				+		-		L
PREV HVIBI	REV PROTEIN	HIMAN DOMINODEFICIENCY VIRUS TYPE I (BHS ISOLATE)	25-59							L
PREV HVIBN	NEV PROTEIN	HIMAN DAMINODEFICIENCY VIRUS TYPE I (BRAIN ISOLATE)	22-59					-		1
PREV HVIBA	NEV PROTEIN	INDIAN INDIANNOBEFICIENCY VIRUS TYPE I (BRU ISOLATE)	35-69				-	-		1
PREV HVIEL	REV PROTECT	HIBLAN BOADWOOEFICIENCY VIRUS TYPE I (ELI ISOLATE)	33-64							1
PREV HVIND	REV PROTEIN	MANAN BARBODE SICIENCY VIRUS TYPE I (HXB1 ISOLATE)	15-49							1
PREV HVID	REV PROTEIN	HAMAN BOATHODEFICIENCY VIRUS TYPE I (INI) ISOLATE)	29-63				4			1
PREV HVIR	AEV PROTEIN	MANAN BANDODEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	31-64			_				\downarrow
PREV HVIMA	REV. PROTEIN	LIABLE AND MODERICIENCY VIRUS TYPE I (NAL ISOCATE)	\$ 1							1
PREV HVINO	NEV PROTEIN	MANAN ILAG MODEFICIENCY VIRUS TYPE I (A.M. ISOLATE)	2							1
PREV HVIOY	REV PROTEIN	INDIAN INDIAN MODEFICENCY VIRUS TYPE I (OVI ISOLATE)	33-69			-				1
PREV HVIPV	AEV PROTEDS	HABIAN INDIGINODEFICIENCY VIRUS TYPE I (PV22 ISOLATE) AN	135-69			1	+	-		1
PREV HVIST	REV PROTEIN	HUMAN DERENODEFICIENCY VIRUS TYPE I (SF1) ISOLATE)					1	+		╀
PREV HVISC	REV PROTEIN	HUMAN INDRINODEFICIENCY VIRUS TYPE I (SC ISOLATE)	\$ *			+	+			1
PREV SIVAI	REV PROTEIN	SIMIAN INDICHODEFICIENCY VIRUS (AGNISS) ISOLATE)	<u>-</u>				+	+		ļ
PREV SIVAD	REV PROTEIN	SPAIN BOARNODEFICIENCY VIRUS (AGMS) ISOLATE)	74.7			1	$\frac{1}{1}$	-		1
PREV SIVAL	nev Protein	STATIAN DANDMODEFICIENCY VIRUS (ISOLATE AGM / CLONE GR					+			1
PREV SIVAT	REV PROTEIN	SIMIAH DARITHODEFICIENCY VIRUS (TYO-1 ISOLATE)	18.75							\downarrow
PREV SIVCZ	AEV PROTEIN	CHD. PANZEE DANIMODEFICIENCY VIRUS	33-43							ļ
PREV VILV	NEV PROTEIN	VYCHA I ENTIVIBUS (STRAIN 1514)	21-62							1
PRIDI ASPAD	AEV PROTEIN		7	10.133	635-483					1
MAI EBV	ALBONACE EOSIDE-DIPHOSPIKATE REDUCTASE LAN	AN ACTUAL STATE CONT. CATALOG SOCIETA	213.247	649-723						4

37.300		All Virgan (no beteriosbers)								
7. C. M. M.	PROTEIN		AREAL	AREA 1	AREA?	ABEA 4	4854	ABEA 6	AREAL	AREAS
1200	PROPERTY EAGINE APPLICATE REDICTASE LAS	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	637-668							
TO THE PERSON		EQUINE HEAPESVIRUS TYPE I (STILAIN AD4P)	24-110							
2007			334-365							
PRIR! VACCV	REDOMINITE EDSIDE DIPHOSPHATE REDUCTASE LAR	VACCIMIA VIRUS (STRAIN COPEMIAGEN)	367-402							
PRIR! VARV	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	367-402							
PAURI VZVD	ALBONUCLEOSIDE-DIPHOSPHATE REDUCTASS LAR	VARIOLA VIRUS	367-402							
PAUL EBY	REBONUCLEOSEDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA-ZOSTER VIRUS (STRAFN DURIAS)	123-257							
PACES HIS VIB.)	ALBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SALA	EPSTEIN-BARR VIRUS (STRAIN 895-8)	19-137							
PRUTAL HSVES	PUBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMA	BOVINE HERPESVIRUS TYPE I (STRAIN 34)	101-135							
PRURA HSVSA	RUBONUCL EDSIDE-DIPHOSPHATE REDUCTASE SMA	EQUINE HERPESVIRUS TYPE I (STRAIN AB4P)	106-140							
PRINC STVKA	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SNIA		125-159							
PRINT VACCC	REMONICE EOSIDE DIPHOSPHATE REDUCTASE SMA	SHOPE FIBROMA VIAUS (STRAIN KASZA)	20173							
PELES VACCE	RIBONUCI EOSIDE DIPHOSPHATE REDUCTASE SXIA		98-132							
VACOV	ALTHORACT FOSIDE DIPHOSPHATE REDUCTASE SMA		98-132							
Pain VARV	IRIBONALCI FOSIDE DIPHOSPHATE REDUCTASE SMA		201-86							
PRL I MSV2H	AUBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SAVA		101.11							
VACOV	NEUROVINIA ENCE FACTOR	HERPES SIMPLEX VIRUS (TYPE 2/STRAIN HGS2)	171-312							
PLP4 VARV	RNA-POLYMERASE-ASSOCIATED TRANSCRIPTION S	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENHAGEN	116-150	465-540	757.791					
PRIOL VACCC	RNA-POLYNGRASE-ASSOCIATED TRANSCRIPTION S	VANOLA VIRUS	41-78	16-130	445-540	187.781				
PRIO VACCV	DNA.DIRECTED RNA POLYMERASE 147 KD POLYTE	VACCINIA VIRUS (STRAIN COFEMIAGEN)	143-191	622-656	754-791	934-948	1006-1057			
VAN IONA	DNA DIRECTED RNA POLYMGRASE 147 KD POLYPE	VACCINIA VIRUS (STRAIN WR)	143.291	622-656	754.791	934-988	1024-1058			
PRIOT CAPVE	DNA DORECTED RNA POLYNOBRASE 147 KD POLYPE	VARIOLA VIRUS	343-291	622-656	184.791	934-988	1006-1057			
Paros Cowex	DNA-DIRECTED RNA POLYNGRASE 133 KD POLYPE	CAPRIPOXYIRUS (STRAIN KS-1)	09-61	114-155	589-630					
PILO2 VACCV	DNA-DRECTED RNA POLYMERASE 133 KD POLYPE			359-400	133-474					
PRIOZ VARV	DNA-DIRECTED RNA POLYMERASE 133 KD POLYPE	S (STRAIN WR), AND (STRAIN COPENHAGEN)	211-245	359-400	13-674					
PRIOR VACCC	DNA-DIRECTED RNA POLYNGRASS 132 KD POLYPE		\$11.245	159-400	133-874					
PLOW VACCV	DHA-DIRECTED RNA POLYNGRASE 35 KD POLYPEP	ENHAGEN)	62-116							
PRIOR VARV	DNA-DIRECTED RNA POLYMERASE 15 KD POLYPEP	(STRAIN WR)	62-116							
PRPOS VACCC	DNA-DIRECTED RNA POLYMERASE 15 KD POLYPEP		63-116							
PLPOS VACCV	DNA-DIRECTED RNA POLYNGRASE 30 KD POLYPEF VACCIMA VIRUS (STRAIN COPENHAGEN)	VACCIMIA VIRUS (STRAIN COPENHAGEN)	=							
PRPOS VARV	DNA-DIRECTED RNA POLYMERASE 10 KD POLYPEP	VACCINIA VIRUS (STRAIN WR)	-							
PILOS VACCV	DNA-DIRECTED RNA POLYNGRASE 30 KD POLYPEP	VARIOLA VIRUS	-	Ĭ						
PRIOR VARV	DNA-DRECTED RNA POLYMERASE 11 KD POLYPEP	I (STRAIN WR), AND (STRAIN COPENHAGEN)	35.50							
PRPOT VACCV	DNA-DIRECTED RNA POLYAGRASE 23 KD POLYPEP	VANOLA VIRUS	65.52							
PILOT VARV	DNA-DIRECTED INA POLITICIASE 19 KD POLITICA	T								
PRIPOR LELY	DNA-DIRECTED MA FOLVMEANS IN RU FOLVTER	FORTAL MAIN	25	1731.1750	1058.1003	3100.3157				
7700	ANA-DIRECTED BAY BOX WAS A CE	FOLIME ARTENITIS VIRUS	Τ	1477-1518	1633-1673					
TANK TANK	BNA. DIRECTED BNA POLYMERASE SUBUNIT PI	MILUENZA A VIRUS (STRAIN MANN ARBONNES)	Т	279-313						
NICE INDIA	ANA.DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN ABEUING/11/54)	171-243	279-313	150-391					
PARPI IAGIZ	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI		171-242	279-313						
PREPI IMAGO	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	DIFLUENZA A VIRUS (STRAIN ANGULLARARYLAND/104/17)		179-313						
PRAPI LAHTTE	INVA-DIJECTED RNA POLYMERASE SUBUNIT PI	DIFLUENZA A VIRUS (STILADI AÆQUINEALONDONI (1671))	160-242	279-313						
PILLE LAKE	MA-DIRECTED RNA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STIVAIN AÆQUINIE/TENNESSEE/SNS)		179-313						
PRUPI LAKOR	ANA-DOLECTED ANA POLYMERASE SUBURIT PI	INFLUENZA A VIRUS (STRAIN A/RIEV/5979)		279-313						
MUP! WE!	RNA-DIRECTED RNA POLYMERASE SUBUNIT PI	DIFLUENZA A VIRUS (STRAIN A/KOREA/426/68)		279-313						
PULL IALES	RNA-DIRECTED RNA POLYMERASE SUBLIMIT PI	INFLUENZA A VIRUS (STILAIN AALENINGRADVI)497)	П	3.50						
PUDI ME	RNA-DIDECTED RNA POLYMERASE SUBURIT PI	DELLENZA A VIRUS (STIAIN ALENINGRADVI)4/17/57)	٦	3.5						
MAN INW	MAN-DIRECTED NNA POLYNGRASE SUBUNIT PI	RFLUENZA A VIRUS (STRAIN ALENINGRADVI)447/97)	T							
PRUDI INVES	RNA-DIRECTED INA POLYMERASE SUBLIMIT PI	INFLUENZA A VIRUS (STRAIN AMALLARDMEW YORKA73071)	Т							
PRILPI IANTA	RNA-DIRECTED RNA POLYMENASE SUBUNIT PI	INTLUBAZA A VIRUS (STRAIN AAGAMHISAMI)	192-16	11.11				1		
PARTI INPUE	RNA-DDECTED RNA POLYMERASE SUBURIT FI	INFLUENCA A VIAUS (SIRAUM ANTIMADA)	7			1				

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PCCLA!		VIRUS	166-242	179-313						
THE PARK			171-242	179-313						
PERPITATION		OTAMINA	171-242	179-313						
100		Γ	171-242	116-911						
Ent in a			160.242	279-313						
PARENT LAUNT		INTLUENZA A VIRUS (STRAIN A TESONATATIVAL)	168-242	118-313						
14740		1126/12)	117-242	179-313						
MOZAL MAGO	RNA DIRECTED BNA POLYNGBASE SUBURIT PI		13.22	179-313						
1477	RNA DOBECTED RNA POLYMERASE SUBUNIT PI	Ī	27.5	279-313						
7464	ANA DIRECTED ANA POLYMERASE SUBLIMIT PI		208.249							1
TRACT INC.	AND MARCHED BINA POLYMERASE SUBURIT PI	Т	306.348							
TANK!	THE PARTY OF WASHACE SUBSECT PI	Mary								
PROFILE DISE	MA-DUELIEU MAN INC. INC. ALLEGA PIL	٦	407-807	745 647	201.363					
PEUT DECT	RNA-DIRECTED MAN POLITICANS (S. C. DILINGT P.		2000	00000						
PREPE LANGE	INA-DILECTED MAR POLIMENAS COMPANY	ARBORUMO)	110-144							
PRUPY IADHO	RNA-DIRECTED IDAA POLTIMEAANE SOUGHT	V4-10)	110-144	177-2118		1	+			L
PRAIL'S LAFFA	RNA-DIRECTED RNA POLYMERASE SUBURIT FA	INTELLEGIZA A MARIE CETTA AN AMOUNT PLACUE VIRUSAOSTOCK 110-144	110-144	177-218						
PRRP2 LAGUE	RNA-DIRECTED RNA POLYNGRASE SUBUNTT P?	INCLUENCA A UNOS (STICKLES A LA PARA PARA AND/DOUT)	110-144	177-218						
MAN IAMO	RNA-DESCRED RNA POLYMERASE SUBUNIT P?		110-144	177-218						1
	BNA DIRECTED RNA POLYNCRASE SUBURIT P?	T	110-144	177.216						1
PIUVZ IANIE	ALL DIRECTED BNA POLYNGBASE SUBUNIT PS	33552300)	1	177.218	-					
TUES INCO	AND PRESENTED BUY DOLY WORLASTE SURUMUT P.			11.311						_
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PLUM LANTE	ANA-DIRECTED RNA POLTMENASII SUBUNII 72	_	110-144	177-2118		$\frac{1}{4}$				L
PLUT LATE	RNA-DIRECTED RNA POLYMERASE SUBURIT PT	ALBERTAII979)	110-144	177.218						
PRINT LAPUE	RNA-DERECTED RNA FOL YACEASE SUBUNIT PZ		₹ 1011	177-316			1	1		
PREPT LARUD	ANA-DIRECTED RIVA POLYNGRASE SUBUNIT PZ		110-144	177-218			1	\downarrow		L
PREPT LASON	AWA-DOLECTED RWA POLYMERASE SUBUNIT PT	Г	110-144	177-218			-			-
PRINT WITH	ANA-DIRECTED ANA POLYNERASE SUBURIT PA	STATE OF THE STATE	110-144	177-218			1		\downarrow	ļ
PREPT LAWY	ANA-DIRECTED ANA POLYNGIASE SUBURILLY	Г	110-144	177-318						L
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14711	RNA-DIRECTED RNA POLYNGRASE SUBURIT PS		10.14	177-218			_			\downarrow
MARY IAZTE	INA-DIRECTED RNA POLYNGRASE SUBUNIT P?	DOLUENZA A UKUS (STICKLE) A KUMPATENAS SEEDATI)	10-14	177-218			-			1
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200	BNA. DIRECTED RNA POLYNGRASE SUBUNIT P2	INCLUENZA B VIXIOS (STICAIN BOANN ANBOUNDED INCLUENZA BOLINGO	2	349-383						\downarrow
7777	BNA DRECTED BNA POLYNGRASE SUBUNIT P2	INFLUENCA B VIDUS (STIMAIN BASINGATURE)	3	363-402	473-514	107-755				4
C. C. C. C. C. C. C. C. C. C. C. C. C. C	BNA.DIRECTED RNA POLYNGBASE SUBUNIT PS		+=	363-403	473-514	118-567	107.735			4
2000	BWA DUBECTED RIVA POLYMERASE SUBLINIT PI		+	141.402	433-514	307-355				4
TRATE INCHES	ANA DIRECTED BNA POLYMERASE SUBUNIT PJ			161.402	473-514	307-755				4
T-N1	BAY OFFICIED BNA POLYMERASE SUBURIT PU	П		141.403	473-514	107.735				4
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MUN IAGU	SAN DESCRIPTION PAY WELASE SUBURIT PO	Ī			21.514	207-755	-			_
MULTI INCOM	ANA POR CITED BUY POR TMERASE SUBUNIT PJ	Ē	 []:		15.165	201.135				
MIN) ININ	ANY MACCAUD BHA ME YMURASE SUBURIT P.				477.614	201.755				
PRRF) IAIRO	AND SIDECTED BUY PAGEASE SUBURIT P.	Г	<u>.</u>		477.516	721-755	-			
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3 H		2	159-619	2769-2803	3586-3620	3821-388	4075-4121	4319-4353	
		\Box		943-1009					
	т	Г	1303-1337	1453-1494	1692-1726	0795-9792			
3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Г	21-42	1303-1337	1433-1494	1690-1724	2627-2668			
>			\$69-059	1460-1494	1509-1548	2246-2287			
>	8523)								
	SEROTYPE 10 / ISOLATE USA)	42	705-748	125-903	1021-1076	<u> </u>	┪		
			10-114	304-363	171-412	1704-1741	1602-1661	1889-1935	
	IN ONDERSTEPOORT)						٦		
	HANTAAN VIRUS (STRAIN 16-118)		134-208	127-71	557-591	969-689	231-363	905.949	1376-1310
	_	=	1342-1776	1993-2027					
	VIRUS (STRAIN A2	٦	127-061	1131-1139	1185-1220	1445-1517			
	KE)		1046-1092	1490-1553	1804-1838	2019-3063	2194-2266		
		٦	1046-1092	1490-1553					
		7	30-624	969-903	1064-1109	1203-1317	\$\$12:1212		
	MUDIPS VIRUS (STRAIN MIYAHARA VACCINE)	2.2.2	220-234	267-304	176-627	733-607	1331-1386	1447.1481	1417.1531
	NEWCASTI E DISEASE VIBILS (STRAIN REALIDETTE CAS)	-1	310,304	1040.3013	1041.100	3160.3143			
	Ī	Ī	100	100 701	700. 300.	1116.1363	1413,1430	1564.1630	1447.1731
		1							
	HUMAN PARATNITUENZA 3 VIRUS (STRAIN NIH 47815)	T	107-163	140-574	147.781	1064-1129	1293-1356	1499-1336	1824-2036
Ш		200	1	100	2 · 5 · 5	80 £	Г	973.556	1119-1133
П		1742-1776	1940-1975	1993-2033					
Ī		3.114	197-231	696-730	1134-1222	1522-1580	1384-1619	1064-2123	
	RABIES VIRUS (STRAIN SAD BIO)	23-114	167-231	696-730	149-783	1174-1222	1522-1580	1504-2133	
2			\$14-\$18	144-671	918-988	1017-1071			
PRAVE SENDS NAN-DOBECTED RNA POLYNGRASE	RUT VALLEY FEVER VIRUS (STILAIN 2H-540 M13)	396-439	641-678	633-667	1001-1115	1833-1683	1819-1870		
Γ	SENDAL VIDUS (STRAIN Z / HOST MUTANTS)	309-343	140-400	612-456	147-781	6111-9901	1239-1280	1499-1536	2000-2034
	2	2146-2216							
PARAL, SENDZ ANA POLYNCHASE BETA SUBUNIT	SENDAI VIRUS (STRAIN ENDERS)		360-420	4)3-476	367-601	864-988	1059-1100	1319-1356	1070-1054
Γ		1966-2036							

		All Viruses (no bacteriophages)	7	ABFAT	AREA 3	AREA 4	AREAS	П	ABEA 2	OBEO!
PCGENE			T	20,000	37.13	Г	6	1239-1280	1499-1536 2	2000-2014
FILENAME		I VIRUS (STRAIN Z)	Т	20.00		T	1			
PRINT SEOUR	ANA POLYMENASE BETA SUBURIT		3146.2316			T	376	1742.1776	1047.1981	1993-2027
		SECOND VINIS (STRAIN 10-19)	98-139	7.2	357-391	Т	Τ,	1	Т	
PRIDE SYSWR			547-627	147.781	1225-1280	Т	1394-1640	Т		
PREPER SYNCY			160-794	123-139	977-1014	1089-1137	1978-2032	Т		
PARM, TSWAR		SONCHUS TELLOW ME! VINOS		199-433	539-573	589-634	1119-1153	П	Т	
200		TOWATO SPOTTED WILT VIRUS (BICALILIAN ISOLATE CONTINUED	١	1117-1196	7213-2127	2154-2200	1206-1147	_	7	2808-2843
THUT OUR			1	100	116-674	1030-1071	1481-1818	3013-2049	3061-3098	
		ULKUNIEMI VIRUS	T			633 1 663	1807-1836			
PRUPL VSVPI	INA POLYMENASE	VESICIALAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA 119-358	T	674-313	100	1001-000				
PLUT, VSVIO	ANA POLYMENASE BETA SUBUM	SECOND AND THIS WALLS (SEROTYPE NEW JEASEY / STRA 119-358		674.715	120.763	lear-ran				
MULL VSVS	JUA POLYMERASE BETA SUBUNIT	VEST. CICKAR STORMS		130-763	1019-1034	1743-1799	200			
PREPO ACLSV	ANA POLYNGRASE BETA SUBUNIT		Γ	357.596	054-914	1115-1269				
SALVAN ON BE	RNA-DIRECTED RNA POLYNGRASE		Γ							
200	MITATIVE RNA-DIRECTED RNA POLYNGRASE									
200	THE PARTY BOLY ACTOR	(121)								
MOVE OWN	PUTATIVE NON-DIECTED TOWN OF THE PAGE		234-285							
PREMO BYDYR	PUTATIVE REA-DUCELIED WAS TOO.	_	234-285							
PIUTO CAUNY	PUTATIVE RNA-DIRECTED RNA POLITMERASE		11111							
PRILIPO CCIONS	PROBABLE RNA-DIRECTED RNA POLYNORASE	CAUTATION MOTITE VINCE OF THE PART ON STRIP AL	147	383-438	446-410	726-767	1445-1479			
SVGE Cesas	PUTATIVE ANA-DIRECTED RNA POLYMERASE	CUCUMBER GREEN MOTILE MUSAIC VINCS (184.412	100-010	L					
120	MITATIVE RNA-DIRECTED RNA POLYNERASE	AVIAN INFECTIOUS BURSAL DISEASE VIAUS (STRAIN 32-14)		266.103	700.757	111.809				
200	THE PARTY OF THE PARTY POLYDERASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRAL			361 101	750-802				
PERO GRAVI	POLATIVE MANAGEMENT BOX YACRASE	INTECTIOUS PANCREATIC NECROSIS VIRUS (SEROTYPE JASPER) 147-181		107						
PREPO IPANS	PULATIVE MAN-DIAECTED MAN BOX VACEDAGE	INTECTIOUS PANCHEATIC NECROSIS VIRUS (SEROTYPE SP)	<u>=</u>	200	2012		1			
PRUPO LYCVA	PUTATIVE MA-DIRECTED MAA FULT FEET	I YARHOCYTIC CHORIOMENINGITIS YIRUS (STRAIN ARMSTRON	301.346	805.416	936-960	1509-1343	1000			
PREMO LYCVW	RNA POLYMERASE	SAMOCYTIC CHORIOMENINGITIS VIRUS (STRAIN WE)	301-345							
PRUPO MONV	RNA POLYNŒRASE	A STATE OF DEPOT PORTIS	111-315	697.731						
PRINO PEANY	PROBABLE RNA-DIRECTED RNA POLYMERASE	MALE CHLOROTTC MOTICE THE	331-358							
PREPO PLAVI	RNA-DOLECTED INA POLYMERASE	PEA ENAITON MOSAC VINCE	26.32	423-457						
WALK OF SAVE	PUTATIVE RNA-DIRECTED RNA POLYAERASE	POTATO LEAFROLL VIKUS (STRAINS)	116.131	5						
2	PLITATIVE RNA-DOLECTED RNA POLYNGRASE	POTATO LEAFBOLL VIRUS (STRAIN WAGENIMIEN)		93.45	197-(19	862-896	L			
	PI ITA TIVE RNA. DIRECTED RNA POLYNGRASE	PEPPER MILD MOTTLE VIRUS (STILAIN SPAIN								
	Т	RED CLOVER NECROTIC MOSAIC VIRUS	3					L		
PRINCE PERSON	T	REOVINUS (TYPE 3 / STRAIN DEARIDAD)	or of		\downarrow		-			
Pinto Medy	Т	REOVENUS (TYPE 2 / STRAIN DISJONES)			-	-	L			
MOO REOM	ANA DIRECTED BINA POLYNORASE	REOVINUS (TYPE 1/STRAIN LANG)	10.70		3	116.140	945	3445	690-734	171-805
MUNO ROIBE	WANDOWS BOWN BON WATERASE SUBUNIT VP)	BOVINE ROTAVIRUS (STRAIN ILF)	8				į	2000	50.72	111-805
PRING ROTEU	MAA-DIMECTED MAKE AN AMERICA STREAM VP.	BOVING ROTAVIRUS (STRAIN UK)	3	2				1001		
PRING ROTTC	INA-DIRECTED ANA FOLIANA OR CONTRACT VPI	PORCINE ROTAVIRUS (GROUP C/STRAIN COWDEN)	ž	23.28				10.00	21.15	
PRUMO ROTTO	ANA-DIRECTED RAY FOLT MELASE SUBJECT VI	PORCTNE ROTAVIRUS (STRAIN COTTFRIED)	62.96	3:10	36.37				191	
PRILITY ROTS!	NA-DOLCTED INA POLTMERASE SOCIALITY	EDITION II ROTAVINUS (STRAIN SAII)	\$. \$	3	22.58	179-671				
PIUNO SBAN	NA-DIRECTED RAY POLINEKASE SUBURITY	CONTINUE NOTAN MOSAIC VIRUS	628-668				\downarrow	1	1	
PIUDO SCYLA	PRODABLE RNA-DIRECTED RNA POLYMENASE	SOUTHERN DESCRIPTION OF THE STATE OF THE STA	180-134	147-191						
PIUTO TACY	ANA-DIRECTED INA POLYMERASE	SALCHARAMITES COMMISSION	155.204	230-278	375-416	484-518	191-925	00 00 00		CIOZ-IM
PREPO TAGACY	ANA POLYMERASE	TACALUBE VICES	677 104	612.720	765-118	_				
Value of the	Γ	TOBACCO MILD GREEN MOSAUC VIRUS (1MV 31 MAIN OL)	1	601.453	665-699					
	Τ	TOBACCO MOSAIC VIRUS (VULGAJE)			87,77					
2	Т	TOBACCO MOSAIC VIRUS (STRAIN KOREAN)				-			L	
PRINC THATO	Т	TOBACCO MOSAIC VIRUS (STRAIN TOMATOR.)	=	\$ \$ \$ \$	100					
PROPORTING	PUTATIVE RNA-DIRECTED MAY FOR THE FAST		ì							

		Att Money day harded as hereal								
PCCENE THE WANT	PROTEIN		AREA 1	AREA1	AREAL	AREAd	\$ V28V	ARCAL	AREAI	AREAI
200 P3 CVA	ANA CARPETTED BNA POLYMERASE	CO NECROSIS VIRUS (STRAIN D)	102-144							
OACO GARAGO	BNA POLYNGRASE ALPHA SUBUNIT	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN AS1908)	851-66	160-216						
7307 0404	THE POLYMERACE ALPHA SURLIMIT		312-373							
INTER PRINT	ANA POLYACERASE ALPHA SUBLATT		851-66	160-216						
PREP HRSVA	IRMA POLYMERASE ALPHA SUBURGT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAI) 99-158	99-158	160-216						
PRRP HOSVI.	IRNA POLYMERASE ALPHA SUBUNIT	HUNGAN RESPUENTORY SYNCYTIAL VIRUS (STRAIN AZ)	99-158	160-216						
PRUP MEASE	RNA POLYMERASE ALPHA SUBUNIT	HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUDGROUP A / STRAUPP-158	99-158	160-216						
PRRP MEAS	RNA POLYMERASE ALPHA SUBUNIT	MEASTES VIRUS (STRAIN EDMONSTON)	315-374	460-495						
PRUP MEASY	RNA POLYMERASE ALPHA SUBURIT		115.374	460-495						
PARP MOO!	RNA POLYMERASE ALPHA SUBURIT	ATA-I)	115.374	460-495						
PREST MODER	RNA POLYNGRASE ALPHA SUBUNIT		149-113	213-275						
PRESE MIDON	BNA POLYMERASE ALPHA SUBUNIT	MONDS VIRUS (STRAIN ENDERS)	214-276							
PREP NOVA	NNA POLYNGRASE ALPHA SUBUNIT	MUMOS VIRUS (STRAIN MIYAHARA VACCINE)	214-276							
PLETP NOVE	RNA POLYNGRASE ALPHA SUBUNIT	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA71) 100-134	100-134							
PREST TING	RNA POLYNGRASE ALPHA SUBINIT	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	100-138							
PRRP PINC	RNA POLYNGRASE ALPHA SUBUNIT	HUMAN PARAINFLUENZA I VIRUS (STRAIN CIS)	10-114	113-364	175-437					
PRES PIND	RNA POLYNGEASS ALPHA SUBURIT	HUMAN PARADITUTIONER 1 VIRUS (STRAIN C19)	60-114	313-364	175-437					
PREST PLINE	RNA POLYNGEKASE ALPHA SUBINGT	HUBLAN PARAINFLUENZA I VIRUS (STRAIN CI-577)	111-00	113-364	175-417					
PARP PIZH	NA POLYNGRASE ALPHA SUBUNGT	6	66-114	237-271	313-364	375-437				
PRESE PERM	BNA POLYNGBASE ALPHA SUBURIT		318-281							
PRR. P. P. D. B.	RNA POLYNGRASS ALPHA SUBUNT	(STILAIN TOSKIBA)	216-281							
PARTY PINE	ANA POLYACELASE ALPHA SUBURIT	BOVING PALAINFLUENZA 3 VIRUS	11-130	414-470						
PRRP PHAIA	INA POLYNORASE ALPHA SUBUNT	HUDAAN PARAINELUENZA 3 VIRUS (STRAIN MH 47885)	410-499							
PRATE PIANG	INA POLYNCRASE ALPHA SUBUNIT	IA)	4.38	222-225						
PRUP PRYV	INA POLYNERASE ALPHA SUBURT	HUMAN PARAINELUENZA 4B VIRUS (STRAIN 48-333)	222-215							
PREST RABVA	ANA POLYMERASE ALPHA SUBUMIT	PRY VRUS	137-174							
PRUTP RABVC	RIVA POLYNORASE ALPHA SUBURIT		93-127							
PAUP TABVE	INA POLYNERASE ALPHA SUBUNIT		93-127							
PRESE BABVE	RNA POLYNGRASE ALPHA SUBUNTI	A), AND (STRAIN PM)	121-08							
PLUTE INBYS	RNA POLYNGBASE ALPHA SUBURIT		93-127							
PRUP SENDS	INA POLYMERASE ALPHA SUBUNIT		93-127	,						
PARTY SENDS	RNA POLYMERASE ALPHA SUBUNIT	SENDAL VIRUS (STRAIN & / HOST MUTANTS)	127.164							
VICTOR SEVON	KINA PUL I MERANSE ALTTAN SUBURITI	DNO	113.364	375-447						
PARTY SENDE	ENA POLYMERASE ALPHA SUBUNIT		313-364	375-447						
PARUP SVS	RNA POLYMERASE ALPHA SUBUNIT		313-364	375-449						
PRUP SYNV	RNA POLYMERASE ALPHA SUBUMIT		205-278							
PRUP VSVIO	RNA POLYMERASE ALPHA SUBUNIT		138-173	33-381						
PRIVE VSVDA	RNA POLYNGAASE ALPHA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN C)	7							
PRACP VSVA	RNA POLYMENASE ALPHA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYFI: INDIANA / STRAIN M)	?							
FRRFF VSVIO	RNA POLYMUKASII ALFIIA SUBUNIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA	5							
PRUPP VSVSJ	RNA POLYNŒRASE ALPHA SUBUNIT	SEY/STIM	2							
PSPHOLANCEV	ANA POLYMERASE ALPHA SUBURIT	N SAN JUAN)	7							
PSPD VACCV	SPHEROIDIN	XVBUS	223-264	361.395						
PSPID_VARV	SEAME PROTEINASE INMIDITOR	S (STRAIN WR)	71-14				•			
PSPD VACCC	SERING PROTEINASE INTIBITOR 2		91:10	770 350						
PSPI) VACCV	SEADUR PROTEDIASE DAMBITOR 3	VACCINA VINUS (STIALIN COPENIAGEN)	118-167	27.57						
PSPIS VARV	SERING PROTEDNASE DAMBITUR >			M77:077]					

					ľ	П	П	П	П	
PCCENE	ALLMOTTS	1963 (no Botternopus La)	ABEA1 A	ABEA1	ABEA2 A	AREAS	AREAL	1	1	
PHEMAME		VIANA VIETA	122-171	9-270			1			
٤	SEATHE PROTEINASE INHIBITION 3									
Γ	HOMOLOG FIRST		1							
Ī,			Ī.	133.207						
T		(STRAIN WR. COPENIAGEN, AND VANCER	T							
Ī										
T		(STRATH WIR) (STRAIN COPENHAGEN)	† 	Ì						
200	TO ANY ACTIVATOR PROTEIN GK!		T	100 100						
Ţ	Machine & Scott	BUDGERIGAR FLEDGLING DISEASE VIRUS	Ī							
T	The state of the s	BOVINE POLYONIAVIRUS	T	10.00	1					
_	LARUE I AMINEM	St	٦	367-671						
PTALA POVIC	LARGE T ANTIGEN		153-117 5	٦						
MALA PONLY	LARGE T ANTIGEN	STEED FOR VOLUME	19-7	206-258	417-478					
PTALA POWO	LARGE T ANTIGEN		\$06-544							
PTALA POWAL	LANCE T ANTIGEN		507.543							
PTALA POVAC	LANCE T AMTIGEN	_	604.510							
ARVOR BALLE	LARGE T ANTIGEN	ICAIN CRAWTON SPINESTER COL	376							
1000	LOTHING T ANTIGEN	HUMSTER POLYOMAVIRUS	Ť						·	
	ADDITION A STATE OF	MOUSE POLYOMAVIRUS (STRAIN 3)	1	77.00						
PIALO POVEA	PROCES I ANTOEN	1)	٦	109-401						
PTAMO POVAC	MUDIC I ANTINCA	(WFORD SMALL-PLAQUE)	193-226	169-403						
PTASM POVBO	MEDDLE T ANTICEN	BOY YOMANTEDS	61-13							
PTASH POVLY	SHALL T ANTIGEN	BOVING TO SELECTION VOLVA VIBILS	7							
PTATA NPVAC	SMALL T ANTIGEN	EAR BOI VICTOROSIS VIRUS	408-442	Г	489-523					
MEN WINTER	O TRANSCRUPTIONAL R	Т	Π		494-528					
PIATE NOVOP	THANS ACTIVATING TRANSCRIPTIONAL REGULAT	BONGYX MOST NUCLEAR PULTHEDROSIS VINUS	T	Γ						
PYAT SIVAL	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT		Ţ							
PTAT STVAL	TAT PROTED									
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		SOLAN DOMINODEFICIENCY VINUS (ISOLATE AUM / CLUME ON		Ī						
7 17 17 17		VISHA LENTIVORUS (STILAIN 1914)								
2 14 74 74	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VISNA LENTIVISUS (STRAIN 1914 / CLURE LV 1:1831)								
2	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	VISNA LENTIVICUS (STICAIN 1914/ CLUME LV 1-16.34)								
	TOTAL RECEIPTOR BETA CHAIN MECURSOR	FEL INE LEUKENDA VIRUS	100							
TECH POLICE	TECH PARATI PROSPHOPROTEDN USP	HENDES SOOLEX VIRUS (TYPE 1 / STRAIN 17)	11-11							
	MANGENCE									
TEG BYES	Lawrence Control									
TIES NO.	TOTAL STATE OF THE PARTY OF THE									
MEG HSVSB	MONSCASE							1	1300-1363	1809-1867
ALC COST	CONTRACTOR OF THE PROPERTY.	EPSTEIN-BARR VIRUS (STRAIN B95-0)	760-802	821-655	214-815	1101-111	1600			
TEGU HOLVA	LARGE TECOMENI PROTEIN		1870-1916	1930-1954	100-1149				100	141.170
	Cattoria Proposition and an annual	HINNAN CYTOMEGALOVIRUS (STRAIN AD169)	34.71	215-249	543-501	8.73	100.00			
PTEGU HSVII	Troates to the second		1237-1296	200-223						1400.1448
	With the Prince of the Park	HERVES SINDLEX VIRUS (TYPE 1 / STIAIN 17)	731-765	101-143	1022-1059	2	1273-1307			
PTECU HSVIO	LACOR I ECOMENI PROTEIN		1673-1714	174-178)	X 81-02	27-0182	961-1900	1001.1181	1102-1233	1357-1400
	A A SCE TE GIDARNI PROTEON	HERPES SINDLEX VIRUS (TYPE 6/STRAIN GS)	10-71	234-262	B		331		171	1487.1549
FIEGO RISVEB	A SECRETARING PROTEIN	EQUINE HEAPESVIRUS TYPE I (STRAIN AB4P)	160-597	63.48)	74	X4-124	100.00			
PTEGO HSVSA			1615-1637	<u> </u>	87.70					
	Manor service and a service an	HERPESYIRUS SADAMU (STILAIN 11)	520-558	260-598	615-632	673-710	77-623	140-59	20.410	10:00
PTECU VZVO	PROBABLE LANGE IEVORETTI FROTE		1434-1502							
		VARICELLA. ZOSTER VIRUS (STRAIN DUMAS)	637-696	113.747	104-141	913-972	1117-1138		310:135	200.00
TTENM ADE02	LAKGE TEGUMENI PROTEST		1633-1705	1719-1756	185-196 196-196	277-276				
	MINISTER TO STATE OF	HUMAN ADENOVINUS TYPE 1	490-572							
TEUM ADED	DATA TERMINAL PROTECT	HUMAN ADENOVIRUS TYPE S	490-593							
PTERM ADES!	DAY ISCHRIST PROTECT	HUMAN ADENOVIRUS TYPE ?	491-559							
PTERM ADEI2	DNA TEXMINAL PROTEIN									

171000	11.00 m	All Vicence (as hacterlashapes)			П	П	П	П	П	П
PLULPE.	PECTET		AREAI	AREA1	AREA?	AREA 4	ABEA 3	AREA 4	AREA! AF	4854
PTEM AVIST	DNA TERMINAL PROTEIN	IN ADENOVIRUS TYPE 12	165-655	497-538						
PTIMAS AVISA	TRANSFORMING PROTEIN TUN		210-214						1	
PTOP1 SFVICA	TRANSFORMING PROTEIN MAF	ROSARCOMA VIRUS AS42	247-288	193-340						
PTOP2 ASTB?	DNA TOPOISOMERASE		137-113	269-310			┪		1	T
PTOP2 ASTNO	DNA TOPOISONERASE II		146-110	411-515	\$0.442 \$0.442	T		┪		
PTSIS_SMSAV		AFIJCAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 2011)	146-180	480-514	17.00	907-604	10	1038-1091	132-1161	
PTYSY VZVD	PDGF-RELATED TRANSFORMING PROTEDY P21-SIS		12					1	+	
PUBIL NO VOP	THYNCOYLATE SYNTHASE	VAUCELLA-ZOSTER VIRUS (STRAÍN DUNIAS)	215-260				1		1	
PULDI HOLIVA	UBIQUITIN-LIKE PROTEIN	ORGYIA PSEUDOTSUGATA MALTICAPSID POLYMEDROSIS VIRUS (1)-40	970					+		T
PCLO3 HSV11	HYPOTHETICAL PROTEIN UL!		169-203						1	
PULOJ HSVZH	PROTEIN U.)		¥.2				1	-	1	
PULO HSVED	PROTEIN UL.)	12)	93-126							
PLEON HSVII	GENE 60 PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN AB4P)	70.104				1		1	
PULOS EBV	PROTEIN ULA	HEAPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	103-136				1	1	1	
PULOS HCD-CYA	VILLON PROTEIN BBILF!		104-145	5.53	240		1		1	
PULOG HSV11	HYPOTHETICAL PROTEIN ULA)	216-250						1	
PULOS HSVEB	VINON PROTEIN UL6		16.94	103-141	194.329	111.111	273	-	1	
PULOS HSVSA	VINON GENE SA PROTEIN	EQUINE HERPESVIRUS TYPE I (STRAIN AB4P)	62-170	157-413	141.503					
PULOS VZVD	VINON GENE 4) PROTEIN		90-140	131-194	303-336	364-405			1	
PULOS HONVA	VIJUON GENE SA PROTEIN		17.131	150-409	704.738					
PLL09 HSVEB	INPODEDICAL PROTEIN ULB		6-50							
PULOS VZVD	ORIGIN OF REMICATION BINDING PROTEIN		107-701							
PULLI HOWA	ONIGIN OF REPLICATION BINDING PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	123-163							
PUL13 HONYA	MONSENSE									
PULIS HOUVA	HYPOTHETICAL PROTEIN ULIS		47.81	165-227				-	1	
PULIS HSVEB	HYPOTHETICAL PROTEIN UL 14		305-343							
PULLIA PRIVAD	HYPOTHETICAL GENE 49 PROTEIN	(AB4P)	52.96	246-283						
אמרוי אבאם	ULI 4 PROTEIN HOMOLOG		43.95						1	
PUL 16 HSVED	HYPOTHETICAL GENE 46 PROTEIN		61-103						1	
PCL17 HSV6U	GENE 46 PROTEIN		266.700					1	+	Ī
PULLU HSVED	PROTEIN ICK	WDA-1102	238-210							
PULLS HOWA	GENE 40 PROTEIN		2.7	431-474						Ī
MA24 HOAVA	HYYOTHETICAL PROTEIN UL 13		213-233				1			T
PULZA ELTVI	HYPOTHETICAL PROTEDIULIA	HUMAN CYTOMEGALOVIAUS (STRAIN AD189)	A.				†	\dagger		T
PLEAS HOWA	PROTEDI UL24 HOMOLOG	KAIN THORNE VE	101-103				1			Ī
POLZS HSVII	HYPOTAETICAL PROTEIN UL25	HUMAN CYTOMEGALOVICOS (STRAIN ADIOW)	117.04	26.16						Ī
PULLS HSVEB	VOUCH TO LEIN ULZS		10.7						t	
אלאט מדוטע	MARION CENT 10 PROTEIN		29.92	10.01	365-406			$\frac{1}{1}$		
MR 36 V7VD	ALLES VEION PROTEIN	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE VIE	7.10	163-206				_	-	
POCE PROPERTY	VINION GENE 24 PROTEIN	WARLELLA-EOSTER YIRUS (STRAIN DURIAS)	340-344							
PULJI HSVEB	HYPOTHETICAL PROTEIN UL31	HUMAN CYTOMEGALOVIRUS (STRAIN AD189)	244-285					-	1	
PULSI VZVO	GENE 19 PROTEIN		5:10				1	1	1	
PULJ2 HSVEB	GENE 27 PROTEIN	٦	163-197					1	+	
PULIZ VZVD	MAJOR ENVELOPE GLYCOPROTED 300	(STRAIN ABI)	342.376					1	1	
PULLS HOWA	PROBABLE MAJOR ENVELOPE CLYCOPROTEDN 26		2.08	296-344				1		
אבא ננשו	G-PROTEDN COUPLED RECEPTOR HOMOLOG UL33		£	28-122				1		
PUL34 EDV	GENE 25 PROTEIN	DUMAS)	19-62							
PULJ4 HCMVA	BFIJF I PROTEIN		139-300				1			1
PULJA HSVII	HYPOTHETICAL PROTEIN UL34		<u> </u>						1	
PULJS HONYA	VILLON PROTEIN UL34		187-221			1	+	1	+	T
PUL17 EBV	HYPOTHETICAL PROTEIN UL35	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	231-268				1	1	1	7
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ACCOUNT ACCO	_		All Viruses (no bacterisphages)	T	T			ABTAG	, , ,	AREA?	AREAL
MATCHER BOTT FULL ALTON IN STRAND AND ST	Ī			T	1	7	2000	ł	Γ	Γ	
The process of the	T			708-347							
CONT. 13 PROTEIN COURT 13 PROTEIN 1411	T			1	T					T	-
CORE 61 PROTEIN MAJCHALA 2057E WIRES (STAND DUALS) 19-13	T			1	Т	14.04	2			1	T
COUNTY C	T				7						Ţ-
MACRITICAL PROTEDULUS MOLACITAL AGOSTE VOLUS GETALAN DION 10-104	T.		VALICELLA-20STER VIRUS (STRAIN DUMAS).	1	200						
MAYER HANDER HANDER VALKELLA-GÜTER VALUG (TYTE I (TITALN MAY) 11-10	Ţ	BOTED UL	HIDAAN CYTOLEGALOVIRUS (STIAIN AD169)	2							1
PRIVATE PLATE PRIVATE PLATE PRIVATE AND THE AND THE PLATE PLATE	T	2	VARICELLA-ZÓSTER VIRU" (STIVAIN DUMAS)	T							
DATA SHOOTED GERE 19 FROTEN EQUAGE GENESYMUS TOTAL MAPP) 11-10			HENDES SDOYLEX VIRUS (TYPE 1 / STRAIN 17)	T	2-12						
HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL FROTERN U.J. HITOTRETICAL TO CONTRACT OF THE LEGISLAND U.S. HITOTRETICAL U.J. HITOTRETICAL TO CONTRACT OF THE LEGISLAND U.S. HITOTRETICAL U.J. HITOTRETICAL U.J. HITOTRETICAL U.J. HITOTRETICAL U.J. HITOTRETICAL U.J. HITOTRETICAL U.J. HITOTRETICAL TO U.J. HITOTRETICAL U.J. HITOTRE	T		EQUINE HELPESVILUS TYPE I (STRAIN AB4P)	138-172			-				
International Company Inte	T			73.109							Ī
CHARGE STANDER PROTECT VALCELLA_COSTER VINIS (STRAND BARS) 11:101	T	101.00		27-68							
Figure 1 Figure 2 Figure 2 Figure 2 Figure 2 Figure 2 Figure 3	T			312-363							T
	T		HERPES SDAPLEX VIRUS (TYPE I / STRAIN KOS)	8.137			1				T
	T		HERPES SDOLEX VIRUS (TYPE I / STRAIN NO)								
VALIGION MOTERN LL47	T		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)		170	245-856					
NEADER POTESTION: NEADEST STATEST 111-106 NET TO ALPIA, TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN 1942) 111-106 NET TO ALPIA, TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN 1942) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN 500/THE READESTAURS TYPE (STRAIN AD149) 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN AD149 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN AD149 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN AD149 111-106 NEADESTAURS TRANS-DOUGHOR PROTEIN AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AD149 111-106 NEADESTAURS TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS-DOUGHOR AND THE STRAIN TRANS		ADJEST OCH TO THE PROPERTY OF	HERDES SIMPLEX VIRUS (TYPE I / STRAIN 17)	473-511							
10.25		TANK TAULT OF THE PROPERTY OF	HEAPES SINOLEX VIRUS (TYPE I / STRAIN F	473-518			-				
111-246	1	2	BOVINE HEAPESVIRUS TYPE I (STRAIN PI.1)				-				
VITO ALTH'S TRANS-INDUCTION STORED COUNTE REAFESTWENS STRAIN AD164) 11-151 1			FOURS HEAPESVIAUS TYPE 4 (STRAIN 1943)		582-620	125.866					
VALPA TAMES INDUCTOR OF STORMS VALUELLA-ZOSTER VIRUS (STRAIN DUPAS) 155.189 PROTEIN ULS) PROTEIN 15 D PROTEIN 15 D PROTEIN 15 D PROTEIN ULS) 15 D	Ī		EOUTHE HERPESVIAUS TYPE I (STRAIN AD4F)		171-412	917-866					
ROTERN U.3)	T	DPROTEC	VARICELLA-ZOSTER VIRUS (STRAIN DUBIAS)		156-209	101-199					
GENE S PROTEIN IGENES SUDCLEX VIRUS (TYPE I (STRAIN 19) 111-163 GENE S PROTEIN ICQUINE IERDESYNUS STRE (STRAIN 1942) 121-163 GENE S PROTEIN ICQUINE IERDESYNUS STRAIN 1942) 121-163 GENE S PROTEIN VALIDICAL SOSTER VIRUS (STRAIN DUNAS) 121-163 GENE S PROTEIN VALIDICAL SOSTER VIRUS (STRAIN DUNAS) 121-163 DIVA REPLICATION PROTEIN U.3.3 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 DIVA REPLICATION PROTEIN U.3.3 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 DIVA REPLICATION PROTEIN U.3.3 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.3 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.3 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.3 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.3 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.4 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.4 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.4 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.4 ICANES SUDCLEX VIRUS (STRAIN DUNAS) 161-131 PROTEIN U.3.4 ICANES SUDCLEX VIRUS (STRAIN DUNADA-1102) 161-131 PROTEIN U.3.4 ICANES SUDCLEX VIRUS (STRAIN UGANDA-1102) 161-131 PROTEIN U.3.4 ICANES SUDCLEX VIRUS (STRAIN UGANDA-1102) 161-131 PROTEIN U.3.5 ICANES SUDCLEX VIRUS (STRAIN UGANDA-1102) 161-131 PROTEIN U.3.5 ICANES SUDCLEX VIRUS (STRAIN UGANDA-1102) 161-131 PROTEIN U.3.5 ICANES SUDCLEX VIRUS (STRAIN UGANDA-1102) 161-131 PROTEIN U.3.5 ICANES SUDCLEX VIRUS (STRAIN SOSTER) 161-131 PROTEIN U.3.5 ICANES SUDCLEX VIRUS (STRAIN UGANDA-1102) 161-131 PROTEIN U.3.5 ICANES SUDCLEX VIRUS (STRAIN V			HINGAN CYTOMEGALOVIRUS (STRAIN AD169)	185.189							
CENE # PROTEIN EQUINE HELVESVIRUS 17PE # (51RAIN 1942) 110-161	٦	KOTEIN ULX	HERPES SINDLEX VIAUS (TYPE I / STALIN 17)	118.169							
CENE FROTEIN EQUINE HEADESVIRUS TYPE I (STRAIN AB4) 120-161	T	KOLEIN OLNI	FOLINE HERPESYIRUS TYPE 4 (STRAIN 1942)	131-162							
CORNELLY FROTEIN VAUCELLA-ZOSTEA VIRUS (STRAIN DUALS) 111-115 111-11	T	ENE O PROTEIN	FOURTH MEMPESVIRUS TYPE I (STRAIN AB4P)	130-161							
PROBABLE DIA REPLICATION PROTEIN U.33 164-35	T	JENE U PROTEIN	VARICELLA.ZOSTER VIRUS (STRAIN DUNIAS)	122-163							
DRA REPLICATION PROTEIN U.33 REDYES SIDGLEX VIRUS (TYPE 1 STRAIN 17) 191-121	T		EPSTEIN-BARR VIRUS (STRAIN B95-1)	100-255							
DHA REPLICATION PROTEIN U.S. EQUINE HELPESYRUS STREE (STAIN ABE) 141-112	T		HEADES SOULEX VIRUS (TYPE 1/STRAIN 17)	П			1				
PROGNALE DIA REPLICATION GENE 59 PROTEIN HEMPESVRUS (STRAIN DIAS) 191-141	T	WA BEN ICATION PROTEDNUES	EQUINE HEAPESVIRUS TYPE I (STRAIN ABAP)	٦	020-020						
PROTEDULA.33 PROTEIN VALICELIA-ZOSTER VIRUS (STRAIN DUBAS) 101-143	T	えど	HEADESVINUS SADAIN (STRAÎN II)	45,483							
PROTEDIUL3	T,		VARICEL LA-ZOSTER VIRUS (STRAIN DUNIAS)	301-342							
HOTER ULS	Ţ		HUDALN CYTONEGALOVIRUS (STRAIN AD149)	13-48							
HYPOTHETICAL PROTEIN ULA* HYPOTHETICAL PROTEIN ULA*	Т	WOTED (E.S	HEADES SOULEX VIRUS (TYPE 2 / STILAIN HOSS)	31:183							
PROGREE DAY NEW LICATION PROTEIN U. PR. MUDAQN CYTOMEGOALOVINUS (STRAIN AD189) 19-19 1	Т	CYPOTHETICAL PROTEDY ULAS	HUNGAN CYTOMEGALDVIRUS (STRAIN AD169)	2,3							
HYPOTHETICAL PROTEIN UL74 HUMAN CTOMEGALOVINUS (STACH AD161) 15-770	Т	PROTEIN	HUNGAN CYTONEGALOVIRUS (STRAIN AD169)	19.50							
INTOPIRETICAL PROTEIN STATE NEDFES VALUE (TYRE 8'S STAIN VOANUA-1142) 145-104 INTOPIRETICAL CAPE SA PROTEIN HEAPESVALUS SADRIES (STRAIN AD169) 147-139 INTOPIRETICAL CAPE DA PROTEIN HEAPESVALUS SADRIES (STRAIN AD169) 147-139 INTOPIRETICAL PROTEIN BOLE* HEAPESVALUS SADRIES (STRAIN AD169) 197-116 INTOPIRETICAL PROTEIN BOLE* HEAPESVALUS SADRIES (STRAIN AD169) 197-116 INTOPIRETICAL PROTEIN BOLE* HEAPESVALUS SADRIES (STRAIN AD169) 197-116 INTOPIREDICAL CAPE 31 PROTEIN HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIREDICAL CAPE 31 PROTEIN HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIREDICAL PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CENE 31 PROTEIN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CAPACIEN ULS* HEAPESVALUS SADRIES (STRAIN AD169) 13-13 INTOPIRETICAL CAPACIEN ULS* 13-13 INTOPIRETICAL CAPACIEN ULS* 13-13 INTOPIRETICAL CAPACIEN ULS* 13-13 INTOPIRETICAL CAPACIEN ULS* 13-13 INTOPIRETICAL CAPACIEN ULS* 13-13 INTOPIRETICAL CAPACIEN ULS* 13-13 INTOPIRETICAL CAPACIEN ULS* 13	Τ	APPOTHETICAL PROTEIN UL74	HUNCH CYTOMEGALOVIRUS (STRAIN AD161)	7.4							
WYPOTHETICAL GENE 19 PLOTED HEBPESVRUS SACHAN STRAIN AD169) 317-391 HYPOTHETICAL GENE 19 PROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 317-391 HYPOTHETICAL GENE 19 PROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 31-31 HYPOTHETICAL GENE 19 PROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESVRUS SACHEN VIRUS (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN UGANIA-1102) 31-31 HYPOTHETICAL FROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN UGANIA-1102) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN UGANIA-1102) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HUDGAN CYTOMEGALOVIRUS (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 31-31 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTHETICAL FROTEIN ULBI HEBPESS SANHIB (STRAIN AD169) 45-100 HYPOTH	Γ	HYPOTHETICAL PROTEIN SR	MEDIES SDOLEX VILLS (1176 8/31 MAIN COMPANION)	207.75	413.414						
WYPOTHETICAL PROTEIN ULB	Γ	HYPOTHETICAL GENE 24 PROTEIN	HEAPESVIRUS SADADU (STRAIM 11)	100.00							
	Γ	HYPOTHETICAL PROTEIN ULUI	HUNCAN CYTOMEGALOVINOS (3 I IAAIIA AD 187)								
VA WYODIETICAL PROTEIN BOLF PATEUR-SALA VILOS (STAIN AD169) PATEUR SALA VILOS (STAIN AD169) PATEUR SALA VILOS (STAIN AD169) PATEUR SALA VILOS (STAIN AD169) PATEUR SALA WYODIGETICAL PROTEIN R. PATEUR SALA SALA SALA SALA SALA SALA SALA SAL		HYPOTHETICAL GENE 10 PROTEIN	HEALESVALUE (STRAIN (1)	103.144	111.222						
HYPOTHETICAL PROTEIN U.S. HUMAN CY TORGECALOVIRUS (STRAIN UCARDA-1103) 101-143 HYPOTHETICAL FOOTEIN R	×	HYPOTHETICAL PROTEIN BOLF	EPSTEIN-BAUG VIRUS (STRAIN BYS-4)	10.00							
HYPOTRETICAL CENE 11 PROTEIN PR. HEADES VARIUS (STRAIN 11) HIP131 H	П	HYPOTIGETICAL PROTEIN UL93	HUMAN CYTOME GALLOVINOS (STRANG SOLO)	101.146	134.216	-					
HYPOTHER LEGIE 11 PROTEIN HEAPTAY LOS SALATION SALATION SALATION 11-17		HYPOTHETICAL PROTEIN 98	HEATER SOUTER VIRUS (1 TTE 8) STAIN COARDAINS	1		l i					
MOTED IL. 19 MUNICAL PROTEIN IL. 19 MUNICAL CYTORIEGALOVIEUS (STANIN ACTOR) 14-71		HYPOTHETICAL GENE 11 PROTEIN	HEALTS VINOS SAMPLING (STRAINT)	31.43	289.184						
WYPOTHETICAL PROTEIN ULS) HUMAN CYTONECAL PROTEIN ACADA 11-151		PROTEIN ULO	HUMAN CYTONELALUS (31 KAIN AD107)	153	160.793						
INTOTINGENCAL PROTEIN INEANS SUPPLIES VINDS 171: 6 / N. N. N. N. N. N. N. N. N. N. N. N. N.		KYYOTHEETICAL PROTEIN ULUS	HUMAN CYTOSIEGALOS INOS (3 HASIS AD187)								
INVOTRIFICAL PROTEIN U. 96 INTRAIN CYTARECALLYNIUS (NRANY ADDITION) INTROTRIETICAL PROTEIN 198 INTROTRIETICAL GENE 33 PROTEIN INTROTRETICAL GENE 33 PROTEIN INTROTRETICAL GENE 33 PROTEIN INTRAINS (STRAINS STRAINS ADDITION) INTROTRETICAL PROTEIN UL 102 INTRAINS (STRAINS ADDITION) INT		IIYPOTIIETICAL PROTEIN 13R	HENNES SIMILEX VIRUS (1 VT. 6 / NIRAIN HOANDA-1102)								
INTROTHETICAL PROTEIN 14R INERTES SIMPLEX VIRUS (TYPIS 67 STICALN UCANDA-1102) INTROTHETICAL GENE 33 PROTEIN (1102) INTROTHETICAL GENE 33 PROTEIN (1102) INTROTHETICAL PROTEIN (1102) INTROTHETICAL PROTEIN (1102)		HYPOTHETICAL PROTEIN U.%	HUMAN CY (CALCAL DVIRUS (NERNIN AD) (4)								
INTOTIETICAL GENE 13 PROTEIN INCINIA INCINIA I INCINIA I INCINIA ADMINISTRATION A	Γ	HYPOTHETICAL PROTEIN 14R	DIERPES SIMPLEX VIAUS (TYPE 6/51RAIN UCANDA-1102)			1		-			
INDIANA CALENDA INDIANA CALONICAL OVINIO CALONICAL CALON		HYPOTHETICAL GENE IS PROTEIN	ILERY SVIRUS SAINING (STRAIN II)	81.6	356.303						
	Г	HYPOTHETICAL PROTEIN ULIO?	INDIAN CYTOMEGALOVINUS (STRAIN AUTO)	1	9	110.164	439.492	31.53			
VIRION PROTEIN UI 104	Γ	VIRION PLOTFIN ULION	HILINIAN CYTONI: GALOVINUS 13 IRAII ADICT								

			-			-			ľ	
PCCENE	ALLAIOTIS	All Virgos (no bisternopueges)	14144	ABGAS	ARFA 3	787	ARFAS	AREAG	AREA?	AREAS
FILENAME	PROTEIN	VIRIO VIRIO VIRIO VIRIO VOLGO	Γ	Г	Ī	Т	Γ	Γ	Г	
PUND HSV11	HYPOTHETICAL PROTEIN ULIDO	HUNIAN CT I WHENALOVING (31 RAIS) ADIO!	32.361					T	Ī	-
PUNG HSV20	URACEL-DNA GLYCOSYLASE	HELDES SINGLEA VIRUS (1778 175 INT.)	200		Ī	+		Ì	1	
MING HSV2H	URACEL-DNA GLYCOSYLASE	PERTES SINTER VIAUS (1778 27 STRAIN 313)							-	-
PUNG HSVSA	URACIL-DNA GLYCOSYLASE	HERFES SOUTER VINUS (TYPE 27 STRAIN 11632							T	
PUNG SEVICA	URACEL-DNA GLYCOSYLASE								Ī	Ī
PUSO2 HSVED	URACIL-DNA GLYCOSYLASE			T					\dagger	-
PUSO1 HSVEX	CENE AS PROTEIN		2 2							
PUSOT HCLEVA	USI PROTEDA	EQUINE HELLPESVIRUS TYPE I (STILAIN KENTUCKY A)	021-90					1	1	
PUSII HOWA	HYPOTHETICAL PROTEIN HOLFS		2.36			-				
PUSI4 HOLVA	HYPOTHETICAL PROTEDN HOLF!	HUMAN CYTOREGALOVIRUS (STRAÍN AD169)				-				
PUSIS HONA	HYPOTHETICAL PROTEDI HYLM		3.51							
AVON USAN	LGLABLANE PROTEIN HWLFS	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	107-125			. 4				
ANON ACIM	INVENTIFICAL PROTECNINGS	HIDAAN CYTOMEGAL OVIRUS (STRAIN AD169)	294-335	\$35-578				-		
ANCH MORA	MYPOTHETICAL PROTEIN HORES	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-172							
MINI HOWA	HYPOTHETICAL PROTEDINGS	HIBLAN CYTONEGALOVIRUS (STRAIN AD169)	\$15-514							
ANON 91318	C. PROTEIN COURT FOR BECEPTOR HOAIDLOG US27		6-40			-				
PV134 AVENT	HYPOTHETICAL PROTEIN HORES	HIBAAN CYTONEGALOVIRUS (STRAIN AD169)	135-169	274-313		-	-			
PANAL MANAC	134 KD PROTEIN	TE LEIDEN	16.52	326-367	591-649		-			
PVIAT TRVPS	MELICASE	VIRUS	113.350	1114-1130	1139-1213			-		
PVICE TRVSY	14 KD PROTEDV	T	38.113							
VALUE A IVO	14 KD PROTEIN	TORACCO RATTLE VIRUS (STRAIN SYN)	78.117						-	
200	IN BROTTEN		Ī	349.405	492-526	710-751	837-864 8	190-924		
100	A PACIFIC AND A		Ī	Τ	Γ	Γ	Γ			
AND VIA	IN TACHER		Ī	T.	346-359	417.226				
200	IATRUIEIN	COLOR DE LOCATION CONTRACTOR CONT		Τ	Τ	244.916				
200	- Trough	CHICAGE MORAL VIBILGACTEAN ON	T	T	\$14.619	868.916		ŀ		
PVIA CAVO	IA PROJECT	CIMINGER MOSAIC VIRUS (STRAIN O)	Ī	Γ		-				
200	A PROTEIN					7-		-		
PV23K HSVTH	IA PROTEIN	TOMATO ASPERMY VIRUS	65-11	182411	\$57-973					
PVZ4K BDV	23.5 KD PROTEIN	(STRAIN HZ)	112:11							
PV25K NPVAC	24 KD ANTIGEN		63.121	130-171						
PV28K PLRVI	25 KD PROTEIN	INICA NUCLEAR POLYMEDROSIS VIRUS	4.50							
PV38K PLAVV	18 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	116-150							
PV790 ASFLS	28 KD PROTEIN	POTÁTO LEAFROLL VIRUS (STRAIN WAGENINGEN)	16-150							
PV29K PEBV	LIS 290 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LISS?)	3							
PVPSK TRVSY	29 6 KD PAOTEIN	EARLY BROWNING VIRUS	261-53				1	1		Ī
PV29K_TRVTC	29 KD PROTEIN	AND (STRAIN PSG)	167-201					1		Ī
MA CON	19 KD PROTEIN	£	4.5				+	1	1	
PVZA CAOMIN	1A PROTEIN		705-106				Ì	1	1	
PVZA PSVI	1A PROTEIN	IN PAY)	27				1	1	1	
PY2A_TAV	2A PROTEIN	נאטא	187-517				1			
PV30K_TRVTC	2A PROTEIN	TOMATO ASPERIATY VIRUS	227.22	1	1					T
PV340_ASFB7	29.1 KD PROTEIN	TOBACCO MATTLE VIKUS (STRAIN TCM)					1	1	1	Ī
PVIGE ASFB?	K740 PROTEDV	AFLICAN SWINE FEVER VIRUS (STRAIN BATIV)	1	1					1	
PV363_ASFB7	KINS PROPER	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	7	161-212	290-324			1		
PVJA BMV	DOS PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	153-199							
PVJA OPMIN	1A PROTEDI	BROME MOSALC VIRUS	₹					1	1	
PVJA CAPM	JA PROTEIN	5	23.33						1	
PVJA CHVO	3A PROTEIN		215-255				1	1	1	
IVIA CHIY	3A PROTEIN		215-35						1	T
PVSIK ACLSV	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Y)	215-255					1	1	
	•									

-			1				V. V.A.V	ATTA	AREA?	
PCCENE	ALLMOTIS	nici (se muzzinen)	AREAL	AKEA	7	1		Т		
5	PROTEIN	TINUS	73-106							
WOLLD BOOM	SELKD PROTEIN	MATE FL.II	113-147	196-233	404-451					
Walk Bulve	the secondary		Γ	196-233	407-451					
PVSIK BWTVU	A PACE STATE OF TH	1000	Γ	438.472						
PVSKK PLRVI	N KU FROIEM		Ţ	411.475						
PVSGE PLEW	S KD PROJEIN	AIN WAGENINGEN)	Ţ	121.131						
PVSEK BSI-IV	S KD PROTEIN		T							
PV66K_BWTVF	SA KD PROTEIN	S (ISOLATE FL-1)	1							
PVYCK_PLRVI	66.2 KD PROTEIN	POTATO LEAFIGIL VIRUS (STRAIN !)	٦		27.71					
PUNCK_PLAW	49.7 KD PROTEIN	MATATO I PAFROLL VIRUS (STRAIN WAGENINGEN)	* - K	2					L	L
PVPOK ANVILE	69.7 KD PROTEIN	AT EAL EA MOSANC VIRUS (STRAIN 425 / ISOLATE LEIDEN)								L
PVADA VACCC	90 KD PROTEIN	ALCALIA MOSKIE COTENHAGEN	12-66	231-275						
WASH WALTV	PROTEIN A4	VACCINIA VIRUS (STICKIN COLEMNICA)	32-46	211-275						
Vaca vaca	PROTEIN A4	VACCIMIA VIRUS (STRAIN W.R.)	33.66	210-265						
ANN MAN	PROTEIN AA		311	114.355						
PVACE VACE	TAULEN AV							L		
PVA06 VACCV	PROJEIN AS	VACCINIA VIRUS (STRAIN WR)	× 4.				_			
PVADE VARV	PROTEIN AS	VARIOLA VIRUS	617-16				-	L		
PVAC VACCC	PROTEIN AN	VACCINIA VIRUS (STRAIN COPENHAGEN)	1.6-2.10					_	L	
PVACE VARV	PROTEIN AU	VARIOLA VIRUS	176-236				-			L
PVAD9 VACCC	PROTEIN AS	VACCINIA VIDUS (STRAIN COPENHAGEN)	199							L
PVACO VARV	PROTEIN A9	VARIOUS A VIRIS	46.93							L
PVA11 VACCC	PROTEIN AS	STATE OF THE ACT OF TH	97-134	11.13	218-203					L
PVAIL VARV	PROTEIN A11	VACCINIA VINOS (3) PORTO (2)	961-86	220-284				1		1
PVA13 VACCC	PROTEIN AIL	VAUGLA VIROS	114-148							1
7877	PROTEDY A12	VACCINIA VIAUS (STRAIN COLLINICALITY)	111.152				-			1
NATE VACCE	PROTEDY A12	VALIGLA VIRUS	433-467	L						\downarrow
VALA VAC	56 KD ABORTIVE LATE PROTEIN	VACCINIA VIRUS (3 FALM COFEMENCE)	307-341	43)-467						-
WALL VARV	56 KD ABORTIVE LATE PROTEIN	VACCINIA VINUS (3 I MAIN WA)	107-341	137467						\downarrow
YAZO VACCC	36 KD ABORTIVE LATE PROTEIN	VACULA VIANO	191					$\frac{1}{4}$		-
PVA30 VARV	PROTEIN A20	VACCINIA VINUS (STROST CO.	1-63							-
PVA32 VACCC	PROTEIN AJO	VALUE A TRUE AND COSCULATION OF THE AND COSCU	38-49						-	1
PVA12 VARV	PROTEIN A22	VACCINIA VIRUS (3) MAIN COLEININGO	39-80				4			1
PVA33 VACCC	PROTEIN A22	VACOLA VIXOS	95.143	133.207	155-200	364-382				-
VAN VANV	PROTEIN A23	VACCINIA VIKUS (STRAIM COFEINIAGES)	95.143	133.307	115-239	344_382				1
VAN VARV	PROTEIN A23	VARIOLA VIRUS	10.136				-			1
2042	PROTEIN A31	VALUEA VINUS								+
200	PROTEIN A33	VACCIMIA VIRUS (STRAIN WR), AND (STRAIN COTENIMEET	317.251		_					4
	PROTEIN A)?	VARIOLA VIRUS	60.03			L				4
	PROTEIN A)	VARIOLA VIRUS	19.0	109-155	L					4
2	SOUTH A14 PRECURSOR	VACCINIA VIRUS (STRAIN WRI, AND (STRAIN COTENIANCES)	13.5				L			4
PVAS VALV	SECURIOR AND PRECURSOR	VANOLA YIRUS	3 2	1		L				4
אאז אינור	TACIENT OF THE PROPERTY OF THE	VACCINIA VIRUS (STRAIN COPENHAGEN)		\downarrow						1
אאס יראא	PROTEIN AJ	VACCINIA VIRUS (STRAIN WR)	3		1	-	-	-		-
PVAJE VACCC	PROTEIN AS	VACCINIA VIRUS (STRAIN COPENHAGEN)	(4.9)			-		-		L
PVA38 VACCV	PROTEIN AU	VACCINIA VIAUS (STRAIN WR)	20.0		$\frac{1}{4}$	-	+	-	-	-
PVAJB VARV	MOTEIN AUS	VARIOLA VIRUS	44.91		-	+	-	-		L
PVAJ9 VACCC	PROTEIN AJS	VACCINIA VIAUS (STRAIN COPENHAGEN)	=		1	+	$\frac{1}{1}$	+	-	-
PVAJ9 VACCV	PROTEIN AJ9	LACCING VIBIS (STRAIN WR)	15.109				+		-	1
PVA46 VACCC	PROTEIN AUP	VACTIONA VIBIS (STRAIN COPENHAGEN)	81-136			-		-	1	1
PVA46 VACEV	PROTEIN A46	DAPPERATE (STRAIN WR)	81-136			1	1	-	-	-
PVA46 VARV	PROTEIN A46	VARIOU A VIRIES	11.126			1	$\frac{1}{1}$	+	1	-
PVA47 VACCC	PROTEIN A 44	VACCEDIA VIRUS (STRAIN COPENHAGEN)	95:29	10-12			1		1	-
PVA47 VACCV	PROTEIN A47	VACCINIA VIRUS (STRAIN WR)	63.96	10.114		-	4	1		-
PVACT VARV	PROTEIN A47	וארנואוא להכי ונייייייייייייייייייייייייייייייייייי								

		All Vicuses (no bacteriophoges)	T			7 7 7 7	AREA S	AREAS	AREA?
PCCENE			I	Т	I	Γ			
THE MARIE	>	LA VIRUS	I	36.160					
PVA49 VACCC		S (STRAIN COPENHAGEN)	1						
PVA49 VACCV		VACCINIA VIBUS (STRAIN WR)		2					
PVA49 VARV		75.0		200					
PVASS VACCC		ENHAGEN	61-132						
PVA32 VACCV			201.18						
PVAST VACCC	PROTEIN ASS.	ENHAGEN)	3						
PVAID VACCV	90.03	VACCINIA VIRUS (STRAIN WR)	34-104						
PVAL1 MSVK	work.	N (SOLATE)	230-269						
PVALI MISVN		6	228-262						
PVALI MSVS		MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	228-362						
PVALI SLCV		COLLACIO FAF CURL VIRUS	117-151						
PV.ALI TYDVA		TOBACTO VELLOW DWARF VIRUS (STRAIN AUSTRALIA)	191-225						
PV N. J. AUSIWW		ABITTI ON MICKAIC VIRUS (ISOLATE WEST INDIA)	44-78	~					
PULL BGNIV		DE AN COLDEN MOSAIC VIRUS	44-78	83-124					
PVALS PYNAV		MTATO VELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	10-78	67-121					
PVAL SLCV		SOLIVERI EAS CIRE VIRUS	46-80	91-125					
PVAL) TGMV		CONTROL DEN MOCALC VIRUS	44.70						
PVAT CAMIVE		CALE IST OWNER ACCOUNT VIRUS (STRAIN CN-1841)	22.70	84-127					
PYAT CAMVD	PROTEIN	CALLIFECTURE MODELIC VIRGIS (STRAIN DAS)	22.70						
PVAT CAMVE	PROTEIN	CAULTIONER MOSAIC VISIG (STRAIN BBC)	22.70	121-04			-		
PVAT CAMVIC	PROTEIN	CALL CONTRACTOR CONTRACTOR (STRAIN NYSIS)	22.70	93.127					
PVAT CAMIVE	MOTEIN	CAUCITOMER MODERIC VIETE (STRAIN POINT)	22-70	121-137					
PVAT CAMVS	PROTEIN	AULT LOWER MOTAL VINCE (CTRAIN STRASBOURG)	23-70	93-130					
PVAT CANTW	ROTEIN	CAUCH LOWER BROAND WASHINGTON WASHINGTON	24.20						
PVAT CERV	PROTEIN	CAULIFLOWER MUSAL, VIACO (SIRCE)	99-138						
PVB03 VACCV	SAUSSION PROTEIN	CAUCA HAM ELCALD MING VINCO	108-142						
PVIION VACCC		VACCINIA VIII. (SI EALIN WA)	88-123	21.372	496-530				
PVBO4 VACCV		VACCINIA VIGOS (31 MAIN COTEN CARE)	19-133	21.32					
PVBOH VARV	PROTEIN B4	VALCINIA VIAMA (STATE OF THE ST	19.134	124.372	492-530				
PY BOS VACCO		VALUE AND STATE AND CIGADA	154.198						
PVB05 VACCC	INGE PROTEIN PRECURSOR	VACCINIA VIEWS (STRAIN COMMANDEN)	254-298						
PVR05 VACCL	PLAQUE-SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIXUS (STRAIN LUTERIA	254-298						
PVDOS VACCV	M. AQUE. SIZE / HOST RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LISTEN)	254-298						
PVB01 VACCV	PLAQUE-SIZE / HOST PLANCE PROTEIN PRECURSOR	VACCINIA VIKUS (SIRAIM WR.)	28-62						
PVD08 VACCC	PROTEIN BY PRECURSOR	VACCINIA VIRUS (STRAIN COSEMACEN)	26-60						
PATON VACCA	PROTEIN 63 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	3 %						
PVB18 VACCC	PROTEIN BE PRECURSOR	VACCINIA VIETS (STRAIN COPENHAGEN)	337-338	491-532					
PVB18 VACCV	PROTEIN B18	VACCINIA VIRUS (STRAIN WR)	337-375	191-333					
PVB18 VARV	PROTEIN BIS	VARIOLA VIRUS	337.378	<u>=</u>					
PVBIS VACCC	PROTEIN BIS	VACCINIA VIRUS (STRAIN COPENHAGEN)	13.131						
PVB19 VACCD	SUIT ACE ANTIGEN STREET OF THE COMPANY	VACCINIA VIRUS (STRAIN DAIREN I)	13-119						
PVB19 VACCV	SIMPACE ANTIOEN STREET MOOR	VACCORD VIRUS (STRADH WR)	85-119						
PVB30 VACCC	2	VACCINIA VIRUS (STRAIN COPENIAGEN)	40.83				-	1	
PVB31 VACCV	PROTEIN 820	VACCINIA VIRUS (STRAIN WR)	61.05						ŀ
PVBLI BGATV	PROTEIN BZI	BEAN GOLDEN MOSAIC VIRUS	130-103				+		
COR THE	all redicin	SQUASH LEAF CURL VIRUS	159-193		\downarrow				L
PVBL1 TGAV	BLITACIES	TOMATO COLDEN MOSAIC VIRUS	139-193			\downarrow			ļ
PVBR BGAV	SCI TACKED	BEAN COLDEN MOSAIC VIRUS	172.20				-		L
PVBR! SLCV	BAI TROITEN	SQUASH LEAF CURL VIRUS	20-61				 -		
VAR TON	BKI TROISIN	TONATO COLDEN MOSAIC VIRUS	25-59		-		-	-	L
PVC02 VACCC	BRITADIEM	VACCENTA VIRUS (STRAIN COPEMHAGEM)	13:63	262-393	1301-442				
PVC03 VACCV	PROTEIN								

ALLMOID Mod Search Re

					ANA					ĺ
	ALLMOTIS		4:	263.20	391-442					
	PROTEIN	VACCOUR VIEWS (STRAIN WR.)	T	174.400						
١	SOUTH STATES	NKASZA)	=						-	
١			12.46							
	PROTEIN CA	ENTAGEN	12-46							
	PROTEIN CO	S (STRAIN WR)	34.51							
	PROTEIN C4		12.124							
VCOI SFVKA	PROTEDICA	VIRUS (STRAIN KASZA)								
WORK VACCC	HYPOTHETICAL PROTEIN CS									
2000	MOTERICS		T							
- AVA				73-151		1				
ANA RIA			45-86			+				
VCBB SFVKA	TROUGHT PROTEIN CH		63-106				-			
VCD9 SFVICA	HYPOTHE III A CONTENT OF		62.116	160-326	259-335	232412				
VCOD VACCC	HYPOTHETICAL PROTEIN CO	MACEN	27.116	162-226	289-323	23412				L
VCO9 VACCV	PROTEIN CO		081 741							
VC10 VACCC	PROTEIN CO	ENHAGEN)				L				
200	PROTEIN C10		2							1
70.4	PROTEIN CIO		21-41			-				1
	PROTEIN CIO	CALLE CONTRACTOR (STRAIN KASZA)	2		45.			_		
V	HYPOTHETICAL PROTEIN CIT	MOTE FIGURE STRAIN KASZA)	1.66	20.65		-	-			
PICIS SVIRA	CIO MISTORE	SHOPE TIBROTIS THE ALL COPENSIA GEN	142-176			-	-			
אלופ זארור	PROTEIN CILEBA	VACCINIA VIRUS (STRAIN COPENHAGEN)	100-155	325-339		-	-			4
אינוז אינור	(10)	VACCINIA VIRUS (3) INC. 11 CONT. 11 CENT	10-01			+			L	
PYCHE VACCC	PROTEIN CHARLE	VACCINIA VIRUS (STRAIN CURENIAGES)	16-91			1	-			L
PVC19 SFVKA	PROTEIN CIPUS	SHOPE FIBROALA VIRUS (STRAIN KASKA)	310.352				\ -\			L
VCIO VACCC	PROTEIN CIO	VACCINIA VIRUS (STRAIN COPENHAGEN)	1811	670-709						ļ
VCAP EBV	PROTEIN CIWETS	EPSTEIN-BARR VIRUS (STRAIN B95-1)	74.7	191-225	260-294					ļ
NTAP HCLIVA	MIANOR CAPSID PROTEIN	MINIAN CYTOMEGALOVIRUS (STRAIN AD169)		146	-					1
NY AP HISVII	MAJOR CAPSID PROTEIN	LEBBER STATULEX VIRUS (TYPE 1 / STRAIN 17)		275	200-111	-	-			1
TIVAL TOTAL	NAJOR CAPSID PROTEIN	STATES SINGLE ST VIBILIS	130-174	3		-	-			
TO THE PARTY	NAJOR CAPSID PRUTEIN	COLUME AFREDECVIRUS TYPE I (STRAIN ADAP)	2		36,736					\downarrow
	MAJOR CAPSID PROTEIN	STATE CANCEL (STRAIN II)	479-520			-				1
MCAC HOVE	NAME CAPSID PROTEIN	HELDEN INC. STEEN	103-160	27.72	+	+	-			4
VCAV PRVIS	ALLEGA CARGID PROTEIN	PSEUDOIXABLES VINCE (STEAM DIBLAS)	_	316-350		1	1	-		
PVCAP VZVD	A PRID PROTEIN	VARICELLA-EUSTER VIRUS (STEAR POLYHEDROSIS VIRUS	110-348			1	+	-		
PYCGS NPVAC	MAKAN CASH PROTEIN	AUTOGRAPHA CALIFORNIA POS	143-181		-	1	-			L
PVD05 FOWP!	DAA-BIKOINO TAN ICA	FOWLPOX VIRUS (STRAIN PC-1)	133-157	-			$\frac{1}{4}$		+	╀
PVD65 VACCC	93.6 KD PROTEIN	VACCINIA VIDUS (STRAIN COPENHAGEN)		-		L				╀
PYDOS VACCV	PROTEIN DS	VACCINIA VIRUS (STRAIN WR.)				-			-	╀
PVD05 VARV	PROTEIN DS	VARIOLA VIRUS	91	-		_				╀
PATOS VACCO	PROTEIN DS	VACCINIA VIRUS (STRAIN COPENHAGEN)		-	-					+
AVOV.	PROTEIN DO	VACCIONA VIRUS (STRADI WR)	20-12	1	-	-			1	+
7877	PROTEDY D9	VANCE A VIRIS	201-021		+					+
	PROTECTION OF	SAME NOT STRAIN FP.1)	4.0		+	-				$\frac{1}{1}$
2	PEOTEDN DIO	SUCCES STREETS VIRUS (STRAIN KASZA)	25.	1						+
200	SECTED DIO	Multiple Committee	67-105			+				4
איםוס אימא	OTO TOTAL	VARIOLA VINCE	1:38	4		+	-		L	
PVD8P CALVC	Т	CAULIFICATER MOSAY VIRIS (STRAIN DA)	§(·)	1			+			
PYDDP CAMVO	Т	CAULIFLOWER MUSACE VECTOR (STEADY BBC)	1.35				-	_		Н
PVDBP CAMVE	Т	CAULIFLOWER MOSAIC VIRGIS (STRAIN NYSIS)	1-38		-	-	+	-		Ц
PUTTER CANVA	Т	CAULIFLOWER MUSACE VIRGO (STEAM STRASBOURG)	1:35		-	-		-	-	H
PVD8P CAMVS	T	CAULIFLOWER MUSAIC VINCE (STEEL)	382-336		1	+	+	+	-	
PVE03 VACCC	CAN DINCE OF THE PROPERTY OF T	VACCINIA VIRUS (SI INSTITUTION COLUMNIA)	282-336		1	1	1	-		-
PVE03 VACCV	Moleur	VACCINIA VIRUS (STRAIN WA)	30.535			+	1	+	-	-
PVE02 VARV	PROTEINEZ	VARIOLA VIRUS	13.61				1			-
PVED! VACCC	PROTEIN E3	VACCINIA VIRUS (STRAIN COPENHAGEN)	1					-		1
	PROTEIN EL	Charles of the Control of the Contro								
		A STATE OF THE PARTY OF THE PAR			l					

MATCHELL		A. P. P. P. P. P. P. P. P. P. P. P. P. P.	All Viruses (no bacterlophages)		ABFAI	AREA 3	AREA 4	AREA S	AREA	ABEAZ	
MARTHER	CCENT		1805	T	Γ		Γ				
MOTORINE WASCESSON, VILLE STRAND BALLED 11-10	THEMANE		ARIOLA VIRUS								
MOTION IS 18-100	VEDS VACCC		ACCINIA VIRUS (STRAIN COPENHAGEN)	3							
MOTION ISSUED MOTION ISSUE	PVE05 VACCD		ACCIDITA VIRUS (STRADI DAIDEN I)	11-103							
MOTERIE MOTERIE WIGGEN VILLE WIGGEN VILLE WILLIAM WILL	PVEOS VACCV		APPRILA VIBINE (STRAIN WR)	10.103							
10.111 11.114 10.1114 10.114 11.114	PVE03 VARV		A POST A VIBILIE	101-103							
10.00 10.0	PVEOF VACCC		ACCOUNT VIDER CETTAIN COPENIAGEN		333-266						
PROTEIN E	PVEOR VACCV		ACCIONAL VIOLES CETO AND WELL	Г	331-266						
FROTEIN FROTEIN FROM F	PVEOS VARV		ALLIPIA VIRUS (3 10 10 10 10 10 10 10 10 10 10 10 10 10		367-401						
1 HOUTEN	PVEIL MPVAC		TOCA A MAN CALL ROBATICA MILICI FAR POLYTEDROSIS VIRUS	112-163							
EL FOOTEIN FIGURAL PARTICION/VILLE TYPE 1 15-10 113-10 1	PVE! HPVIA		UTUCKATA CALICANACA HOLLEN	137.171			•				
II FROTEIN	PVEL 11PV31		IDNAN PAPILLEMAVIAUS 117E IA	06-90							
11 FOOTEN	LANGE I JAMES		RAIAN PAPELCHAVIRUS TYPE 11	19.11	131.167						
ENOTEH HOUSE HOU	1		ILDIAN PAPILLOMIAVIRUS TYPE 3)								
ENOTER FOUL FOUR FOUR FOUR FOUR FOUR FOUR FOUR FOUR FOUR	ייבו שאיז		ADAM PAPILLOMAVIRUS TYPE 15	2							
11 FOURTH 11 F	AVEL HAVE		IDMAN PAPILICALAVIRUS TYPE 19	2							
18 FOOTEN	PVEL HOVE		ADIAN PAPEL CASAVIRUS TYPE 41	2	317-71						
EMOTERN	PVEL HOVE		PRIAM BARN I CHANNELIS TYPE 43	15-47							
EMOTERN	PVEI HPVS		DALAN BARTI CALAVIRUS TYPE SE	13-47	119-174						
19 10 10 10 10 10 10 10	PVE1 HPV60		Charles and a fact where Type 48	165-199							
ELALY 29 FOR PROTECH ALTICGRAMA LEAD POLICIA POLITICAS POLITICAS 1-11	PVE! PAPVE		ILIMAN PATELLIANA VINOS 1115 C	174-310							
EALLY 19 FOR PROTEIN	PVEM NOVAC		TRUMAN ELL PATLLMAN TIRES	73-117							
PROGRAME ENTOTEIN	MARY CROWN	KD PROTEIN	AUTOGRAPHA CALIFORNILA NUCLEAR POLITICADOS	7							
MOGABLE EI PROTEIN MALANA PARLLOAA/NILS TYPE 1-15 11-19 11-1			COTTONTAIL BABBIT (SHOPE) PAPILLUNIA VIRUS (SIRVERINA)		916.310	147.183	437-471				
MODABLE ES FROTEIN	LA LA MA		ADAM PAPELOMAVIAUS TYPE S	200					L	L	
ET ROTEEN HUMAN PARLICOLAVIRUS TYRE 16 61-100	PVE2 HVG	THOUSAND STATE OF THE PARTY OF	HUMAN PAPELOMAVIRUS TYPE &	3.55	201-201						
ET ROTEIN HIGHAN PAPILLOMAYNUS TYPE 1A 11-37	PVE3 POVIS		HEALAN PAPELICALAVIRUS TYPE 16	69:100	200						L
E3 FROTEIN HIGHAN PAPILLOMAVRUS 177E 1 14-15	PVE1 HOVIE	E TRUICAN	HISTAN PAPILLOMAVIRUS TYPE 18	8							
13-47 13-4	PVE3 HOVIA	EJ PROJELIV	RIDGAN PAPILICALAYIRUS TYPE IA	257	138-183						
E1 PROTEIN HUBANI PAPLLOMAVRUS 177E 31 11-103	PVE2 HDV2A	E2 PROIEIN	HEBLAN PAPELOMAVIRUS TYPE 2A	3	158-193						
E1 PROTEIN HIGHAN PAPILLOMAVBUS 177E 31 42-109	PVE3 HDV31	EZ PROIEZA	HIBIAN PAPELOMAVIRUS TYPE 31	103							
E1 PROTEIN	PVE3 HDV3	EJ TRUIELM	HIBAAN PAPILIDAAVIRUS TYPE 33	101	297-331						
E. PROTEIN HOLAN PAPELOMAVBLIS TYPE 11 6-14	PVE3 HDV35	EJ FROTEIN	HIDALAN PAPELLONAVIRUS TYPE 35	20.00	139-193						
2.2 PROTEIN FIGHALN PAPELGRAVTRUS TYPE 41 5-54	PVE2 HPV39	E2 PROTEIN	HOMAN PAPILLOMAVIRUS TYPE 19	74-110	333-333		-				
E. PROTEIN MOBALN PAPELOBAVRIUS TYPE 41 154-191	PVE2 HPV41	E2 PROTEIN	HEMAN PAPILOMAYRUS TYPE 41	3							
E3 PROTEIN HODALN PAPILOGA/VILUS TYPE 31 154-191	PVE3 HDV47	E2 PROTEIN	HIMAN PAPELOMAVEUS TYPE 47	2	146-102						
22 PROTEIN INDALAN PAPILLOMAVRIUS TYPE 31 13-14	PVE1 HDVSI	EZPROIEM	HUMAN PAPELOMAVORUS TYPE SI	2							
12 PROTEIN INDALAN PAPILLOMAVIRUS TYPE 59 2-14	PVE1 HDV57	EZ PROTEIN	HIDAN PAPELOWA VIRUS TYPE 57	2	175.213						
PLOGABLE E2 PROTEIN PRIDALAN PAULOAKVRIUS 1YE 5B 5-21	PVE1 HOVE	EZ TROTEIN	HUNGAN PAPILLOMA VIRUS TYPE SI	2							
PROBABLE ES PROTEIN DEER PAVILLOBANVRUS 101-150	PVEZ HAVS	SPORARI E ST PROTEON	HUNGAN PAPILLOMAVIRUS TYPE SB								
FORMATILE ET PROTEIN	LACE PARTY	PEORADI F ES PROTEDA	DEER PAPILLOMAVIRUS	101							
E3 PROTEIN PYCANY CHADA ANZEL DALAVIALUS TYPE 41-164	200	PRODUCE ES PROTEON	EUROPEAN ELK PAPILLOMAVIRUS				-				
E3 FACTERN AUTOGALVARUS TYPE 14 EALT Y 19 KD PROTEIN AUTOGALVAR CALL'EGALEA POLYMEDROSIS VIRUS 116-154 EALLY 19 KD PROTEIN AUTOGALVAR CALL'EGALEA POLYMEDROSIS VIRUS 116-154 PAGALE E PROTEIN REALLY 19 KD PROTEIN 63-46 PROBALE E PROTEIN REALLY 19 KD PROTEIN 63-47 PROBALE E PROTEIN REALLY 19 KD PROTEIN 63-47 PROBALE E PROTEIN REALLY 19 KD PROTEIN 641-719 PROBALE E PROTEIN REALLY 19 KD ROTEIN 641-719 PROBALE E PROTEIN REALLY 19 KD ROTEIN 641-719 PROBALE E PROTEIN REALLY 20 REALL 20 ROTEIN 641-719 PROBAL 20 ROTEIN REALL 30 ROTEIN (19 KD GL VCOP TRACHOPALUSA IN GRANILOSIS VIRUS (19 KD V) 111-344 BENYELOF E ROTEIN (19 KD PROTEIN) (TVES PLY	ESPECIEN	PYCANY CHEGOANZEE PAPILLOMAVIRUS TYPE I	2	101.101						
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EALLY 19 KD PROTEIN PROMABLE EN PROTEIN PROMAB	PVEJ9 KIVAL	CATACOLOUR SECUEDA	ALTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS				-				
PAGALILE E O ROTEDN	VED KYC	SAN PROTECTION	DRIGHTA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRU	200			-				
PLOBABLE E PROTEIN	PVE4 POVIE	POOL P PA PROTEIN	HEBITAN PAPILLONIA VIRUS TYPE 18								
PROBABLE ES PROTEIN VIDAL ENANCHOS FACTOR (VEF) (104 KD GL YCCP TILCHOPLUSIA NI GRANILOSIS VIRUS (TNGV) SENVELOPE PROTEIN GAVELOPE PROTEIN ENVELOPE GL YCOPROTEIN PLECUASOR DALONS ENVELOPE GL YCOPROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (STRAD INDIANY) (DHO) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (CORTAGIOSIAN VIRUS SUBTYPE 1 (ACVI) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (CORTAGIOSIAN VIRUS SUBTYPE 1 (ACVI) 111-344 MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (CORTAGIOSIAN VIRUS SUBTYPE 1 (ACVI) 111-344 111-345 MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) 111-344 111-345 MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) 111-344 MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) (19-346) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) (19-346) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) (19-346) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PA3K MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) (19-346) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PASK MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) (19-346) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PASK MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) (19-346) MALONE ENVELOPE PROTEIN (19 KD PROTEIN) (PASK MOLLIASCIA) (TRUS (19 TYPE 1 (ACVI)) (TRUS	PVEA HOVE	PROPARI R EL PROTEDA	HUMAN PAPILLOMANIUS TYPE 41		95,78						
VIDAL ENGACING PACTOR (VEF) (104 KD GLYCOP ITACHORLUSA NI GIANNILOSIS VIRUS (17NGY) ENVELOPE PROTEIN ENVELOPE GLYCOPROTEIN PRECLASOR ENVELOPE GLYCOPROTEIN PRECLASOR MAJOR ENVELOPE PROTEIN (13 KD PROTEIN) (19 KD PROTEIN)	PVC CVC						-			L	
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MAJOR ENYELOPE PROTEIN (4) ED PROTEIN (PAIK MOLLISCUM CONTAGIOSUM VIRUS SUBTYPE 2 (DACVII) LANCOR ENYELOPE PROTEIN PRECINCOR (SUBFACE THOGOTO VIRUS (THO)	WENT MEN	ALL TOP ENVEL OPE PROTECU (4) KD PROTECH (PAS)	MOLLUSCIDA CONTAGIOSUM VIRUS SUBTYPE I (MCVI)	200			\downarrow	1	1		
MANA CAL WOODEN THE PRECURSOR (SURFACE TWOODTO VIRUS (TWO)	PVENV MCV2	1	MOLLUSCUM CONTAGIOSUM VIRUS SUBTYPE 2 (MCVII)	20.00			+	1		-	
	PVENY THOGA	1	THOOOTO VIRUS (THO)	71.71X							

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MARTING CONTROL 1972 1				157-295							
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		LIANOR ENVELOPE PROTEIN (17 KU PROTEIN)	ALIFORNICA KINCLEAR POLYTIEDROSIS VIKUS	1	124-151						
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MODIENT INTERNAL PROTEIN PACCESS WING THE MODIENT CONTRIVERS 11-13		PROTEINFI		T							
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WICERA WILLIAM CONFORMACE) 11-17	Ī	20011001	VACCINIA VIRUS (STANIS)	71-110							
NECTION OF SERVICE AND STATEMENT 11-13 1			VACCINIA VIRUS (3 I PARIS TO TO TO TO TO TO TO TO TO TO TO TO TO	621-11	283-370						
M. E. MACHELLI, M. M. CECHAN MUST FILLY, M. M. M. M. M. M. M. M. M. M. M. M. M.	1	S ACENTRA NE PROTEIN PRECURS	VACCINIA VIRUS (3) RAIN CONTINUE	871-18	282-320						
NEGITIEM NATIONAL STATES	VACCE	TO NICOLA PIECURSOR	VACCIMIA VIRUS (STRAIM L-197)		121-131						L
14 CONTRIBUTE 14 CONTRIBUT	VACCV	THE MINIOR PIECUSOR	VACCINIA VIRUS (STRAIN WR)		281-322						L
11 12 12 12 12 12 12 12	VARV	16 KO MAJOR PLEADING THE PROPERTY OF FOLISTOR	VARIOLA VIRUS	3							
PROTEIN 11 VACCION VIRIG (STAMP COPENACEN) 11-34 15-31	VARV		VARIOLA VIRUS	200	269-315						
PROTEEN ! PROTEEN	VACCC.	PROTEIN F	VACCINIA MILIS (STRAIN COPENIAGEN)		111.37%		L				
PROTEIN 11 VACCIOLA VILLE VACCIOLA VILLE VACCIOLA VILLE VACCIOLA VILLE VALCIOLA	V.ACCP	PROTEINFIL	VACCIONA VIRUS (STRAIN L-1VP)								1
19 19 19 19 19 19 19 19	7877	PROTEIN FIL	STATE A VIBIL	6:5		100.236	330-388	\$44.585			\downarrow
PROTEIN 1		PROTENTI	CONTRACTOR AND COPENIAGEN)	Q.		1	100.00	1844.511			
PROTEIN 11 VALCOLA VIRUS 115-194 115-1	NACK.	PROTEIN F12	VACCIMIA VINOS (STELLINE)	1.63	61-181		187.58				
PROTEINT VACCHIA VIRUS (STANIN COPERALGEN) 151-194	AALL	2004504	VACCIMIA VINUS (STEAM)	1-67	14.230				L		
MODIEM M	VANV		VARIOLA VIRUS	155-194			1				
PROTEIN 11 PROTEIN 12 PRO	VACCC	PROIEURIS	VACCINIA VIRUS (STRAIM COFEMINACES)	155-194			$\frac{1}{4}$		-		Ĺ
PROTEIN 11	4 VACCP	PROTEINFIL	VACCINIA VIRUS (STRAIN L-1VP)	153.184					1		L
PROTEIN 19 PROTEIN 19 FOW-DOX VILUS	6 VARV	PROTEINFIE	VARIOLA VIRUS	3	L						L
PROTEIN PACE	1 FOWPV	PROTEIN F16	FOWLPOX VIRUS	136173	230-273						
FACTER IF A	4 FOWPV	PROTEINTP	FOWN POX VIRUS				_				1
PROTEIN PROTEIN POWLOX YRUS (STAM COPENIAGEN) 10-44	VOWOR	PROTEIN FP4	FOWN POX VIRUS				-				1
INTOTIBETION CAPENTY VACCHIAN VRIUS (STRAIN WR) 190-10-10-10-10-10-10-10-10-10-10-10-10-10	FOWE	PROTEIN FP?	FOUND OX VIRUS (STRAIN FP.1)			-			1		1
14 KD FUSION PROTEIN	איניני	FPLEFT PROTEIN (FRAGMENT)	VACCIDITA VIEUS (STRAIN COPCINITAGEN)	1		-					\downarrow
INTOTRETICAL GENE PROTEIN ICTALUMD NEMESYRUS ICHANNEL CATFISH VARUS (CCV) 111-304 111-314		14 KD FUSION PROTEIN	CACLINIA VISITE PETRIN WE)	ş ğ		677.00	20.00				1
	NAC.	IA ED FISSON PROTEIN	VACCINIA VINUS (SELECTIFISH VINUS) (CCV)	33.38	212-21				_		
PROTEIN GI PRO	OI HSVII	INVESTIGATION GENE I PROTEIN	ICTALUMUS NEW COST AND COPENHAGEN)	301-339		+	1				4
PROTEIN CI (TRACATENT) VALCHA VILLS STACKH VILLS	OI VALLE	10 10 10 10 10 10 10 10 10 10 10 10 10 1	VACCINIA VACO (STATE OF THE STA	240-278		4	+	1			
PROTEIN CITY CENE 1 MOTERN VALIDIA VRAUS	OI VACCV	PROTEIN OF THE PARTY OF THE PAR	VACCING VIRUS (3) INVITATION TO	301-339		$\frac{1}{4}$	+	-	-		
GENET PROTEIN GENET PROTEIN GENET PROTEIN GENET PROTEIN GENET PROTEIN GENET PROTEIN GENET PROTEIN GENET PROTEIN GENET PROTEIN GENET PROTEIN FROTIEN GIA FROTIEN	OI VARV	PROTEIN CI (FRANCISCO)	VARIOLA VIRUS	141-131			-		+	-	
GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN GENE 1 MOTERN VALIGATA VILLIA VALIGATA VIL	OS HISVED	PROTEIN G1	EQUINE MEMPESVIRUS TYPE I (STRAIN ABAT) (EIVT)	101.17				1	1	1	L
CENE 1 PROTEIN (OW L.1)	O HSVEK	CENE 1 PROTEIN	FOUNCE HELPES VIRUS TYPE 1 (STRAIN KENTUCKT A) (CHITT)		-	-				1	1
PROTEIN G3	VARV	CENE 1 PROTEIN (ON L!)	VARIOR A VIRUS		344.386	335.389	-			$\frac{1}{4}$	$\frac{1}{1}$
PROTEIN G PROTEIN G PROTEIN G	2047	PROTEDIO	WASCINIA VIELS (STRAIN COPENHAGEN)			115.18	-			1	+
PROTEIN GE	7847 30	PROTEIN GS	V31215	┱				-			+
HYPOTHETICAL GENE I AGEAGRANE PROTEIN (CTALIND PEARSYRUS I (CHANNEL CATRISH VIRUS) (CCV) (4-103) HYPOTHETICAL GENE I PEAGLANE PROTEIN (CTALIND PEARSYRUS I (CHANNEL CATRISH VIRUS) (CCV) (4-103) HYPOTHETICAL GENE I PROTEIN ON (TAGAHAN VIRUS (STRAIN COPENHAGEN) (14-11) (150	PROTEDUGS .	CHANNEL CATFISH VIRUS) (CHANNEL CATFISH VIRUS) (CCV)	_ [\downarrow	+	-				1
TATOTHE TICL. CENE 1 MEMORING PROTEIN COTEMHACEN) TATOTHE TICL. CENE 1 MEMORING PROTEIN VACCORA VIRUS (STAJIN COPEMHACEN) TATOTHE I (PROTEIN CO) TA	3	LYSOTHETICAL CENE & MENBRANE PROTEIN	CCV)	_		+		-	_		4
PROTEIN GT	100 M2	ANY DESCRIPTION OF STREET	ICTALULUS TENENT COPENDACEN			-	+	-	-		4
PROTEIN CONTROLL OF TAXOLAY THE STALL COPENHAGEN) PROTEIN FI (PROTEIN CO) VACCINIA VALUS (STALM WR) PROTEIN FI (PROTEIN CO) VALUA VALUS (STALM WR) PROTEIN FI (PROTEIN CO) VALUA VALUS (STALM WR) PROTEIN FI (PROTEIN CO) VALUA VALUS (STALM WR) GENE 13 PROTEIN WYPOTHETICAL GENE 10 PROTEIN HYPOTHETICAL GENE 10 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 12 PROTEIN HYPOTHETICAL GENE 13 PROTEIN HYPOTHETICAL GENE 14 PROTEIN HYPOTHETI	Sol VACE	13 712 11	VACCINIA VIAUS (STINGING)	114-139	134-358		1	1		L	
HOTEIN FI (PROTEIN G9) WACCINIA VILLS (STALIN COFFERENCE) WACCINIA VILLS (STALIN WR) FROTEIN FI (PROTEIN G9) (TALINGHERY) WALCINIA VILLS (STALIN WR) FROTEIN FI (PROTEIN G9) (TALINGHERY) WACCINIA VILLS STALIN FROTEIN G9) WATCHIEFICAL GENE IS MEABLANE PROTEIN WATCHIEFICAL GENE IS PROTEIN WATCHIEFIC	CO) VARV	racium Ci	VARIOLA VIRUS	304.338				+	-	-	L
PROTEIN FI (PADIENT OF AGAZEMY) VACCORA VBLIS (STAAN WR) FROTEIN FIGUREN OF (FAGAZEMY) FROTEIN FIGUREN OF (FAGAZEMY) FROTEIN FIGUREN OF (FAGAZEMY) FROTEIN FIGUREN OF (FAGAZEMY) FROTEIN FIGUREN OF (FAGAZEMY) FROTEIN FIGUREN OF (FAGAZEMY) FROTEIN FIGUREN OF (FAGAZEMY) FROTEIN FROTEIN FROTEIN FROTEIN F	COP VACCC	PROTEIN G	VACCINIA VIRUS (STRAIN COPENIANCEN)	104.118				1	+		-
PROTECT I (PROTEIN OF) (PACHALLY) PROTECT I (PROTEIN OF) PROTECT I (PROTEIN OF) PROTECT I (PROTEIN OF) PROTECT I (PROTEIN OF) PROTECT I (PROTEIN OF) SPROPLASA VALUS SPRIAN I (PRANTEIN OF) REPOYDET CALGE IS PROTEIN REPOYDET CALGE	CON VACCV	PROTEIN FI (PROTEIN CV)	VACCIDALA VIRUS (STRADA WR)	1	-	-			1		1
HYPOTETH II (PROTEIN CO) HYPOTETH II (PROTEIN CO) HYPOTETH CALL GENE IS PROTEIN HYPOTETH C	OOS VARV	PROTEIN FI (PROTEIN OF) (PRACHES)	VARIOLA VIRUS	Т	-				1		\downarrow
HYPOTHETICAL GENE 10 PACKAROVE TO THE STROPLASMA VRIUS SPVI-MAALD B 11-95 GENE 12 PAOTEIN HYPOTHETICAL GENE 10 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 11 PROTEIN HYPOTHETICAL GENE 12 PROTEIN HYPOTHETICAL	CIO HSVII		ICTALURID HERPESVIRUS I (CHANNEL CATFISH VIXUS) (CL.	7	-	-				+	$\frac{1}{1}$
GENE 11 PROTEIN KYPOTHETICAL GENE 11 PROTEIN KYPOTHETICAL GENE 11 PROTEIN KYPOTHETICAL GENE 11 PROTEIN KYPOTHETICAL GENE 11 PROTEIN KYPOTHETICAL GENE 11 PROTEIN KYPOTHETICAL GENE 11 PROTEIN KYPOTHETICAL GENE 11 PROTEIN KANTALITA MOOREI EKTOMOPONYINUS (AMENY) GIL PROTEIN	GIT SPVIR		SPIROPLASMA VIRUS SPVI-REAZ B	Т	1	-				+	+
HYPOTHETICAL GENE 18 NOTEIN ICTALIND NEWESWINGS (CHANNEL CATTISH VALUS) (CCV) 19-129 HYPOTHETICAL GENE 18 NOTEIN ICTALIND NEWESVINUS (CHANNEL CATTISH VALUS) (CCV) 114-209 HYPOTHETICAL GENE 18 NOTEIN ICTALIND NEWESWINUS (CHANNEL CATTISH VALUS) GLI PROTEIN GLI PROTEIN	GIE HSVSA	GENE 13 PROTEIN	HERPESYTHUS SADMIN (STRAIN !!)	Т	115.211		-			1	+
HYPOTIETICAL GENE 13 PROTEIN ICTALINED REAPESYTAUS 1 (CIANOREL CATFISH VAUS) (CAT ANTOINETICAL GENE 13 PROTEIN ANTAINET	HSVII	HYPOTHETICAL GENE 16 PROTEIN	ICTALLIND HEAPES YINUS I (CHANNEL CATFISH VINUS) (CC)	т	2					+	+
HYPOTHETICAL GENE IS MOTEUN AMEACTA MOGRES ENTORIOPOXYIRUS (AMERY) GIL PROTEIN	HSWIT	HYPOTHETICAL GENTE 17 PROTEIN	KTALURD PERPESYINGS I (CHANNEL CATFISH VIRUS) (CC.	т					-	-	$\frac{1}{2}$
GIL PROTECT	Add to	Τ	AMERITA MOGREI ENTONOPOXVIRUS (AMERV)	7	$\left\{ \right.$						
	100	T									

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		417.670	660-89	1033	-		
INTO INTO		74.108					
1170 111	1 1 1					Ì	
17.70 18.10 17.70 18.10 17.70 18.10 18.10 17.70 18.1	1 1 1					j	
GENT PROTECT INTO	1 1	104-218					
INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVINU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVIRU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO IERRESVIRU I (CIANNEL CATESII VIRUS) (CCV) INFOITE III.AL. GENE 31 PROTEIN CELAURO I	1	205-336					
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INTOINE IECAL GENE 15 PROTEIN CTALUND IERAESVINUS CICIANNEL CATISIS VIRUSISCON	I (CHANNEL CATTISH VIRUS) (CCV) 145-179					Ì	
INTO III ETAL GESS IPPOTEN GEALGIAN TOTAL GENERAL CATTESI VIRUS SEVIANI SI CHANNEL CATTESI VIRUS SECTION SI CHANNEL CATTESI VIRUS S	I ICHANNEL CATFISH VIRUSHCCV) 17:90						
INFOILERICAL CENS INFORMS INFOILERICAL CENS INFOIRMS INFOILERICAL CENS INFOIRMS INFOILERICAL CENS INFOIRMS INFOILERICAL CENS	STATES CATTISH VINUS (CV 135-47)						
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PVCLB HSVB2	GLYCOPROTEIN I PRECURSOR	CONSTRUCTION OF STRAIN BAIL	440.474	141.903						
PLGLE HISVEC	GLYCOPROTERN B-1 PRECURSOR	THE PROPERTY OF THE PARTY OF TH	163.400							
	CLYCOPROTEIN I PRECURSOR	DOVINE LEADER STATE LISTON AT INCOME.	943.570	196-116						
1	GLYCOPROTEIN B PRECURSOR	CONT. ILEGA STATE	474.515	141.800						
l	GLYCOPROTEIN BPRECURSOR	COINE TRACES THE STATE OF THE S	142.536	198-1-10						
1	GLYCOPROTEIN B PRECURSOR	FOUND HEAVES VILLE (STEAKY AND	417.174	196110						
15.00	GLYCOPROTEIN B PRECURSOR	FOUND INTERPRETATION TYPE 1 (STEAM AD-P)		910.010						
ı	CLYCOPROTEIN B PRECURSOR	EQUINE HEAPESVIRUS TOPE I (STRAIN ALTHUM TO		110.613	317.145					
2000	CI V COPROTE IN B PACCURSOR	PLAKEK'S DISEASE IEAPESVIRUS (STRATS ROTE)		104.401				L		
1	CI VCOPROTEIN B PALCURSOR	IEEDESVIAUS SABILITI (STRAIN I I)		15.65	401.716	346.378	160-091			
	CL VOORDOTE DE PRECURSOR	MUMINE CYTOMEGALOVIRUS (STRAIN SAUTH)	•••						L	
	C. C. C. C. DEL C. DEL C. DEL C. D.	PSEUDORABIES VIRUS ISTRAIN INDIANA-FUNKILAUSER / DEUAE				-				
200	SOLUTION OF THE PROPERTY OF TH	VAINCELLA-ZOSTER VIRUS (STRAIN DUNIAS)		200		<u> </u>	 -			
200		JERPES SINDLEX VIRUS (TVPE I / STRAIN I')	98.310							
Cic IISVIK	CLY CAROLEIN C TALCONSON	IGENES SLADLEX VIRUS (TYPE I / STRAIN KOS)	3				-			
VCIC HSVI		IGENES SUPLEX VIRUS (TYPE 1)	-			-	-			
VOLC IISV	COLORDIES CHARLES	HEAPES SOULEX VIRUS (TYPE 27 STRAIN 191)	1			1	-			
איכור ווצאשנ	CLYCOROLEIA C PACCONSON	BOVING ISTANCESVIRUS TYPE I (STRAIN COOPER)								
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FILE WANIE		VAC:	Ţ	SELA!	OFFICE	1	Т	1010	7	1
PVILC PRVIF	SECRETURY GLYCOPROTEIN GP! T . S PRICLASOR	STAREN'S DISEASE HEAPES VIRUS (STR.NE) SIDIS								
אמנ מיצים	GL YCOFROTEIN GIII PRI CL'R SOR	PSEUDORADIES VIRUS (STRAIN INDIANA-FUNKTIAUSER/ DECKE								
PVGIC VZVS	GL VCOPROTEIN GPV	VANCELLA ZUSTER VIRUS ISTRATY DUNIUS)							1	
PVGLD HSVEA	GLYCOPROTEIN GPV	VAUCELLA-TOSTER VIRUS ISTRAIN SCOTT)	7							
PVGID HSVTB	GLYCOPROTEIN D PRECURSOR	EQUINE METALS SYNCE I (STEATS AND)								
PYCAD HSVTK	GLYCUPROTEIN D PRECURSOR	FOUND IN MINISTER IN THE PROPERTY AND INC.								
MCLE HSVII	CL VC IIPOTEIN D PPF CLASOR	EQUING HEIGHTS LIKE HISTORIAN MENTON MATA					Ī			
PY GLE 115V2	CANCOPROTEIN E PRECURSOR	IERPES SINGLEX VIRUS (1VPL 1/STRAIN 17)								
PVCH F BRSVA	CLYCOPROTEIN E PRECURSOR	HERDES SIMPLEM VIRUS (TVPE 2)	Ī							
PACE BROVE	PUSION OF YCOPROTEIN PRECURSUR	BOVINE RESPIRATIONS SYNCYTIAL VINUS (STRAIN ASSISTED)	Î	96.56						
Ĺ	IT SHOW GLYCOPROTEIN PRECURSOR	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGE	Ī	\$47.302	56-51					
1	ILISHING VOOROIEN PRECENSOR	POLINE ALSHILATORY SYNCYTIAL VIAUS (STRAIN ABBA)	Ī	141.101	106-551					j
10871	TUSION GLYCOPROTEIN PRECLASOR	CANINE DISTENDED VIRUS (STRAIN ONDERSTEPOORT)		140-181	\$68-603					
I LIBSVA	PUSHING OF YCOPACIEIN PRECURSOR	HUDIAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP BY STRAI		167-102	506-549					
Tusul I	PUSION CA YCOPROTEIN PRECURSOR	HUSTAN RESPIRATORY SYNCYTIAL CIRUS (STRAIN AS	107-91	167-102	\$06-549					
15	FINANCE VEORADIES PRECIDENT	HIGHAN BESPIENTORY SYNCYTIAL VIRUS (SUBGROUP AVSTRA	116.302	261.302	506-547					
PACIFICACION PACIF	PUSION CLYCOPADTEIN PARCUASOR	HUNIAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSS-2)	116-302 20	267-303	906-349					
PACAL MEASI	FUSION GLYCOPADIEIN PRECURSOR	MEASLES VIRUS (STRAIN EDMONSTOM) AND (STRAIM HALLE)		328-269	133.500					Ī
TIEST SHASY	PUSION GLYCOPROTEIN PRECURSOR	MEASLES VIRUS (STRAIN IP.) CA)		271.172	155-501					
	ILUSION GLYCOPROJETH PRECTURSIN	ARASI.ES VIAUS (STRAIN YAMAGATA-1)	111-114		453-500					
	PLUSION CLYCOPROJETN PRECURSOR	MUNIPS VIRUS (STRAIN SOL.1)	30.50	103-179	115-217	447.502				
	#05E7ULE4 713T0E4ULA 13 703013	ALIANDS VIBUS (STRAIN MITTALIARA VACCINE)	20.55	Π	315-372	117.502				
	FUSTON CLYCOPROTEIN PRECURSOR	AUMOS VIRUS (STRAIN AW)	20.52		115-272	447.502				
	TOSON GLYCOPROJEIN PRECURSOR	MUNDS VIRUS (STRAPN SOL)	30.54	103-179	335.312	447.503				
	PUSION GLYCOPROTEIN PRECUSSOR	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA))	201-111		31-511					
PVGET NOVICE	I USION GLYCOPROTEIN PRECURSOR	NEWCASILE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	137:103		436-513					
PLUE KOVIE	FUSION GLYCOPROTEIN PRECURSON	NEWCASILE DISEASE VIRUS (STRAIN HERVI)	117-113	111-111	116-317					
PICE ROV	PUSION CLYCOPROTEIN PRECUESOR	NEWCASILE DISEASE VIRUS (STRAM DI-HITCHNERAT)	-		436.519					
וימנ ושע	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN ITALIEWAS)	٦	٦	3					
PICE NOW!	FUSION CL YCOPROTERN PRECURSOR	NEWCASTLE DISEASE VIAUS (STRAIN LAS/46)	٦	٦	18.51					
PVCLF MOVO	PUSION CLYCOPROTEIN PRECURSOR	MEWCASTLE DISEASE VAUS (STRAIN MIYADERASTI)	П	Ì	200					
PUCLE NOVE	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLANDMA)	Ì	Ì	215					
PVGLF HDVTG	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIAUS (STRAIN TEXAS)	Ī	Ī		1		1		
TIGE MOVE	PUSION GLYCOPROTEIN PRECURSOR	MEWCASILE DISEASE VIKUS (SIKAIM IEKAS CE AL)	701-77					1	Ì	Ī
VICE PHODO	FUSION GLYCOPROTEIN PRECURSOR	PHOCENE DISEASE VINOS (31 NAIN OLS LENDA)	T	Т	Τ	19:41	Ī	T		Ī
1000	FUSION OF POPROTEIN PRECUESOR	INDIAN PARAMETURNZA I VIRUS (STRAIN C19)		Τ	T					
PVGLF PIZING	FUSION GLYCOPROTERN PRECURSOR		Γ	T						
PYCLE PINT	FUSION GLYCOPROTEIN PRECURSOR	(STRAIN GREER)	93-183	477-533						
PVGLT PID	FUSION GLYCOPROTEIN PRECURSOR	(STRAIN TOSHIBA)								
PVGLF PINIS	FUSION GLYCOPROTEIN PRECUISOR		Ì		136-518					
PVCA F RINDK	FUSION CLYCOPROTEIN PRECURSOR	IN MIII 47105)	Ī	٦	462-533					
PVCR.F RINDS.	FUSION CL YCOPROTEIN PRECURSOR	(DETE CI)	Ī	Ī	448-493					
	I USION CLYCOPROTEIN PRECURSOR		Ī	Ī	20.32	1			Ť	
PUCILI SENDI	FUSION CLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN Z / 110ST MUTANTS)	Ī	T	100				Ì.	T
P.CLF SENDI	FUSION CLYCOPROTEIN PRECURSOR	SEMDAI VINUS (STRAIN FUSIONI)	Т	ī		1	T	T	Ī	
•	FUSION CLYCOPROTERN PRECURSOR	SENDAI VIRUS (STRAIN HARUS)		1		Ì			Ì	
_	LUSION CLYCOPIO EIN PRECURSOR	SENDAI VINUS (STRAIN HV)								Ī
200	POSION GLYCOPROJETN PRECURSOR	SENDAL VIELE	T	107.70				Ì		Ī
٦.	TOSION OF TOO ROLL ON THE CONTROL	CONTAN VIEW (1618 AND 1611)		I.	131.447		Ī			Ī
	CUSION CLYCOPROTEIN PROCURSOR	TIMERY VEINOTRACIETTS VIRUS	Τ	Т	137.491	Ī	Ī	T	T	Ī
-1	The state of the s		1	1						

		AS Virues (no berterioginoffet)		ABFA 2	ARCA 3	98.6	7			
	ALLWOTTS		Ì	Ī	Γ					
- 1		E EPHENERAL FEVER VIRUS	Ì							
i		VIRUS ISTRAIN COPENHAGE							-	
1		SESSION TONY CYNCYTIAL VIRUS (SUBGROUP B. STRAIL	10.01							
COC HEST			50.00							
ł			10.00							
IN SV			00.00							
VELO 105V	MAJOR SURFACE GLYCOPROTEIN G		500							
	NIAIOR SIMPACE CLYCOPROTEIN G		200							
	NILLON STIMP ACE GLYCOPROTEIN G	_								
	NI STORE OF ACCUSED AND ACCUSE	_								
	THE PROPERTY OF THE PROPERTY O	-								
- 1	MANDE STREAM OF THE PROPERTY OF		3							
III SVL	MA YOR SLIRE ACE GLYCHTROICING		25-05							
15 VE	MIAKON SUNTACE GILYCOPNOTEIN G	STATE OF THE PARTY STATE OF THE	111.105							
1	GLYCUPAGIEIN G PALCURSOR	•		161-191						
1	CHIKE GLYCOPROTEIN PRECURSOR		111.111							
1	SPIKE GLYCOPROTEIN PRECURSOR	T	141.107							
	TOTAL COMPONENT OF THE PARTY OF									
ای	STATE OF TOTAL PROPERTY.	2	470-310		90.					L
- 1	SPIKE GLYLOPROTEIN PRESCRIPTION		Т	107.00						
	CLYCOPIOILIN CYD TALCORSON	MAIAN CYTOMEGALOVIRUS (STRAIN ADIAS)	١	376.31						
_	GLYCOPHOTEIN II PRECURSOR	HALAN CYTOMEGAL OVIRUS (STRAIN TOWNE)	101-136	692.740						
	CLYCOPROTEIN II PRECLIFIOR	STATE OF THE CANADA IN STRAIN IN	187.481							
ì	GLYCOPROTEIN HPRECURSOR	ILEACE STANCES AND COMMENT OF THE PARTY OF T	443.483							1
1	GLYCOPROTEIN II PRECUASOR	HERPES SIMIPLEX VIXUS (177E 1/3) INCHAINTING	113.404							
1	CI VODEDTEIN II PRECIMSOR	IERPES SINDLEX VIRUS (TYPE OF STRAIM US)	***				L			
1	CONTRACTOR IN THE PROCESSOR	BOVINE IGENESMBUS TYPE I (STRAIN COOPER)	Ī							
1	CONTRACTOR PRECISEOR	EQUINE HERVESVIRUS TYPE + (STRAIN 1942)	1							
1	C. COORDOTE IN IN PRECISE SOR	EQUINE HERPESVIRUS TYPE I (STRAFN ABIP) AND (ISOLATE NY			11.					
- [SCALL STATE OF SCALL	IE RPESVIRUS SAIMIN (STRAIM II)								
VGLII MICNIVS		NIUME CYTONEGALOVIRUS (STRAIM SMITH	440-474							
VGLH PRVKA	LL TCOTROICES IN PACCAGE COM	PSEUDORABIES VIRUS (STRATM RAPLAM)	20-20							
VOL II PRVNI	GLYCOROLEIN II PRECURSOR	PSEUDORABLES VIRUS (STRAIN MIA-1)	126-260							
PVGI.H PRVIL	GLYCOPROTEIN IF PACCUASOR	SCHOOLANIES VIRUS (STRAIN RCE)	236-360							ļ
אכנוו עצעם	GLYCOPROTEIN H PRECURSOR	VARIETI A PROTER VIRUS (STRAIN DURIAS)	455.306							ļ
PVGLI HCNIVA		CONTRACTOR OF STRAIN ADIES	111-10	333-359						1
PVCLM BUNGE	INDIEDIATE EARLY GLYCOPROTEIN PRECURSOR	TONIAN CTIONE CALLESTON	\$12.567	665-737	1336-1267					1
PVGLM BURLT	NEPOLYPROJEDY PRECURSOR	DUNTAVIACS GENERALISM	641.437	916-950						_
MACHINE BIDAN	IN POLYPROTEIN PRECURSOR	BUNYAVIRUS LA CRUSSE (1300A 1 E L'A)	(17.17)							
	AT POL YPROTEIN PRECURSOR	BUNYAYAUS SHOWSHOE HARE		100	916					
100	LA POLI VEROTEIN PRECURSOR	BUNYAKWERA VIRUS	140.374							L
ארד או מחספ	Section Sectio	DUGBE VIRUS	411.414	ON CALL						L
PVCLN HAMIS		HANTAAN VIRUS (STRAIN B-1)	601.717							L
PVCLM HANTH	IN POLYTHUIEN PRECORSON	HANTAAN VIRUS (STRADN HOJO)	12-106							1
PVCLM HANTL	M POL YPROTEIN PRECURSOR	HANTAAN VIRUS (STRAIN LEE)	13-106							\downarrow
PVGERI HANTV	M POL YPROTEIN PRECURSOR	HANTAN VIRES (STRAIN 76-118)	301-64							1
PVCI M INSV	M POL YPROTEIN PRECURSOR	A STATE OF COURT CITY	1011.101							1
PVCLM PHV	NI POLYPROTEIN PRECURSOR	IMPAILERS AND ACTUAL								4
PVGLN PTPV	M POLYPROTEIN PRECURSOR	PROSPECT HILL VIAUS	149.131							
PVGLM SEOUR	M POLYPROTEIN PRECURSOR	PUNTA TORO PILEBUVINOS	1			L				_
PVGI M SEOUR	M POLYPROTEIN PRECURSOR	SEOUL VIRUS (STRAIM BE-17)	1111			_				_
STORE IN SECURI	NI POLYPROTEIN PRECURSOR	SEOUR, VIRUS (STRAIN RZZ)	91. 100							
				970						
2 3	MONETH INTINAL GLYCOPROTEIN GNS PAECURSO	BOVINE EPIENIERAL FEVER VIRUS				2001.000		-		L
200	PEPE ONER GLYCOPROTEIN PRECURSOR	BERNE VIRUS	200				-			L
NOT Y AND	CECTETED GLYCOPROTEDY GX	PSEUDORABIES VIRUS (STRAIN NUCE)	1020			1	1	-		L

PCGENE	ALLAIOTIS	ares (no besteriophygra)	ARCAL	ARCA 1	AREAJ	AREA 4	AREA S	AREAS	ABGA1	AREAL
HERAPIE			36.10	7						
PVGLY LASSI	GLYCOPROTEIN POLYPROTEIN PRECURSOR		18.361	18-433						
PVGLY LYCVA	CLYCOPROTEIN POLYPROTEIN PRECURSOR			105.413					-	
PVGLY LYCVW	GLYCUPROTEIN POLYPROTEIN PRECURSOR			111.167	105.432					
PVGLY MOPEI	CLYCOPROTEIN POLYPROTEIN PRECURSOR	CHORIOMENINGINS VINUS (SINAME)								
P'GLY PIARY	GLYCOPROTEIN POLYPROTEIN PRECURSOR									
PVGLY TACV	GLYCOPROTEIN POLYPROTEIN PRECURSOR	VIRUS								
PVGLY TACVS	CL YCOPROTEIN POLYPROTEIN PRECURSOR		13:303							
PVCI V TACVI	GLYCOPROTEIN POLYPROTEIN PRECURSOR		101-111	207-710						
ı	CI VERDITEIN POR YPROTEIN PRECURSOR		101.150	31-13						
	CI CLORED TEIN POL VALORETA PRECISSOR	rt. 11590)	161-161	161-116						
- 1	OF TOTAL STATE OF THE STATE OF		135-149							
- 1	CENTRE TOLITICAL INC.	TOWER AND AIR VIELK	160.301							
_	GENOME FOLTERNA	COURSE A SENSE AND AND VIEWS AS THE AM INC.	192.236	150.792	114-918					
2	GENOMIE POL VPROTEIN MI		13.63	917.046						
PVC#1 COV	GENONIE POLYPROTEIN MI									
PVCP EBOV	PROBABLE MEMBRANE ANTIGEN GP15				100					
PVGP BIABVAI	STRUCTURAL GLYCOPROTEIN PRECURSOR		780.37	200	20.40					
PVGP MABVP	STRUCTURAL GLYCOPROTEDY PRECURSOR		361.5%							
PVIID VACCC	STRUCTURAL GLYCOPROTEDN PRECURSOR		562.596							
VACCV	LATE PROTEIN HI	VACCINIA VIRUS (STRAIN COPENITAGEM)	50-92							
2442	TATE DECISION NO.	VACCINIA YIRUS (STRAIN WR)	11.54							
	A A TE PROJECT IN	VARIOLA VIRUS	10.05							
2000		VACCINIA VIRUS (STRAIN COPENDIAGEN)	110-110							
AVIES AVECA	TROILE	CAPONIA VIBILE CORANGE WITH	111.115							
PURS VARV	PROJEINIIS		114.301							
VSILEL LSV	PROTEINHS	VAUGLA VIRUS								
PYINE VACCC	PROBABLE HELICASE	LILY SYNCTONILESS VIKUS								
PUTINE VACCV	HOST RANGE PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)								
PVIDI VACCC	HOST RANGE PROTEIN	VACCINIA VIAUS (STAAIN WR)	417							
PVIOS VACCV	PROTEINIS	VACCINIA VIRUS (STRAIN COPENHAGEN)	Ŕ	10.70						
PVIO1 VARV	PROTEIN	VACCINIA VIDUS (STRAIN WR)	30-163	210-244						
PVID& VACCV	PROTEIN	VALIOLA VIRUS	20.00	210.244						
PVIDG VARV	PROTEIN 16	VACCIPILA VIRUS (STRAIN WR)	20.03							
PVIOT VARV	PROTEIN	VARIOLA VIRUS	20-92							
PVIDS VACCC	PROTEIN !?	VARIOLA VIRUS	113-407							
PVIOD VACEV	PUTATIVE RMA IGELICASE ID	VACCIMIA VIRUS (STRAIN COPEMIAGEN)	241.500							
PVIOL VARV	PUTATIVE RMA ITELICASE 18	VACCINIA VINUS (STRAIN WA)	346-316							
PVIET RCMVA	PUTATIVE KNA IELICASE II		540.580							
PVIET HOMYT	SS KD DOCEDIATE EARLY PROTERT		200	171-205	368-402	27				
PVIET MCMVS	SS KD INDEDIATE-EARLY PROTEIN I	HUBIAN CYTOMEGALOVIRUS (STRAIN TOWNE)	76-12	507-12	368.403	0.0-4.50				
PVIET MPVOP	INDIEDIATE: EARLY PROTEIN I		144.197							
PVIEW MPVAC		21		103-193						
PVIF CAEVC	U.D.EDIATE.EARLY REGULATORY PROTEIN IE-H	3	177-407							
PVIF FIVE	VINION INTECTIVITY FACTOR	CAPRIME ARTIOUTIS ENCEPHALITIS MINUS (STILAIN COILK)	13:62							
PVIF FIVSD	VINION INTECTIVITY FACTOR	FELINE INDAUNODEFICIENCY VIRUS (ISOLATE PETALUMA)	*							
PVE NVIAZ	VINION INDECTIVITY FACTOR	FELME WOUNODEFICIENCY VIRUS (ISOLATE SAN DIEGO)								
PVIF IIVIBI	VINION IN ECTIVITY FACTOR	IRBIAN INDRINODEFICIENCY VIRUS TYPE I (ARVYSF7 ISOLATE		2.75						
PVIF HVIBS	VINON INFECTIVITY FACTOR	IRAGAN INDUMODEFICIENCY VIRUS TYPE I (BHIO,BRU,HXB1,PV		2.2						
PVIF IIVIES	VILLON INTECTIVITY PACTOR	HADAN INGONODEFICIENCY VIRUS TYPE I (BHS ISOLATE)	7	53.56						
PVI IIVI	VIRION INFECTIVITY FACTOR	INDIAN DOUNODEFICIENCY VIRUS TYPE I (ELI ISOLATE)	775	62.96						
PVIE HVIMA	VIRION INFECTIVITY FACTOR	INDIAN LIBRANDOEFICIENCY VIRUS TYPE I (INCSF ISOLATE)	17	96-29						
PVIF IIVIER	VILLON INTECTIVITY FACTOR	_	97.							
PVIF HVIMS	VILLON DO ECTIVITY FACTOR	HUMAN BOATHODEFICIENCY VIRUS TYPE I (MONISOLATE)	7	2						
PVIF IIVINA	VINION INFECTIVITY FACTOR	HUMAN INDICHOPERICIENCY VIRUS TYPE I (NEW YORK-\$ 1504.	7	2.5						

	VIT NOTIS	see (no hecterlephoge:)	1414	AREAL	48541	4854	ABIA2	2010	OREA!	4854
TH. LYANE	נעטזגענ	-		27-28						
-	VIBION IN ECTIVITY PACTOR	1		9.:						
l	VIRION IN ECTIVITY FACTOR	THE TANK THE PROPERTY VIEWS TYPE I (OVI ISOLATE)	-	62.96					-	
١	VIBION IN ECTIVAL V FACTOR			62.96						
2012	VINDA IN ECTIVITY AND ION	THE LISTENSION OF THE PARTY OF THE PARTY OF THE PROPERTY OF TH	7							
۱	VIRION IN ECTIVITY I AL TOR		7	62.76						
į	VINOS IN ECTIVITY OF SOIL	HINIAN INNIANDES ICIENCY VIRUS TYPE I (ZAINE & ISOLATE)	27:	63.46						
-	VALON IN ECTIVITY PACTOR	HANTAN MARINODE FICIENCY VIRUS TYPE 1 (SOLATE D205.9)	147.195							
באניון וויא	VISION IN ECTIVITY FACTOR	MANAN MANANCESCIENCY VIRUS TYPE 2 (ISOLATE NULZ)	133.193							
	VIBION IN ECTIVITY FACTOR	AND THE PROPERTY COMES TARE THE ADD	161-191							
	VINION IN ECTIVITY FACTOR	HUNDAR INCHIDENCE THENCE AND THE CONTRACT								
	VIRION INTECTIVITY FACTOR	OVINE LEWINING STRAIN SACONARY		10.707						
PVII SIVAC	VIRION IN ECTIVITY FACTOR	SIMILAN INDICATE REPORT VINUS (AGAILT) ISOCALES								
l	VIRION INFECTIVITY FACTOR	SINDAN DEREMODE PICIENCY VIRUS (AGAI) ISOLATE)								
١	VINDS IN ECTIVITY FACTOR	SIMILAN INDIAMODEFICIENCY VIRUS (ISOLATE AGAIT CLONE CA	Ī							
	VIBION INTECTIVITY FACTOR	SINITAN INDIANODE FICIENCY VIRUS (TYO. I ISOLATE)]	20.102						
	CHICK TAR COLVETY FACTOR	CHINDANZEE IMMUNODEFICIENCY VIRUS	7							
	VIETOM DE ECTIVITY FACTOR	SINITAN INDICINCIPACITY VIRUS (ISOLATE GO!)	=							
	PROPERTY OF THE PROPERTY	HERPES SINDLEX VIRUS (TYPE 1/STRAIN 17)								
2000	PRODUCE PURCEAN MENTRANE PROTEIN	EDUINE HERPESVIRUS I VPE I (STRAIN ABAP)		111.169						
LAND HONE	PROBABLE INTERNATIONAL PROPERTY.	HERPESVIRUS SABIRU (STRAIN 11)	10-136							
שאוואם אלאם	INTEGRAL MEMBRANG TRUILIN	VARICELLA. 2057ER VIRUS (STRAIN DUNIAS)	107.151	135-110	167.301					
PVINT SSVI	PROBABLE DATE OF THE PERCENT PROTECTION			23:12						
PVIDI VACCC	PROBABLE INTEGRASE		Ī							
PVIOL VACCV	PROTEIN	VALCINIA VOLDS (STITALIN CONTRIBUTION)	37.62							
PVIDI VARV	PROTEIN !!	VACCIPIA VIRUS (STRAIN WIR)								
PVK03 VACCC	PROTEIN	VARIOLA VIRUS								
PUTED VACEV	PROTEINKI	VACCINIA VIRUS (STRAIN COPEMIANEM)								
PVK01 VACCV	PROTEINKI	VACCINIA VIRUS (SIRAIN WA)								
PVL02 VACCC	PROTEIN K7	VALCED A VINO (3) PAIN WAY, AND (3) PAIN CO. L. C. C. C. C. C. C. C. C. C. C. C. C. C.								
PVL01 VACCV	PROTEIN L1	VACCINIA VIRUS (STANIA CUTENTIACEN)								
PVL03 VARV	PROJEIN L2	(STRAIN WR)								
PVLI CRPVK	PROTEINLY		T							
PVLI FPVL	PROBABLE LI PROTEIN	AFILICATA VIRUS (STICAM RAPS								
	PROBABLE LI PROTECIN	AVIAN PAPELOMAVIRUS IPV-L	R							
PVI.1 10 VOS	PROBABLE LI PROTEIN	HUMAN PAPILLONA VIRUS TYPE 3	147-667							
	PROBABLE LI PROTETN	HUMIAN PAPILLONIAVIRUS TYPE I	194-193							
	PRODABLE LI PROTEIN	HERIAN PAPILLONIA VIRUS TYPE IA	10.17							
	PROBABLE LI PROTEIN	HUMAN PAPILLORIAVIRUS TYPE 47	141.161							
PVL! REOVD	PROBABLE LI PROTEIN	DEER PAPILLONIA VIRUS	T							
PVL1 IEVOS	NAJOR CORE PROTEIN LANGEDA I	AEOVIRUS (TYPE) / STRAIN DEARING)	707-24							
PVL2 10PV08	PROBABLE L2 PROTEIN	FIGNIAN PAPILLUMA VIRUS 1 VPE	144.303							
PVL1 10V16	PAOBABLE L2 PAOTEIN	TOWN THE PROPERTY OF THE PROPE	1117							
PVI.3 HPVIA	PROBABLE L2 PROTEIN	MINISTER CONTACTOR TYPE IA	20.00							
PVI.2 11PV31	PROGABLE LI PROJEIN	TINGS AND AND AND AND AND AND AND AND AND AND	101.126							
PVL2 - 10 V35	PROBABLE LZ PROTEIN	TO DESCRIPTION OF TAXABLE TAXA	10.25							
7413 10443	PROBABLE LA PROTEIN	INDIAN PAPEL CALANDERS TYPE 42	141.175							
PVL2 10 VS	PROBABLE LI PROIEIN	INDIAN PAPE LOSIAVIRUS I YPE SE	101.101							
1000	TAUGABLE LA TRUISIN	HANGAN PAPIT LOMANDUS TYPE SB	141.175							
000	MONOR CORE PROJECT ANGROA I	REDVINUS (TYPE 37 STRAIN DEALDING)	97:10	1117.1170						
500	AUDION COME PROTEIN LANGOA	AEOVIAUS (TYPE 1/STRAIN DYIONES)	-							
IVE IN	AIDIOR CORE PROTEIN LANDON)	REDVINUS (TYPE I / STRAIN LANG)	П	391-166	1112-1170					
200	- C. PROTEEL	TIPULA INDESCENT WAUS	144-110	198.334						
							İ			

:ENE	ALLAIOTIS		Ī				Ī	Ī	Ī	
"CEALU	regium	Nata.	N N	48541	3	1	2000	1	N N	4
VALL REOVE	PROTEINALI	VACCINIA VIRUS (STRAIM CUPENHAGEN)	2							
PUNIT REOVU	MINOR VIRION STRUCTURAL PROTEIN MU-1	REOVIRUS (TYPE 1 / STRAIN LANG)	1							
REOVD	MAJOR VIRION STRUCTURAL PROTEIN MULIANUIC	AEDVIRUS (TYPE) / SIRAIN DEARING)		619-643						
PUNIT REOVE	MAJOR VIRION STRUCTURAL PROTEIN MU. MATU-IC	REOVIRUS (TYPE) I STRAIN DEARING)	416-450	618-662						
VAIL REOVE	MIAIOR VIRION STRUCTURAL PROTEIN AIU-IMIU-IC	REOVEN'S (TYPE 2/51 PAIN DIJIONES)	416-650	616-642						
PUNI REOVD	MAIOR VIRION STRUCTURAL PROTEIN MULIMIU-IC	REOVIRUS (TYPE I / STRAIN LANG)		616-662						
A1 BRSVA	PIATOR HONSTRUCTURAL PROTEIN NIU.NS		133.180	111.111	523-558	618-490				
PUNIAN HRSVA	MATRIX GLYCOPROTEIN MIZ	BOVINE RESPIRATORY SYNCYTIAL WIRUS (STRAIN AS1908)	04:20							
PUNIAN TRIV	MATRIX GLYCOPROTEIN MI	VIRUS (STRAIN A2)	2·0							
PINIAI COVO	MATRIX GLYCOPROTEIN NIZ	TURKEY RUINOTRACIENTS VIRUS	36.70							
VALUE (MC)	MATRIX PROTEIN	JONDERSTEPOORT!	193-334							
AVON TA	NA PRINCIPAL PROTEIN	1	1	111.700						
NOV TANK	NATE OF STREET	AUSTRALIA: VICTORIA: 121	10.11							
	2131004 X	_	174.150				1			
SOLIT PINE		j	Ī	204.353						
ALCO AND A		100000000000000000000000000000000000000	Ī						Ī	Ì
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NA MAY	PIAIRIAFIC									
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AI KABA	MAIRIX PROFEIN	HEALTH RELIE	60.00	İ						
AT RABVS	MATRIX PROTEIN		101							
NAS THE	PIAIRIX PROTEIN		66.103							
VIAT VSVIC	MAJRIK PROIEIN	_	:46.260							
VAIE CVBM	MAIRIX PROTEIN	PE INDIANA / STRAIN C	101-333							
CVPFS	EI GLYCOPROTEIN	_								
	EI CLYCOPROTEIN PACCLASOR			112.357						
. !	ELCH YCOPROTEIN PRECURSOR	VIRUS ES	312.257							
CVIKE	EI GI YCOPROILIN PRECURSOR	VIAUS (STRAIN RNI)	112-157							
	EI GI VCOFROITIS			175.300						
77.61.67.6	EI CLYC DPROTEIN PRECL'RSON	9	_							
P. VE1 13/13	EI CLYCOPAOILIN			177-218						
P. V.E. 18VB)	EI CLYLUPAOTEIN			117.318						
PLNEI IBVK		TTEN		177.218						
PLANE KOV			117-216							
PLYIP CAME	E PROTEIN	_	76-94							
PLYED CANIND		CAULIFLOWER MOSAIC VIRUS (STRATIV CAL-1841)		270-324						
CAMINE			187.254	370 334						
PI COLIVE		CAULIFLOWER MOSAIC VIRUS (STRAIN DDC)	187.254 2	170.114					İ	
CAMIVS				170.134						
PIND CANVW				170-324						
PLU CERV	MOVENENT PROTEIN	KAIN W260)	117.234	316-314						
PLAIP FAIVO	AIOVEAIRMI PROTEIN		212-246							
PUNIP SOCAIV	MONEMENT PROTEIN		111.131							
VAISA IDBDB	MONTAGENT PROTEIN	_	16-110							
PINISA IDBDC	MAJOR SURFACE ANTIGEN PRECURSOR	DUCK IEPATITIS B VIRUS (BROWN SIJANGITAI DUCK ISOLATE S		136-361					<u> </u>	
PINISA IDBOU	NAJOR SURFACE ANTIGEN PRECURSOR			333.360						
PINISA IOTBOW	MAION SUNFACE ANTIGEM PRECURSOR	_	234-275	10.333						
PINISA IDBGS	MAJOR SURFACE AMINGEN PRECURSOR	UNCHIAI DUCK ISOLATE SI	111-111	136.361						٠
SA HOBIE	MAJOR SURFACE ANTIGEN PRECURSOR	ITIS VIRUS	210-244							
PLYISA WITVE	MAJOR SURFACE ANTIGEN PRECURSOR		294-330							
VAISA WHIVS9	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS I	108-343							
F1 100 A 100 P117	activities of the second second									

	IALLMOTIS	7.17.10.001.00.00	ARCA L	4854	AREA.	7	111	1854	10136	
FII E NAVIE	PROJECT	THE STATE OF STATE CORES	113-247							
NAISA WHYDI		ACCITIONS CLONE)	111.10							
PUNITI DAINTI	PROBABLE MIAJOR SURVACE ANTIGEN PRECURSOR		101.115	į	į				-	
PUSITE IAANN	MATRIX PROTEIN !	m14078/44/03	!	114-111	į					
1	WILLIAM TO THE PROPERTY OF THE	A VIBILE AS BACK DIVINOS		111111						
PVNII IACAO	NIA IMIN (MII) PROFEIN	(1948)	11.70		:					
	VIAIRIX (ATT) PROTITIV	SI CSTR	41.126	14.23						
1	NA IRIX (MILI PROILIN	NI ULAZA A VIRUS AS DEL VIRUS ROSTOCK	950.50							
TYNI INTE	MAIN (NII) PROTEIN	STATE AND AND AND PLAGUE VIRUSANE VORIS	921-14	174-272						
H	MAJRIN (MI) PROILIN	THE CLARK A LINE OF THE LAND AND A PARTY OF THE LAND A	92:130	174-122						
	MATRIX (MII) PROTEIN	1	97:126	111.222						
73.74	MAJEN CHI PROTEIN	т		14-312						
1	MATER WILLPROTEIN		Ī	136.333						
	NAME OF TAXABLE PROJECT	A/PORT CHALMERS 1773	Ī	34.322						
	NECOSION AND AND AND AND AND AND AND AND AND AN		Ī	14.11						
3	7.1.000	AATDORIN 1971)	Ī							
111111111111111111111111111111111111111	ALALIA TROUBLES		Ī	77.77						
111 14211	NATRIA (AII) PROTEIN		1	74-222						
Į	NIATRIX (MI) PROJEIN	OLD-ADAPTI	13.209							
VAITI INBAD	MATRIX (MI) PROTEIN		135.209							
3185	MATRIX (MI) PROTEIN	STATE OF STATE STRAIN BA EU/O)	13.200							
202 IN	MATRIX (NII) PROTEIN	CONTRACTOR AND BACKING APORE/12/19)	11.209							
	MATRIX (MILIPROTEIN	INTURNATION OF THE STANDARD COLD AUAPTE	11111							
	PROBABI E MIA IRLX (FIL) PROTEIN	TATE DE PARTY OF THE STREET OF THE PARTY OF	133-114							
1	PROBABLE MATRUX (MI) PROTEIN	INCLUENCE OF THE PROPERTY OF T	131.114							
•	PROBABLE MATRIX (MI) PROTEIN	INTUENCE & VARIATION OF BATHGAPORE/22/19)	1							
PWILL MYXVL	PROBABLE MATRIX (MI) PROTEIN		66.80	145-197						
PYNOI VACCC	N. 10 PROTEIN	3	2:3							
PVROI VACEV	PROTEIVAL	VACCINIA VIBLIS (STRAIN WA)	64-113							
PVX M RO185	PROTEIN	BOVING ROTAVIRUS (GROUP C / STRAIN SHINTOKU)	61-169							
PVN14 ROTPC	NOWSTRUCTURAL PROTEIN PASS	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	64-113	3						
PVNCA AAVI	NONSTRUCTURAL PROTEIN	ADENO ASSOCIATED VIRUS 1	81.13	=						
NYCA RSV	DNA AL PELCATION PROTEIN	INCE STUPE VIAUS	3							
LUCH PAVEO	MACHINE MONCAS SID PROTEIN	BOVINE PARVOVIRUS	اء							
N.K.S. ADVG	TACOMOLE POST OF THE PAST OF T	ALEUTIAN MINK DISEASE PAR VOVIRUS (STRAIN G)	Ī	20.00			879.081			
VNCS ALDEV	MONEY AND SECTION	AEDES DENSONDELEOSIS VIRUS (STRAIN CKV 002 002)	276-339	231-371	200	2				
ANCS IDAIN	NOW AND SECTION AS .	FELINE PANLEUKOPENIA VIRUS (STRAIN 193)	2							
CKCS SIEVA	TOWN THE PROPERTY OF THE PROPE	MINK ENTERITIS VINUS (STRAIN ABASHIR!)	-							
WHO THE	MONTA COST A PROPERTY NS. I	ATURINE MINUTE VIRUS (STRAIN MIVALI)	13.01	24.101						
ANCO MICHAEL	LOSAL APEDIN BELLE	ATURDAE ATRAUTE VIRUS		147-461						
NUA VICE	PROBABLE NONCAPSID PROTEIN NSI	BOVING PALVOVIRUS								
MICHAEL PANIE	MONCAPSID PROTEIN MS-1	CANINE PARVOVIRUS (STRAIN M)								
INVAC PANIE	NOWCAPSID PROTEIN MS.1	HUMIAN PARVOVIRUS BIO	27.01	140 303						
New	MONCAPSID PROTEIN NS.1	HANISTER PARVOVIRUS HI			45.					
VAXI BIVIO	NONCAPSID PROTEIN MS-1	PORCINE PARVOVIRUS (STRAIN NADL-1)								
VINSI BIVIT	HONSIAUCTURAL PROTEIN HSI	BLUETONGUE WAUS (SEROTYPE 1871SOLATE USA)								
VKKI BIVIA	MONSTRUCTURAL PROTEIN NS!	OLUETONGUE VIRUS (SEROLTTE 1771SOLATE USA)	171.00							
PVNS: BIVIS	NONSIAUCIUMAL PROTEIN MSI	BLUE TONGUE VIRUS (SEROI TYR. IV ISOLATE AUSTRALIA)	1		L					
PVNSI BTV20	MONSIBUCTURAL PROTEIN NS!	BLUE TOWOLE VIRUS (SERVIT TO 1150 ATE ALISTERIAL)	101-141				•			
PVNSI EIDV	HONSI RUCTURAL PROTEIN WSI	BLUE LONGUE VINUS LIEROL LIFE AV 130LALE ACTIVITIES AS TO 1 YEE 2 STRAI	_							
PVNSI IAAM	MONSTRUCTURAL PROTEIN NS	DELLENZA A VIBUS (STRADA AANN AABORNES)	18-61							
PVINSI IACAO	NONSTRUCTURAL PROTEIN WAS	INTELLENZA A VIRUS (STRAIN ACAMELA:ONGOLIAR)	11.11							
PVNSI IACKG	HOMSTRUCTURAL PROTEIN PSI			•						

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NYS 1 ACK! NYS 1 ALDE! NYS 1 ALDE! NYS 1 ALDE! NYS 1 ALDE! NYS 1 ALCH NYS 1 ALKAN NYS 1 A	NOMS THE CUTALL PROTEIN WITH WAS INCOMED THE CUTAL PROTEIN WITH WORSE HELT LIBERT PROTEIN WITH WORSE HELT LIBERT PROTEIN WITH WONS THE CUTALL PROTEIN WITH WORSE HELT LIBERT PROTEIN WITH WORSE HELT LIBERT PROTEIN WITH WITH WITH WITH WITH WITH WITH WITH	INTURNA A VIRUS (STANIA ACHICKENIARIANA) ONTURNA A VIRUS (STANIA ACHICKENIARIANA) NOTURNA A VIRUS (STANIA ADUCKALBER FANDA)				ĺ		
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SACE LABOR OF THE PROPERTY OF	NONSTRUCTURAL PROTEIN NSI NONSTRUCTURAL PROTEIN NSI	INTLUENCE A VIILUS (STRAIN ACOUCEAEMCLARUMINA)	01-10					
1834 (MONSTRUCTURAL PROTEIN NST	INFLUENZA A VIRUS (STRAIN ADDICKAKRAINEIM)	00.00					
POWS IN FREE POWS	NOWSIEUCTURAL PROTEIN MS!	INFLUENZA A YRUS (STRAIN AFORT MONMOUTIVIVI)						
PVEST LARIA PVEST LARIAN PVEST LARIAN PVEST LARIAN PVEST LARIAN PVEST LARIAN		INTIUENZA A VIRUS ISTRAIN AFORT WALLEWIYS, AND ISTRA						
PVNS LALEN PVNS L	HONSTRUCTURAL PROTEIN NSI	INFLIENZA A VIRUS (STRAIN AGON'L PLAGUE VIRUSMOSTOCK	19.00					
MASS TARIAN WYSE TARIAN WYSE TARIAN WYSE TARIAN	HONSTRUCTURAL PROTEIN WSI	INGLUENZA A VIRUS (STRAIN AR ENINGRAPY) 4/31)	10:00					
PVYSI IANIAN PVXSI IANIAN PVXSI IAPII	HONSTRUCTURAL PROJETN NSI	INTLUENZA A VIRUS (STRAIN ALENINGRADYSU)	10.00					
PVNSI IANIAO PVNSI IAPIO PVNSI IAPIO	HONSTRUCTURAL PROTEIN HSI	INCLUENZA A VIRUS (STRAIN AAIMI LALDVALBERT AAIMTA	19.61					
PVNSI IANIYN PVNSI IAPIB	ACASIRIAC TIMAL PROTEIN NS:	INFLUENZA A VITUS (STRAIN ARIALLARDARW YORKA 19078)	39.81					
PVNSI IAPIO		INCLUENZA A VIRUS (STRATH ARIALLARDINE W YORKASTATE	3.5					
PVNS LAPII		INTERNAL A VIRING STRAIN ANIVALIMANEDA. TILAUM	01.90					
74.5		NAME OF STREET A PUBLIC ACTION OF A STREET AND DESIGNATIONS						
	WONSTAIR LUKAL PROJECT AND	THE COURT A COURT OF THE ABOVE AND A STATE OF THE PERSONS ASSESSED.		-				
	NOW STRUCT UNIAL PROTECT MAST	I V LUCKER A VIRUS IS INVIN APPLIANTAL AND APPLIANT						
5	NONSTRUCTURAL PROTEIN NS	INCLUENCE A VIRUS (SIEVAIN APINI ALL VALOERI ALGORIA						
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PYNSI IATKO	NOWSTRUCTURAL PROTEIN NSI							
PYNS INTRC	HONSTRUCTURAL PROTEIN NSI	GLILIT/						
PASS INTRA	NONSTRUCTURAL PROTEIN NS!	INFLUENZA A VIRUS (STRATH ATURKEYCANADAM))	19:11					
PUNS IATRS	HONSIAUCTURAL PROTEIN KSI	INFLUENZA A VIRUS (STRAIN ATURKEYORE CONTI)	19:01					
PUTSI TATRI	NONSTRUCTURAL PROTEIN NSI	INSLUENZA A VIRUS ISTRAIN AMERINSOUTH AFRICASI	79.90					
PVNKI IAZII	NONCINITION OF PROTEIN MS.		19:63					
PANCE CARAC	MONSTELL TIRAL PROJEK NS		10.0					
PVPS I INBGA	NOWSTRUCTURAL PROTEIN NS	OLD ADAPIC	10.13					
NAME OF THE PERSON	MONGENCE AND PROPERTY OF		10:00					
PVNSI DABIIT	NOWSTRUCTURAL PROTEIN NSI	PULLENZA B VIRUS (STRATH BAIONG KONGENT), AND (STRATH	10.01					
0.000	MONGE PLANTED AT DECISION OF	PACLIFIED A PARTIC (CREAN MATRIA)	11:11:			T		
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PVAC DABA	MONSTALL TRANSPORTER ME	D VIDES (STRAIN DAIABY) ANDVID				Ì		
11000	LANCIBLE OF A PROTECT PER	b Visits and Brazes	10.00			Ī		
NOVE DEBE	NOMSTRUCTIONAL PROTEIN NS		T					
PVNS: D/BS!	NONSTRUCTURAL PROTEIN NSI	POLENIZION	143-177					
PVNS1 DOVI	NOWSTRUCTURAL PROTEIN WS!	INTLUENZA B VIRUS (STRAIN BYSINGAPOREMA)	101:171					
PVMSI DABYA	MONSTRUCTURAL PROTEIN MS!	INFLUENZA B VIRUS (STRAIN BIVICTORIANS)	10.01					
PVNS1_AJISV9	NONSTRUCTURAL PROTEIN NSI	INFLUENZA B VIRUS (STRAIN BIYAALAGATAJIÑ))	143-177					
PVNS2 BIVI?	NONSTRUCTURAL PROTEIN NS?		\$7.101					
PVNS2 BTV1X	MONSTRUCTURAL PROTEIN NST	ISOLATE USA)	201:23					
PVSS CVAJH	MONSTRUCTURAL PROTERN WS		101.137					
PVNS3 EIDV3	MONSTRUCTURAL PROTEIN MS	_	Ī					
PVNS1 IAALA	HONSTRUCTURAL PROTEIN MS2		206-273					
PVMS3 IAANA	NOWSTRUCTURAL PROTEIN INS	-	16.93					
PVNS3 IAAM	NOWSTRUCTURAL PROTEIN MS?	INTLUENZA A VIRUS (STRAIN AVANAS ACUTAPRIMORIEMPS/NS)	6.0			1		
PVNS3 IACHII	NOWSTRUCTURAL PROTEIN NS	_						
PVNS3 IACKG	MONSTRUCTURAL PROTEIN NS		6:0				Ì	
PVMS3 IACK3	HONSTRUCTURAL PROTEIN MS	(Mark)	16.79			1		
PVNS3 IADA3	NONSTRUCTURAL PROTEIN MS	INDICENZA A VINUS (STRAIN ACHICREMIA/ANZO)	2					
ZANSZ TADEL	NONSTRUCTURAL PROTEIN NST		2.3					
PWS2 (ADU)	MONSTRUCTURAL PROTEIN MSS	PATUENZA A VILUS (STRAIN ADDUCK/ENGLAND/179)	R					
PVNSZ IAJOM	MONSTRUCTURAL PRUTEIN NS		2	-				1

PCGLME	ALL MOUSE			ARIA	1					
	7.00	The state of the s								
	HOME BUILTIEAL PROTEIN MS		18.0							
A L	SV NEDERINA PROJECT NE	-							1	
2	MONTH PROJECT NO.		-							
PVKS JALES	MONOTON TO THE PROPERTY NO.									
P. P. J. IALER	MONGTON THEAT PROTEIN NS	1	2							
ST IANIA	MONSTELECTURAL PROTEIN NS?	Ī	5							
LAND INVITA	CONCLETE PROTEIN MS	-	-							
200	CONCESSION TO PROTEIN NS	÷								
ON INVINO	CONCERNITION AND PROTEIN NS									
PVRSZ IANITE	CONCLUSION TO SEE WAS	7	2 5							
NASZ IANU	CONSTRUCTION OF THE PROJECT INC.	Ī								
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VNS2 IAPI2	NOW STRUCTURE AND ADDRESS AND									
PVNS1 IAPUE	NONSTRUCTURAL TROUBLES	-								
VNS2 IATE	NOWS INC. LORAL PROPERTY.	M-GLILITYIN								
PVNS3 IATKA	NONSTRUCTURAL PROTEIN NO.	INTLUENZA A VIRUS ISTRAIN ATURKEYOREGONTI	-							
VNS2 IATRS	POPSITION OF THE PROPERTY NAS	\$	2							
PVNS2 IAUSS	ACCUSATION AND PROTECTION NS.	3)		40.119						
PVNS) INBLE	NOTE THE PROPERTY AND					-	-			
PVMS1 (NBYA	MONSTRUCTURAL PROTECT PASS	SATAVITI)	=	34-114						
VNS2 PACE	NONSTRUCTURAL PROTEIN 155	İ								
PVNS3 PVNI	NONSTRUCTURAL PROTEIN TO		20.104							L
VNS) AJISVI	NONSTRUCTURAL PROJECT		22	66.213		-				
PVNS3 AHSV9	NONSTRUCTURAL PROTEIN NO		13:38	771-01						
PVHS3 BRD	NONSTRUCTURAL PROTEIN ASS		7.00	107:10		1				
PVNS) CVPFS	MONSTRUCTURAL PROTEIN FAST	BLE GASTROENTERITIS CORONAVIRUS IS	13.51							
NS CVHIL	NONSTRUCTURAL PROTEINS	HIDLIAN CORONAVINUS ISTRAIN 179E)	=							
NS4 BSV	NONSTRUCTURAL VACABLE NA	ALCE STRIPE VIRUS	0,-1							
NS) CVCAE	KIND OF INC.	CANINE ENTERIC CORONAVIRUS (STRAIN K)10)	3 13							
CALL ST	SOCIETY PROPERTY	FELINE ENTENC CORONAVIAUS (STRAIN 19-1643)								
ANS LIFE	MONATOR TOWN PROJECT 3	FELINE INTECTIOUS PERFOUNTIS VIRUS (STRAIN 79-11-46)		5179						
NASC COAC	CONCIDENTIAL PROPERTY C	CRSTEPOORTI								
VASC PIEASE	WOLCE BLOTHE AT PROJECT	TON)								
NWSC MEASI	CONTRACTOR AL PROTEIN	NEASLES VIRUS (STRAIN IP-) CA)								
VNSC MEAST	NONE INTERIOR PROTEIN	MEASLES VIRUS (STRAIM YANIAGATA-1)								
NAC STREET	MONSTRUCTURAL PROTEIN C	IIIDIAN PARAING LUCHZA I VIRUS (SIRAIN CTS)								
CILL SALE	MONSTRUCTURAL PROTEIN C	HEBIAN PARAINSTURNEA I VIRUS (STRAIM C.39)								
VNSC PINE	NONSTRUCTURAL PROTEIN C	HIGHAN PARAINFLUENZA I VIRUS (STRAIN CL. 2013)	50.33	133.167						
VNSC PINIA	NONSTRUCTURAL PROTEIN C	TICHAN PARAINELUI AND COMPANY AND AND AND AND AND AND AND AND AND AND	=	101.100						
VNSC SENDA	MONSTRUCTURAL PROTEIN C	HUNLAN VACAINT LUENTA A VINCE	9:10							\downarrow
PLNSC SENDH	NONSTRUCTURAL PROTEIN C	SENDAL VIEW CTBAIN HABBIS	13:161							1
VYSC SENDS	NONSTRUCTURAL PROTEIN C	CENTAL VIEW STEAM 2)	13)-16)						\downarrow	1
VASH MSN	KONSTRUCTURAL PROTEIN C	INDATIENS MECROTIC SPOT VIRUS (INSV.)	44.103	£						-
VINST BUNGE	NOWSTRUCTURAL PROTEIN MS.A.	RIPSYAVIRIS GERMISTON	=							
VNST BURG?	NOWS TRUCTURAL PROTEIN NS S	BUNYAVIRUS LA CROSSE (ISOLATE L74)	5		<u> </u>	1	1	\downarrow		
PVNST BUNGC	MOSSIBILITITAL PROTEIN PS. 3	BIDAYAVIRUS LA CROSSE	=				-			ļ
VNST MAGV	NOWSTRUCTURAL PROJECT PRO	NAGUAD VIRUS	3				-			
VSOI ISN	NONSTRUCTURAL PROTEIN PS	TOSCAMA VIRUS (TOS)	=				1			
NNSI GUK	KONSTRUCTIONAL PROTEIN ASS	UNKUNIEM VIRUS (UUK)	2		1	+	-			
PLYUA PRVKA	NONSTRUCTURAL PROTEIN NO.	PSEUDORABIES VIIUS (STRAIN KAPLAN) (PRV)	200				-	1		L
PVYC DHAT	PROBABLE MUCLEAR ANTINET		304.74	-	_	-	-	-		

PCCCNE	IALLAIDTIS	ires (ne bacteriophsges)	Ī	Ī	Т	100	7867	7 7 2 4 7	4864.9	ARTAI
וונצאונ	ZADJEJN		7	7	1	T	Ī	Г		
PVNUC IAANA	MUCLEOPROTEIN	EDOLA VIRUS	Ī	Ī	157.408					
PUNCE INAMA	MUCLEOPROTEIN	INTUENCE A VIRUS (STATIS AND ACOTAMINATION OF	Ī	T	İ				-	
PVNUC IABIA	MUCL EOPROTEIN	IN LUENCA A VINUS (STRAIN AVAIN AND UNION)	Ī	\$7.406						
PVX:UC IABUD	MICLEOPROTEIN	INTEREST A VIEWS (STEAM AND ACTUALISTS)		Ī	157-408					
PWUC IACAL	MUCLEOFROIEIN	INTERNAL A CIPITO COLPANA ANTA I BOD CIANDO	Ī	1						
NAME INCHES	MUCLEOFICIEN	CALLENA A VIBIR REPAIN ANTHER PARTERNANY AND		Ī	157.406					
PVNIC IACK	MUCI EDINOIEIN	INCLUENCE A VIRIA CATE AND ACTUCK ENDENNEYS VANIALISM		Ī	357-406					
PYNC IADAU	NUCLEOPROTEIN	DELIGENZA A VISITE SETTANA AMERICANISTRALIA (AMAND)	Ī	Γ	337-408					
PLYUC IADBE	MACLEGRADIEIN	INCOCATA A MINISTER SELECTION AND AND AND AND AND AND AND AND AND AN	Ī	Ī	157.404					
PYNC IADCZ	MACLEOPAGIEIN	INTUENCY A VIRUS (STRAIN WULCHESELINGENIS)	Ī	Ī	140.408					
PWINC IADE!	MUCLEOPROTEIN	IN LUENZA A VIRUS (STRAIN ADUCEAC CECHOSEUVANIAM)		T						
PYKUC IADEI	MUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN A/DUCK/ENGLAND/1/94)	Ī	T						
PVMK IADIOK	NUCLEOPROTEIN	ROLLENZA A VIRUS (STRAIN ADUCK/ENGLAND/14/2)	Ì	Ī						
PANC IADAI	SOCI EOPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKAIONG KONGAMI)		Ī	37.400					
PVNUC IADAIA	NUCLEOFROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKAIENDHISMIN)		Ì	23.40					
PUNC INDAZ	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCKALANITOBAVIYI)			32,408					
PVNUC IADUJ	HUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ADUCKARW ZEALAND/11/16)		96-134	357-408					
PLYNC IAENS	NUCLEOPROTEIN	INITUENZA A VIRUS (STRAIN ADUCKAJKRAINE/240)	96-150	153.406						
PVNUC IATOM	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ACENCIL ANDVINSS)	1.42	153.400						
PANUE IAFOW	NUCLEOPROTEIN	DELUENZA A VIRUS (STRAIN AFORT MONNIDUTIVIAT)	142	337.400						
PANIE IAIPO	MICH EDPROTEIN	INFLUENZA A VIAUS (STRAIN AFORT WARRENVISO)	137-408							
PASSIC AFPE	MXTEOPHOTECN	INTLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUS/DOBSOW	271	20.2	117-408					
1000	Nich sound in the	RELUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSAOSTOCK		96-134	960-408					
1000	NICE CONTROLLER	INTELEBUSA A VIRUS ISTRAIN AGREY TEAL/AUSTRALIA/UT)		× :	157-404					
1000	NISCI EDISTON	Т	Ī	23.40						
THE PERSON	Marci Fossorie IV	ء	200	\$1-400						
PORT INCH	MACLEOPEOIEIN	INTLUENZA A VIRUS (STRADI AGULLADARYLANDI 112-11)	1.43	151-30	157-406					
PVWIC IAGUA	MUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AGULLANARYLANDVIBIS79)	=	<u> </u>	157-409					
PYNUC IAGUN	NUCLEOPROTEIN	POLUENZA A VIRUS (STRAIN ACID L'ASTRAKHANZITA)			117-409					
PVINIC IAGUN	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AGULLAIASSACHUSETTS/2019)	27.	151-34	157.409					
PUNIT INIIC	MUCLEDPROTEIN	BIFLUENZA A VIRUS (STRAIN AGULLAINOFESOTAM SAU)		21-8	157-409					
PYNUC INIU	NUCLEOPROTEIN	RELUENZA A VIRUS (STRAIN AFUCKOX/40)	141	357-409						
PYNUC (A)B.O	MUCLEOPROTEIN	DELUENZA A VIRUS (STRADA AVEQUINE/IRLINU/IR)	1-42	154	357-408					
PYNUC IAIDA	NUCLEOPROTEIN	DE LUENZA A VIRUS (STRAIN AEQUINEALONDOMIAIATI)	7	1 1 24	157-408					
PVAUC IAIDI	NUCLEOPROTEIN	DELLENZA A VIRUS (STRAD) AEQUINEAHANIVIM)	X	M-134						
PVNUC INIOS	NOCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/HONG KONG/IMB)		157-409						
PVNUC 1AIPR	MUCLEOFROIEIN	INFLUENZA A VIRUS (STRAIN AMONG KONGMI)	1-41	337.409						
PVMUC IAHTE	NUCLEOPROTEIN	NG LUENZA A VIRUS (STRAIN A/EQUINE/PRAGUE/174)	•						İ	
PYPAUC IAKIE	NUCLEOPROTEIN	INFLUENZA A VIRUS		١	157-408					
PVANC ILEN	MUCLEOPAOIEN	DALLENZA A VIRUS (STRAIN AIKIEVISMIS)		357-409						
PUNUC IALIAA	MUCLEOPROTEIN	NFLUENZA A VIRUS (STRAM ALENINGRAD/14/1)	7	87.400						
PUNIC INMAN	MUCI EOPROTEIN	INTLUENZA A VIXUS		181-181	157-408					
PUNC INCH	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRATH AMIALL ALDMEW YORKK 1907B)	¥ (7-)	96.134	153-408					
PVNUC IANEL	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AAUNK/SWEDENNA)		1 96-134	803-456					
PVPCUC IANTE	MIKLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ANEW JERSEYATA)	143	94-154	357-408					
PVNUC IAOIU	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ANTMONS)	175	137-400						
PLYNC IAPAR	MUCI EOPROTEIN	INGLUENZA A VINUS (STRAIN AOHIO/461)								
PVPUC LAPUE	PUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN APARROTAR STERM)			157-408					
PVAUC IARUD	NUCLEOPROTEIN	INGLUENZA A VIRUS (STRAIN APUERTO RICOAM)								
PVMUC IASEO	MUCLEOPROTEIN	BOLUENZA A VIRUS (STRAIN ARUDDY TURNSTONGAEW IERSE			157-404					
PYXUC IASHU	MUCLEOPROTEIN	DELUENZA A VIAUS (STRAÍN ASEALAGASSACHUSETTS/1/A0)		П	337409					
PVNIK IASIN	MICLEOPROTEIN	INFLUENZA A VIRUS (STRAM ASHEARWATERAUSTRALIAM)	1.01	157-408						

		All Visuses (no bacteriophoges)	П	П	1		4874	48644	AREAT	AREAI
	ALLMOTIS		4	J		Τ	1			
١	KROJEK	INFLUENZA A VIAUS (STRAIN AVSINGADURE/1951)	Ī	J	100					
PYNC INTEL	MUCLEUMOLEIM	INFLUENZA A VIAUS ISTRAIM ATE AL/ICEL AND/19/10)		Ī						
Ì	NIKI BOTRUEM	DIFLUENZA A VIRUS (STRAIN ATURKEYAIINNESOTA/1661/81)		Ī						
PVPOC IATEO	MCCLFORMICIN	DITLIENZA A VIRUS (STRAIN ATURKEYONTALIOM112/64)		100	0, 0,					
PVNUC IAIRS	MACI ECONOMIC DE LA COMPANION	INTLUENZA A VIRUS (STRAÍN AMERINSOUTH AFRICAMI)			3	Ī				
STATE INTE	NEC EQUELLE	INFLUENZA A VIAUS (STRAIN ATERNATURKAIEMIATI)	Ī							
311111111111111111111111111111111111111	N. S. C. C. C. C. C. C. C. C. C. C. C. C. C.	INTLUENZA A VIRUS (STRAIN ATEXASII77)								
NOC YES	NICE COMPANY OF THE PARK OF TH	INT. UENZA A VIRIIS (STRAIN AUDORAVIONIL)								
PARKE AUSS	NICLEOPOTECA	INTLUENZA A VIRUS (STRAIN ANDSSIMONT)	~	1						
200	The sound in the second	INFLUENZA A VIRUS (STRATH AVICTORIAVISE)	3							
PVPUC IAWIN	NOCIE CANOLEIA	INFLUENZA A VIRUS (STRAIN AWHALERIAINE/118/14)		7. 2	137.403					
PUNC IAWIE	NIA, LOTROSCIA	INTELENZA A VIRUS (STRAIN AWITALEPACIFIC OCEANISMS)	-62	27.2	27.408					
PUNIC IN WILL	MACHORIOTEIN	INTEREST A VIRUS (STRAIN AWILSON-SAILTWID)	-	157.40						
PUNIC IAWIS	NICHEOTHORN	THE LIENZA A VIRUS (SIPAIN ANYISCONSIN) \$2/41)	1.42	9¢-154	33.40					
PVNUC IAZZO	KOCLEUTROICIN	DELIENZA A VIRUS (STRADI ASWINE/1997)	1.42	12.0	137-00					
NAUC IAZAI	MUCLEOFICE	HALLIENZA A VIRUS (STRAIN ASWINE/1149)	1-43	96-15A	157-406					
PUNDC 1AZCA	NUCLEOPROTEIN	NET TENZA A VIRIS (STRAIN ASWINE/CAAIBAIDGE/1/) 1)	9-43	357-409						
PVNUC IAZDA	MUCLEOPROTEIN	SALLENDA A VIEW COLDAIN ASSENCE DANDONG AND INC.	Ĩ	157-409						
PVNUC JAZGE	MUCLEOFROTEIN	THE CHARLES OF A STATE OF A STATE OF THE STA	7	M-134	157-408					
PVNUC IAZHII	MUCLEOFROTEIN	INTEREST A SOUTH AND AN AND MANAGEMENT OF THE PARTY AND AND AND AND AND AND AND AND AND AND	7	157-400						
PVNUC 1AZII)	MUCLEOPROTEIN	INTELLEGIZA A VINCE STRAND AND AND AND AND AND AND AND AND AND	1-42	2 2	157-400					
PYNUC IAZIIA	MUCLEOPROTEIN	THE CENTER OF THE PERSON AND ADDRESS OF THE PERSON OF THE	÷.	\$6.150	111-406					
PYNUC IAZII	MUCLEOPROTEIN	DALIGENZA A VIANE CERANA A AMBREADA A LA LA LA LA LA LA LA LA LA LA LA LA	3	251.36	153-408					
PVRUC IAZI3	NUCLEOPROTEIM	TOTOTO A CONTROL OF THE PROPERTY OF THE PROPER	7	\$ 13¢	357-408					
PVMUC IAZII	MICLEOPROTEIN	INFLUENZA A VIKUS (STRAIM ASMINE/IOMALIVIE)		100	157-608					
PVMUC 1A211	MUCLEOPROTEIN	DIFLUENZA A VIKUS (STRAIM ASWIREAUWANS)		7	157.404					
PVNUC 1AZII	NUCL EOFROIEIN	INCLUENZA A VIRUS (STRAIN ASWINGTIAL VIRUS		¥134	157-608					
PVNUC_IAZII	MUCLEOPROTEIN	THE LIEUX A VINUS (SIRVIN ASTWORMS IN VIOLEN	3	#	357-406					
PVKUC_1A234	MUCLEOPROTEIN	INTEREST A VIEW CONTRACTOR AND ACCORDING TO A 19-19-19-19-19-19-19-19-19-19-19-19-19-1	3	21.28	357-408					
PVNUC 1AZJA	MUCLEOPROTEIN	DECLERACY A VIEW CORPANY ARMONISTRATES BEING CARD	7	M-154	157-408					
PYNUC IAZKIA	MUCLEOPROTEIN	THE COUNTY A VINDE COMMENDENCE AND ACCUMENTANCE AND ACCUM	7	2 2	357-406					
PVNUC IAZNE	MUCLEOPROTEIN	CALLERYA A CHILD STRAIN ASWINGAGTIER AND STRUS	7	# 1X	157-408					
PVNUC IAZON	MUCLEOPROTEIN	THE LEAD A VIBING ACTORNIA AND INTERCENCIAL STATES	7	20.38	157-408					
PUNDC IAZON	MUCLEOPROTEIN	ING. (ENZA A VIRUS (STRAIN ASWINGSONTALIOZA))	7	¥-1%	157-406					
PVMIC IAZIE	NUCLEUROI EIN	INCLUENZA A VIRUS (STRAIN A/SWINE/TENNESSEE/14/1)	77	151.96	117-408					
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NICI EOPOTEIN	INGLUENZA A VIRUS (STRAIN A/SWINE/WISCONSINVINI)	=	2	20.00			<u> </u>		
PVNIT DIBAA	MUCLEOFKOTEIN	INTELENZA A VIRUS (STRAIN ASWINEAVISCONSINVINI)	-		137-408					
PVAUC INBAC	MUCLEOPROTEIN	INTLUENZA B VIRUS (STRAIN BVANN ARBOBVIAK)								
PV:NUC INBAD	MUCLEOPROTEIN	INSTITENZA B VIRUS (STRAÍN B/AIN ALBOWING COLD-ADAPTE	7							
PVPUC WOLE	MUCLEOPAOTEIN	DOLLENZA B VIRUS (STRAIN BANNA AKBUNION WILLD-11TE)								
PVNUC INBSI	MUCLEOPROTEIN	INCLUENZA & VIRUS (STRAIM BAREAM)		1						
PVMUC INCCA	MUCLEOPROTEIN	INTEREST OF THE PERSON OF THE	107.101	5.6						
PVNUC MABVM	MUCI EOPROTEIN	INTOCACA CAROLINAMIA COMPANIA	13.201	322-407						
PVNUC MABVP	MUCLEOPROTEIN	PLACEURO VIEWS (STRAWN PROPERTY)	173.201	133-401						
PV001 VACCC	NUCLEOPROTEIN	CACCAGA CHILLEGETH AND COREMANDER	5.55	265-279	341-302	21413				
PVOOL VARV	PROTEIN OI	VALUE A VIBIL	25-15	305.279	341-382	21412				
PVORI FXDAY	PROTEIN OI	FONTA B MOSAIC VIBILS	187.53							
PVOR! NAV	153 KD PROTEIN	DARCHER LOCAL WHIS DAIN	1516-1575							
PVORI PMV	I I KD PROTEIN	PARALISOS MOCAIC POTEXMENS PAIN	5	111.111	1474-1532					
PVOR! PVMR	176 KD PROTEIN	POTATO VIRIS MISTRAIN RUSSIANI (P.VA)	307-638	617.130						
PVORI PVX	123 KD PROTEDI	POTATO VINUS X (PVX)	516.530							
PVORT PVXCP	165 KD PROTED	101101 July 2011								

PLORI SUYEA			Ī					Ī		4
PLORI SUVEA	24747	7.00	3:	1	1	1	2010	4	7000	4
NORT WON'S	145 KD PROTEIN	FOLKIUS K (SIRKIN CP) (PVA)		971 041						
CHILD INTER	ISO KO PROTEIN	STAAWBEARY MILD YELLOW EDGE-ASSOCIATED VIAUS (SAITE	,							
Cultural Park	147 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN MI) (WCMV)	180-1284							
PLP10 NPVAC	147 KD PROTEIN	WHITE CLOVER MOSAIC VIRUS (STRAIN O) (WCMV)	740.136							
PLPIG NPVOP	PIOPROTEIN	AUTOCRAPIIA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS (-							
PAPE BASOV	PIOPROIED	ORGYIA PSEUDOTSUGATA AKULTICAPSID POLYIEDROSIS VIRUS	3						ŀ	
PY PIO RGDV	PRUIE IN \$10	RICE BLACK STREAKED OWARF VIRUS (RBSDV)	39-312	105.479	106-556				1	
71.W OId 14	NONSTRUCTURAL PROTEIN PASIO	NCE GALL DWANT VIRUS (AGDV)	166-273							
N. P. I. R.D.V.	NONSTRUCTURAL PROTEIN PUSIO	WOUND TUSTOR VIRUS (WTV)	120-254							
71% 114	NONSTRUCTURAL PROTEIN PASSI	NICE DWAN VIRUS (NDV)	25.60	273-314						
Pi Pi I NOV	NONSTRUCTURAL PROTEIN PHSTI	WOUND TURIOR VIRUS (WTV.)	16-74							
Press wry	NOWSTRUCTURAL PROTEIN PLI	RICE DWARF VIAUS (ROV))	140.181							
PILL WINE	NONSTRUCTURAL PROTEIN PASTS	WOUND TURIOR VIRUS (WTV)	801 · 83							
PLP19 115/18	NONSTRUCTURAL PROTEIN PASTS	WOUND TURIOR VIRUS (STRAIN NI) (WTV)	89.108							
PLP13 HENNA	CAPSID ASSESSIBLY AND DNA MATCRITION PROTE	EQUINE HEAPESVIAUS TYTE I (STRUM ABAP) (EHV-I)	169-331							
P. P. 3 115VeU	PROBABLE CAPSID PROTEIN 1921	HUNLAN CYTONIEGAL OVIRUS (STRAIN AD 189)	~	\$ 5 1 5						
P. F. 1 F110V	PROMABLE CAPSID PROTEIN (72)	HERES SIMPLEX VIRUS ITVPE 4/STRAIN UGANDA-1102)	13.61							
Pi Fit 115/EB	MINIMANE ASSOCIATED STAUCTURAL PROTEIN	EBOLA VIRUS	166-200							
P1 F36 115VSA	CAPSID PROTEIN VP26	EQUINE HERPESVIAUS TYPE 1 (STAXIN ABIP) (CHV-1)	14.11							
PLESS HPUOP	CAFSID PROTEIN VP26	HERVESVIAUS SAINING (STRAIN 11)	÷.1							
0121 9:414	P26 PAOSEIN	ORGVIA PSEUDOTSUGATA NAM TICAPSID POLYTIEDROSIS VIRUS	111-159							
PV FT AIISVO	CAPSID PROTEIN VP26		47.81							
PARI BIVIO	OUTER CAPSID PROTEIN VP3	LAIN VACCI	136-111	170-304	410.465	114-662	684-720	976-1056		
P. P. BIVII	OUTER CAPSID PROTEIN VP2	BLIETONGUE VIRUS (SEROTVYE 1071SOLATE USA)	161-125							
P. P. BIVII	QUIER CAPSID PROJEIN VP3	BLUETONGUE VIRUS ISCROTYPE II / ISOLATE USA)		559-593						
PLP1 BIVIS	OUTER CAPSID PROTEIN VP2		111-111	61.209						
PYP1 EMDVI	OUTER CAPSID PROTEIN VP2	_	119-133	376-610	£01 · 109					
PVP2 ROTER	OUTER CAPSID PROTEIN VP2	EPIZOOTIC HENIORALIAGIC DISEASE VIRUS ISEROTYPE IJ (EHDV	72-106	147.301	405-453	565-190	626-661			
P. P. ROIBU	ANA-BINDING PROTEIN 172			411-316	513-557		673.334			
PLF1 ROTIN	ANA-BINDING PROTEIN VP2	BOVINE BOTAVIRUS (STRAIN UK.)		41.517	526.558		616-319			
PVP1 ROTPC	ANA-BINDING PROTEIN VT?	HUMLAM ROTAVIAUS (SEROTYPE I / STRAIN WA)	19:61	402-526	111-567	417-438	685-764			
PVP1 ROTSI	KNA-BINDING PROTEIN VP?	NIN COWDEN)		53.00	194-338	315-331	100-005	705-746		
PVP10_ASFE?	RMA-BINDING PROTEIN VP3		16.96	413-517	969-809	111-011				
PUPIL FREIV	PHOSPHOPROTEIN P.10	VER VIRUS (STRAIN E-15) (ASF V)	19.66							
P. P.11, ASFB?	EARLY 31 KD PROTEIN		22.6							
P. P.15 E80V	PHUSPHOPROTEIN P12	NE FEVER VIRUS (STRAIN DATIV) IASFV)	=							
PVP19 KPVAC	POLYMERASE COMPLEX PROJETS (P.1)	_	91.00							
MAN SIANA	EARLY 19 KD PROJECT	AUTOGRAPHA L'ALIT URAILA MULLEAR PUR VIEDROSIS VIRUS								
איננים	INCOMPONDATION BY THE OPE PROFESS PIL	Ī	Ī	110-130					1	
PVP35 VACCV	INCHINODOMINANT ENTEL OPE PROTEIN P13							T	Ì	
PVP15 VARV	INDICHODOMINANT ENVELOPE PROTEIN P15		1							
PVP1 A115V4	ININIOMODOMINANT ENVELOPE PRUTE IN P.11		10 m					Ī		
PVP1 BTV10	VPI CORE PROTEIN	SICKNESS VIRUS (SEROTYPE 47 STRAIN VACCE		40.234	667.700					
PVP1 D1V13	VP) CORE PROTEIN		314.335	53.184						
PUP) OTVIA	VP) CORE PROTEIN			83.PM						
PVP) EIIDVI	VP) CORE PROJECIV	_	316.333	83.EM						
PVP1 ENDVA	VP1 CORE PROTEIN	SEROTYPE I) (EIW)	200.346	M-102	131.072					
	VPI CORE PROTEIN	VIRUS		135.770	748-813	151.302				
VD1 RDV	P) PROTEIN		I							
PVP1 ROTPC	NIAJOR 114 KD STRUCTURAL PROTEIN	RUCE DWARF VIRUS (RDV)	_	13.873		٦				
PVF) ROISI	INNER CORE PROTEIN VP)		-	129-163	379-195	98748	10.41		1	7

CUNE	ALLNUTIS	ner fes betteriophoger)	ANTAL	CBEAL	ABEA?	40534	1628	ABEAS	ORFA!	AREA
ULEANE	CAPIELL	-	14.76	344.376	1		27.28			
P. P.40 EBV	INER CORE PROTEIN (7)	HENLY HERPESY IRUS 4)	133.467							
11.48 1137.11	CAPSID PROTEIN PAD	_	204-257	199.633						
PYP40 115VEB	CAPSID PROTEIN P40	(F11V.11	10.103							
PVP40 B.TVT	CAPSID PROTECN P40	DRYE VES	13	596.557						
PVP40_SCMVC	CAPSID PROTEIN P46	_	137.400							
0124 OF 414	CAPSID PROTEIN P40	SINIAN CYTOSE OF CYTOS (STRAIN DIDING) (VZV)	167-346	116 933			İ			
PLPII NPVAC	CAFSID PROTEIN P40	SIS VIAUS (13:16							
PY PAI ROISI	STRUCTURAL CLYCOPROTEIN GEN	_	Ē	115.10	330.630					
PVP-13 ROTS!	OUTER CAPSID PROTEIN VP4	STATE OF STA	=	11:31	\$31-646					
PAA VACCC	OUTER CAPSID PROTEIN VP4	SINISA II KOI ANIKUS ISINISA SAIN	151-159	137.01	964-828	183.481				
PVP1A VACCV	MAJOR CORE PROTEIN PAR PRECURSOR	VACCINIA VIAUS (SIRAIM CONCINCION)	161.28	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	116.763	794-828	857-891			
PLPAN VARV	AILIOR CORE PROTEIN PAA PRECURSOR	VACCINIA VIRUS (SIRAIM "A)	11:11	3.5	205.030	150-892				
PLP48 FOWPV	MAIOR CORE PROTEIN PIA PRECUMSOR	VALUELA VIRUS	111.133	104.330						
VP4B VACCC	MINION CORE PROTETIN PAR PRECURSOR	FOWLPOX VINUS	113	135.163	105-203					
PVP IS VACEV	MAJOR CORE PROTEIN PAU PRECURSOR	VACCINIA VIRUS (STILAIM CUPENIAUEA)	-	13:163	149-103					
PYP40 VARV	MIAJOR CORE PROTEIN PAR PRECURSOR	VACCEMIA VIAUS ISTRAIN WAS	13.1	133.163	149-203					
PVP4 BTV10	MIAJOR CORE PROTEIN PAD PRECURSOR	VARIOLA VIRUS	130.611	619-613						
PVP1 BTV11	VP4 CORE PROTEIN	BLUETOYGUE VIRUS (SEROLTYPE 1971)SOLATE CASA	140.607	19.60						
EVP4 DIVID	VP4 COME PROTEIN	BLUETONGUE VIRUS (SENO) VIE 11 (1905-15 027)	109.695	(19-60)						
PVP4 DIVIA	VPA CORE PROTEIN	BLUE LUNCOS VINUS (SENOTIVE 17 CONTRACTOR ALE USA)	\$49.607	[17:60]						
PUP NCDV	VP4 CORE PROTEIN	BLUE ICHOUS VINOS (SERVICE A VIBIR ACTIVATION ACTIVATIO	110.00	818-518						
PVP4_RDV	OUTER CAPSID PROTEIN VP4	REMARKA LALI DIANNILA VINCENZIA	111.03	164.438	637-679					
PVP4 R0104	MONSTRUCTURAL PROTEIN PAST	SOUTH BOTA VISITE (SEROTIVE A. STRAIN BALL)	=	#1:E	336.374	484-518	128-65)			
rvre ROIBC	OUTER CAPSID PROTEIN VP4	SOURCE BOTA VISITS STRAND CASE	=	10.5	338-430					
PVP4 ROIBU	OUTER CAPSID PROTEIN V74	POWER BOTAVIBLE SERANGIES	=	113:104	136-379	484-518	138-453			
PVP4 ROTEH	OUTER CAPSID PROTEIN VP	FOUND BOTA VIRUS (STRAIN 11-2)	=	113.146	111.114	145.176	12.51	37453		
PVP4 R01G1	OUTER CAPSID FROITING VA	ROTAVIRUS (GROUP B / STRAIN IDIR)	113.131	476-519						
10 M	CAPTER CAPTED PROTEIN VP4	HUBIAN ROTAVIRUS (SEROTYPE I / SIRAIN 1076)	5	236-273	1.5	9	2			
7110	CALLER CAPSID PROTEIN VP4	INDIAN ROTAWRUS (SEROTYPE 1/STRAIN RV-S)	2	116-273			76-175	277		
TO POLICE	CHIER CAPSID PROTEIN VP4	HUNDAN ROTAVIRUS (SEROTYPE I / STRABH 69%)	=	3	37.276			-		
0101	OUTER CAPSID PROTEDY VP4	ILDALAH ROTAVIRUS (SEROTYPE 27 STRAIN DSI)	÷				100			
VP4 ROTIE	OUTER CAPSID PROTEIN VP4	HORIAN ROTAVIRUS (STRATIV KB)								
PVP4 ROTIE	OUTER CAPSID PROTEIN VP4	IGMIAN BOTAVIRUS (STRAIN RU)					11.631			
PVP4 ROTIDA	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN LZO)			11.11	2005				
VP4 ROTIEM	OUTER CAPSID PROTEIN VP4	TOPING TO SERVICE (CEDOSAN SERVICE)		21.21	25.35	404.510	3			
PVP4 ROTED	OUTER CAPSID PROTEIN VP4	THE LANGE OF THE COMPANY OF THE LANGE OF THE	15	114.11	15.6	65.53	117-452			
VP4 ROTIO	OUIER CAPSID PROTEIN V74	MONTH BOTANTEUS (SEROTYPE) / STRAIN RAV)	=	91:146	111.114					
PAPE ROTHT	OUTER CATSID FROILIN VIT	MINIAW BOTAVIBUS (SEROTYPE 4 / STRAIN ST THOMAS I)	=	116-111	337-378	403-313	170-011		ļ	
V.P. ROTIIV	OUTER CASSID PROTEIN VP	HIDAN ROTAVIRUS (SEROTYPE 4/ STRAIN VATO	3.	111.111	144-178	40.513	331-433			
V.P4 ROINW	COLER CASILO FROIEN VI	HISTAN ROTAVIAUS (SEROTYPE I / STRAIN WA)	55.	111.111	344-378	411.513	20.5			
NA ROLLS	COLER CASE DESCRIPTION OF	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN 05U)	113.146	116-511	\$20.039					
VP4 ROIN	COLER CASE DECISION COL	PORCINE ROTAVIRUS (GROUP C.I STRAIN COWDEN)	8.	137-160	341-378	31.15	205			
VP ROING	CLUSE CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN GOTT) RED)	=	26-33	2	3	300	264.63		
najoa ran	CHITER CAPSID PROTEIN VPA	PORCINE ROTAVIRUS (STRAIM YA!)	=	3	217.174		AF0-976	***		
2010E 2010E	OLINER CAPSID PROTEIN VP4	NICESUS ROTAVIRUS	=	=						
PVP4 BOISS	OUIER CAPSID PROTEIN VP4	SIMIAM 11 ROTAVIRUS (STRAIN SAIL FEN)			019-016		1			
VIW MAY	DE OUTER CAPSULPROTEIN VP4	SIMIAM II ROTAVIRUS (STRAIM SAIT-SENI)	2							
PVP1 AHSV4	MONSTRUCTURAL PROTEIN PASS	WOUND TUNIOR VIRUS (WTV)				1				
ONE SAV	OUTER CAPSID PROTEIN VPS	AFRICAM HORSE SECRESS VIAUS (NEROLINE: 47 STRAIN ALL								
PVP1 BEVIO	OUTER CAPSID PROTEIN VPS	BROADHAVEN VIRESTERIN								

	11140416	All Vieuses (no bacteriophages)	T	Γ	2 7 2 4	ARCA	AREAS	AREAG	AREA1	AREAS
יייייייייייייייייייייייייייייייייייייי			4	999	20.31	101.10	Γ	Γ		
	CHITER CAPSID PROTEIN VPS	ONGUE VIRUS (SEROTYPE 10/150LATE USA)	I	27.10	150.222	604-645				
	CHIER CAPED PROTED VP.		T		100				-	
	CALTER CAPSID PROTEDA VES	T				157.00				
	OUTER CAPSID PROTEIN VP3	i	Ī			117.707				
	CATER CAPSID PROTEIN VPS									
NAME OF THE PARTY	CHIEF CAPSID PROTEIN VPS	PLUETONGUE VIRUS (SEROTYPE 2/15OLATE USA)		77.74		201.125	188-433			
200	CATTER CAPEID PROTEIN VPS			A.C. 168						
200	Outre COAT PROTER PS	RUCE DWANG VIRUS (RDV)	2	24 64						
	The state of the s		434-303	347.386	131.78					
DIAIG 194Ad	GOICE COAL PROJECT	TPE 107 ISOLATE USA)	163-215							
PUPEL AIRDY	VPS PROTEIN		120-202							
PVP61 KPVAC		A POLYNEDAOSIS VIRUS (29.96	151-166						
PUPE BIVIO	SI KD PROTEIN		17:01	159-207	314-351					
PUPEL MPVOP	VP6 PROTEIN	ROSIS VIRUS	194-341	431-470						
PVP61 NPVAC			14.78	209-364	413-411					
PYPET NEVEN			206-381							
11/10	MAJOR ENVELOPE OF TLOPROTEIN		119-211							
PVP6 BTVE)	VP6 PROTEIN		139-211							
7.76 01/17	VPOPUOLEIN		101-103	139-211						
7. F6 BTVIS	(Po PROTEIN	I AJ RICA)	===	163.211						
P. P. 01V2A	V Pt PROJECT	ī	4.3	135.107						
	(Pe PROTEIN		190.191	294-344	160-401					
VIW 6114	STRUCTURAL PROTEIN PO		44.17	104.31	100-434					
PLP6 WTVN	STRUCTURAL PROTEIN PA	Z En Cultu	100.17	106-334						
PLPIN NPVAC	STRUCTURAL PROTEIN PA	A VICEIROSIS VIRUS (27.12							
N. P. S. N. C.F	PARPLETA		105-453							
P. P.13 115VSA	P14 PROTEIN	-	6.8	15.50	170-110					
PLP IN NOVAC	PROBABIL MENIBLANT ANTION IN	EAR PULYICIDADSIS VIRUS	2:2	201.10	406-440					
27.0	W KO PROJEKY		114-131				-			
	VA COME PROBLEM	-	201-335							
P. PIVI	CALCONE PROFILE		104-220							
P. P. BIVIA	CONF PROTEIN	ALIA)	110-115							
P.P. BIVIS	INTI CORE PROTEIN	BLOE LONGE THE SECTION OF THE SOUTH AFRICAL	16.278							
P. P. BTV2A	VP CORE PROTEIN	ALUETONGIS VIBUS (SEROTYPE 27/150LATE USA)	124-311							
TYPI EIDVI	VP/COLE PROTEIN	VPE 1) (CHOV	16.50	24.13						
V2.	VP CORE PROTEIN		\$4.19	113.255						
VIN (4.4	CONSTRUCTURAL PROJECT PASS		12.5	105-243	181.181					
PY PEG NPVAC	NONSTRUCTURAL PROTEIN PRO	AUCLEAR POLYIII.DROSIS VIRUS (3.	271-66	154-304	321-396				
P. PET NPVOP	CAPSID FROTEIN 700	ORGYLA PSEUDOTSUGATA MULTICAPSID POLYIEDROSIS VIRUS		410-451						
P. P. BTV10	CAPSID FROILIS FEE	BLUE TONGUE VIRUS (SEROTYPE 107 ISOLATE USA)	_	165-219						
NA PARA	SE TILLOR OF THE STATE OF THE S	BLUETONGUE VIRUS (SEROTYPE 11/150LATE USA)	¥-102	=						
1	NOT THE PROPERTY OF THE PROPER	BLUETOMOUE VIAUS (SEROTYPE I) / ISOLATE USA)	24.103	1					1	
	SOCCEPT OF PROPERTY PE	BLUETONGUE VIAUS (SEROTYPE 17/1SOLATE USA)	26-102	=		-		\downarrow		
	CONSTRUCTIONAL PROTECT PO	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE AUSTRALIA)	24-102	2						1
100	NOWSTRUCTURAL PROTEIN PL	BLUETOWGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	20.00				1			
VANOT 14 14	MONSTRUCTURAL PROTEIN PE	BLUETOWGUE VIRUS (SEROTYPE 2/150LATE USA)	26-102							
700	STRUCTURAL PROTEIN VPB PRECURSOR	FOWLPOX VRUS					-			
213	NONSTRUCTURAL PROTEIN PMS9	NICE DWARF VINUS (NDV)		22.00	-		-	-		
NATA AL	STRUCTURAL PROTEIN PT	WOUND TURIOR VIRUS (WTV)	2		1		+			
NOAR DAY	STRUCTURAL PROTEIN PO	_	140-2112				-			
77.67	PLITATIVE GENOME LINKED PROTEIN PRECURSOR	R BARLEY VELLOW DWAJS VIRUS (ISOLATE MAV-PSI) (BYDV) 135-39	AC-42				+			L
TALK PARTY		۳			_	-		•		

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				I	ì					
				106-165						
		11	Ī							
	IND POLYHEDRAL ENVELOPE PROTEIN		5						_	
	20 000 15 DE		1.3							
			17.7							
	VIOLEN CONTRACTOR CONT									
	- NOTEIN	INTERIOR BURLINODEFICIENCY VIAUS TYPE I (BILL ISOLATE) (TILL)								
llil	VPU PROTEIN	THE SAME AND THE PACK VIRUS TYPE I (DRAIN ISOLATE) (14	3							
lil	VAU PROTEIN	THE PARTY OF THE PARTY OF TARREST AND ISOLATES (III) 4.	F-3				1			L
il	70.000	٠.	44.							
	VTU PROTEIN			-						
	VPU PROTEIN	•	2							
Ì	VPU PROTEIN		5.2							
	Miles		9.2							
	VAU FROIE EA	IN BLAN INDIGNODEFICIENCY VIRUS TYPE I (III) INCLUING								
Ī	N. PROTEIN		4.30				-			_
١	7130000	INDIAN INMONOCATION OF THE PARTY OF A TELLUM	2							
١	The state of the s		1							
DAN OXIVI	NISTORA DA		3	1				L		_
Ī		HILIAM INCHES OF THE PARTY OF T	6.72	_						
i	,									
THE INTERIOR	LAU PROTEIN	-	•				L			
Ī	NA TROPIES		t-39				-		L	
	100 miles	•	6.40							
Ì						_				1
JAN ZIVCZ NAV	NAU PROTEIN			j			L	_		
	VPU PROTEIN	Ę	42.15						L	
Ī	Mark as well		90.34	157-150						L
١	, and the second									ļ
PVS05 ROTS1 AL	ALPIIA.A PROTEIN						L	_		
Ī	NOWSTRUCTURAL PROTEIN NCVP?		4-44			1			L	_
1	Maloue Act	RAHEA ROTA	69.144				-			L
			1	44.103					1	-
١	's radicus					_				1
PVSOB ROTHC VP	VP# PROTEIN							_		
	VPS PROTEIN	-								
	VP PROTEIN		÷:	207.72			1	1	-	L
Ī	CONTROL VE		18:131	195.236						1
	A CONTRACTOR OF THE CONTRACTOR			100.316						1
PUSOI ROIPS	ONSTRUCTURAL PROTEIN	S/STRAIN OSU)					-			
Γ	NONSTRUCTURAL PROTEIN MCVT		88-133					-		L
1	MANY TRUE THAT PROTEIN NCVP)	SELECT INC. STATE OF THE SELECT INC. SELEC	3.70		160-226				-	L
I	CONTRACT PROTEIN NS2/VP	BOVINE ROTAVIRUS (STRAIM OR)	1	164-212	117.255					1
	UNDIRECTION TO THE PROPERTY OF THE PARTY OF			١						
PV.509 BO184	NOWSTRUCTURAL PROTEIN PLANT	RAIN DEATH	-	101.10		+			-	L
	GLYCOPROTEIN VP?		1-4)	31.370			1	-	-	-
Ī	CL VCOPROTEDA VP	BOVING RUIN VINCE CONTRACTOR OF THE PAIN CONTRACTOR	3.54	311.330		-		1	+	1
Ī	The state of the s	BOVINE ROTAVIRUS (SERUTTE & STRAIN STATE		363.130		_			-	4
	LICOTODE NATIONAL PROPERTY OF THE PROPERTY OF	BOVING ROTAVIAUS (STRAM A44)					-			_
V.509 ROTES	CL VCOPROTEIN VP	BOWINE BOTAVIRUS (SEROTYPE 10 / STRAIN B221)	2							
	GLYCOPROTED VP?	TOTAL SAN AND MARKED AND MARKED	1.54	201-170		+	+	-	ļ.	L
	CL YCOPROTEIN VP 1	TO THE POST OF THE	ž	113-330			+			L
Ī	CL VCOPROTEDY VP!	COVER TO SECOND	1-43	163-320			1	-	+	
Ī	CI VERSEDITEIN VP7	BOVING KUIN IKOS (SENOTINE)	\$ 2	163-370				-	+	-
Ī		BOVINE ROTAVIRUS (STRAIN UK.)	104.134			L				+
PUSON ROTCE	A TLOFACIETY W	CHICKEN AOTAVIAUS A (SEROTYPE 1/51KAIN CIVI)								
	CLYCOPROTED VP?	FOURINE BOTAVIRUS (STRAIM LIM)	201.702					-		Ц
PVS08 BOTCA	CL VCOPROTEIN VP7	A OTAVIRUS (GROUP B / STRAIN ADRV) (ADULT DIABBLEA ROTA			İ					
Γ	CL VCOPROTEIN VP 7 PRECURSOR	SOTA VIBING (CROUP BY STRAIN IDIR)					-			
	CLYCOPROTEIN VP) PRECURSOR	AND AND STANDARY SEROTYPE 4/ STRAIN RV-4)	143	267.22		-	-	-		-
	CL VCOPROTEIN VP?	TOPON ROLL SEE SEED STORY OF STRAIN BKOS	262-520					-	1	l
T	CL VCOMOTEDA VP	INDIA ROTAVIRUS (SERCITIE CT. ST. ST.	313.330				-	$\frac{1}{1}$	-	+
T	STATE OF THE PARTY	HUNGAN ROTAVIRUS (SENO) THE 31 STRAIN 1103)	5	017:11		L			1	+
٦	GL TCOPROTEIN VE	HABLAN BOTAVIAUS (SEROTYPE G/STRAIN DIT)				-				4
	CLYCOPROTEIN VP?	HABITAN BOTAYAUS (SEROTYPE 37 STRADY DS1)		1		1		-		
Γ	CL YCOPROTED! VP?	THE ASSESSMENT OF PROPERTY BE 2 / STRAIN HOUSE	203-320			1	1			
	CL VCOSEOTE IN VP1	MUMON HOLIVIEW STATES OF THE S								

	A NOTES	All Vieners (no becersiophoges)	Ţ	Т	1 1 1 1	ARTAG	AREAS	ARKAS	AREAT	AREAS
777	PROTEIN		4		Γ	Т	Γ	Γ	Г	
101 PO 101	GLYCOPROTEIN VP?		T							
9110	CI VCOPROTEIN VP	-	T							
210	CLYCOPEOTE IN VP	O AND STRAIN D)	T	R						
	SI VEDENCIE NEW	HURIAM BOTAVIRUS (SEROTVPE 1/STRAIN P)	03.370							
100	CI COSEDITED 193	(,)	200							
NA ROLLS	CLUCOSOCIETY IN		20.70	Ì						
	CALCACIAN AND AND AND AND AND AND AND AND AND A	ILDIAN ROTAVIRUS (SEROTYPE 4/ STRAIN ST THONIAS))	36 30	٦	182-370		1			
ALION AN	OLYCOPROJECT VY		2.50		163-170					
CA ROTIN	CLYCOPROIRIN VF7		17.5	181.170						
	CLYCOMOTEIN VP	161	201.330							
500 ROTP)	GLYCOPROTEIN VP)		382.330							
SON ROTPA	CLYCUPACIEIN VP?		Ī	108.242	383.330					
1.509 ROTPS	CLYCOPROTEIN VP)		2	T						
1 SOF ROTP	CLYCOPROTEIN VP?									
See Botton	CL VCOPROTEDA VP?	PORCEME ROTAVIRUS (SEROTYPE 57 STRAIN TFR-41)		Ī	-					
30104 003.10	GLYCOPROTEIN VP?	PORCENE ROTAVIRUS (SEROTYPE 4/STRAIN BEX:144)	1	Ť	184-340					
1	C1 < C0000 15 17 19 1	PORCENE BOTAVIRUS (STRAIN K)		Ī						Ī
200 800 50	CONTRACTOR OF THE CONTRACTOR O	PORCINE ROTAVIRUS (SEROTYPE 4/STRAIN BAIL-1)	10.56	206-242	283.370					
200	C. L. Consolin View	PORCINE ROTAVIRUS (STRAFA YAL)	1.33	2 2 2						
NO TOTAL	C LOTAGE AT THE STATE OF THE ST	RAESUS ROTAVIRUS	921-130							
V SOV ROTS!	GUICORDIEM VI	JS (STRAIN SAII)	212-530							
Y STO ROTEN	GLYCOPHOILEM VF	BOUNE BOTAVIBLE (STRAIN NCDV)	11.161							
PVS10, RO10S	NONSTRUCTURAL CLYCOPROTEIN POLYP	POWER POTANIES CAPAGE CASTALL SHINTOKUI	17.58							
PVS10 ROTBU	AITHOR OUTER CAPSID PROTEIN	BOVING ROLL KUING (CROAD) CONTROL CONT	37:161							
PVS10 BOTH?	MONSTRUCTURAL CLYCOPROJEIN NCVP)	BOVERS ROLAVINOS (STRAIN ON)	11.162							
P1 \$10 ROTH?	MONSTRUCTURAL GLYCOPROTEIN NCVPS	HUMAN HULAVIRUS (STRAIN AND)	71-167				 			
PVS10 ROTH	MONSTRUCTURAL GLYCOPROTEIN NCVPS	HUNIAR RUIAVIRUS (3) RAIN ARTICLES (2)	100							
VS 10 ROTHC	HONSTRUCTURAL GLYCOPROTEIN NCVPS	SCRIMA ROLAVIROS (STRAIN AND CLOSE OF	123-131							
VS10_BOTHW	MINOR OUTER CAPSID PROTEIN		91.10							
PVS10_ROTS1	NONSTRUCTURAL GLYCOPROTEIN NCVTS	MUNICIPALITY (SCHOOL OF THE TOTAL OF THE TOT	37.163							
VSII ROTGA	NONSTRUCTURAL GLYCOPROTEIN NCVPS	A TOTAL TOTAL	Ţ	94.130						
PVS11_ROTG	MONSTRUCTURAL PROTEIN		T							
VSII ROTIIS	HONSTRUCTURAL PROTEIN	ROTAVIRUS (CROUP B / SIRAIM IDIA)	100	T						
VSII ROTIM	MUNOR OUTER CAPSID PROTEIN	HUMAN HOTAVILOS (SENOT TEL 27 STRAIN RV-5)	103.144							
VSII ROTID	MINOR OUTER CAPSID PROTEIN	HUNDAR ROLL VIEWS (SENS) (SE 1) STRAIN COM	107-144							
VSII ROTID	NINOR OUTER CAPSID PROTEIN	TOWARD TAVIETY (SEROITYEE 2/STRAIN DSI)	10.11							
VSII ROTIIW	ATINON OUTER CAPSIO PROJETIN	IDDIAM BOTAVILIS (SEROTYPE 1 / STRAIN WA)	111:13							
VSII ROTSI	AUROR OUTER CAPSID PROTEIN	STATEM II ROTAVIRUS (STRAIN SAII)	111-145							
VS48 TBRVC	NAMED COLLECTION AND PROPERTY	TOWATO REACK RING VIRUS ISTRAIN C) (TBRV)	217-265							
VSI MUMBE	SATELLITE DAY 40 KD TROICIN	JS (STRAIN SOL	9-48							
CENT PROPER	SWALL INTUROFFICER FROITER	MINGS VIRUS (STRAIN EDINGBURGH 2), AND (STRAIN EDINGB	17-11							
VSH MUND	MALL HTUROTHORN FROIDS	MARGE VIRUS (STRAIN EDINGBURGH 4)	13-43							
V.SH PROPOR	SMALL HUNGARIDAN PROJECT	AND S VIRUS (STRAIN MATSUY ANA)	13-51							
A STI MILANT	MINITE INCOMPRESSION AND AND AND AND AND AND AND AND AND AN	IMINITS VIRUS (STRAIN BELFAST)	13-52							
Vall Pilonire	NISTON CHARGOS IN THE PROPERTY OF THE PROPERTY	INDUM SIRUS (STRAIN ENDERS)	9-46							j
A PROPERTY	STORE III COMPANIE PROTEIN	MARIPS VIRUS (STRAIN JERYL-LYNN)	97-6							
PVSII PIUPUR	STATE STATE OF STATE	JAUDAPS VIRUS (STRAIN KILHAN)	16.9							
200	SUALL HYDROPHOBIC PROTEDA	MUNDS VIRUS (STRAIN DRUSTOL!)	13:33							
A COLUMN	SAAL HYDROPHOBIC PROTEIN	MUNDS VIRUS (STRAIN MIT ANIAMA VACCIME)	17-51							
LASH MONEY	SUAL I KYDROPHOBIC PROTEDA	ALLAUS VIRUS (STRADA TAXAHASIH)	17-13							
STORE STORE	SMALL HYDROPHOBIC PROTEIN	NUMBER VIAUS (STRAIN URABE VACCINE AMIS)	7							
PACIF PEDAI	SIGNA I PROTEDY PRECURSOR	REDVINUS (TYPE) / STRAIN DEALING)		137-173	£ 1					
200	SIGMA I PROTEIN PRECUBSOR	REDVIRUS (TYPE 2 / STRAIM DY/ONES)	201							

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PCGENE	ALLAIOTIS	and the Best State of the State]	T	2010	Т	Г		Γ	
C NAME		TOWNER STANK I STRAIN LANG)	1	M1.21	1					
OVER REOVO	PRECURSOR	NC)	20.00		+		1			
PLOW.			30.384				1	-	1	
5000			911.8			1	†			
LAU STORY	12	AEOVIAUS (177E.) SURAIN DEANGACH	57-			1	Ť	†		
THE VALLE		100	111.352				1	+		
311 115 120	CIBILCTICAL PROTEDY 2 PRECURSOR		117.331					+		
VSI2 HEVE	TOTAL SECTION OF CHANGE		9							
VST2 IEWAY	STRUCTURAL PROJECT CONTROL									
VS12 HEVPA	STRUCTURAL PROTEIN 2 PRECURSOR		110-331	1	İ	Ì	 			
VST2 HEVEN	PRECURSOR		66-220		Ì	Ì				
VI IA CABVI			120-158					\dagger		
			130						T	
VICAPVI			1					1		
TH CAPVK			7							
VIER EDV	TA PROTEIN	895-1) (HUNIAN HERDESVIRUS 4)	٦							
VIER SICHVA	PROBABLE DNA PACKAGING PROTEIN		417-458	11-438			T			
LIAVED HISVALL	PROBABLE DNA PACKAGING PROTEIN	ANDA-1102)	161.502					Ì		
10.00 m	PRODUMENT DINA PACKAGING PROTEIN		197					1		
	PROBABILE DNA PACKAGING PROFELN	T		646.744						
100	BECRAPI & DNA PACKAGING PROTEIN	יייייייייייייייייייייייייייייייייייייי	114.167							
TER INVA	MISTOR COURT AND STORY							-		
VIER VZVD	PROBABLE LINA FALLANCING		388-465							
VV PIGIA	PROBABLE DWA FALKAUMU PROTEIN	DA) (PIV-4A)	5		1					
PVVI SENDA	VAROIEN	10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	104-138							
VIOL SEVI	YI PROTEIN	SENON VINCE CONTRACTOR	01-10							
VINE SEVI	HYPUTHETICAL 10 I KD PROTEIN	SULPCIONED VIACOTINE	197							
100	HYPOTIETICAL TO BKD PROTEIN	ארש לעו משתם אושרה ביאים והיה ביאים והיה של היאים ביא	25.50							
	HYPOTHETHCAL IT O KD PROTEIN	Statologus villus-Like Parinete 33 vi	10.00							
1	WYPOTHETICAL 119 KD PROTEIN	77	19:15							
2000	AVPOTUTE TICAL IL DED PROFETS	TOBACCO VELLOW DWARP VINCS (SIRS)	=					j		
200	INVESTIGATION IN THE PROPERTY IN COAT PROTEIN	FELINE CALICINIAUS ISTRAIN CRUS CALINIA								
	INTEREST 13 1 KD PROTEIN IN COAT PROTEIN		9							
A I EN	WANTETICAL IS SED PROTEIN IN COAT PROTEI	INDIT IENOLUIGE DISEASE VIECS (#101)	9							
A PER MINISTRA	ACCOUNTS AND PROFESS IN COAT PROFEIN			Ī						
VIIK CLVK	STORESTON IN THE PROPERTY.									
יווא כראא	HILLIAN STATES	CASSAVA LATENT VIRUS (STRAIN NICERIAN)								
VIJK MOVOP	NYPORE IN A 11 TAU PROTEIN		9							L
YIJK SSVI			3.36	*						
VISE SSVI	HYPOTHETICAL 13 7 KU PROTEIN	SOLI CALLO CARRIED FOR PARTICLE SSVI	1.10							
VIAS ADEO?	HYPOTHETICAL 13 3 RD PROTEIN	SUCCESSION VINCENTIAL TOPE 3	19:16							
NEW COVI	HYPOTHETICAL PROTEIN C-164	HUNIAN ADEXONINGS THE CO.	=	13:111						
1000	HYPOTHE HEAL 19 6 KD PROTEIN	SULFOLORUS VIRUS LINE PARTY CONTROL	3	118-130) 					
173	hiveond rical to and proofin	ואת נמיסטת אשת זרוער ביצוור ביצוו	102.114							
	ILVEGILIETICAL IN O KD PROTEIN	SULFOLORUS VIRUS-LIKE FALTIKLE SSVI	19.103							
1 m	INCOME THE ALE BOARD PROTEDY	SULFOLOBUS VIRUS-LIKE PARTICLE 33VI								
VZIK SSVI	7131000 CA 00 11310111	SULFOLOBUS VIRUS-LIKE PANTIKLE SSVI	2							
PI SOCHV	IN POLIUE CICAL 10 3 M.D. M.D. M.D.	SOYDEAN CID OROTIC MOTILE VIRUS	2		1					
PYSIK SSVI	ILYPUTIG TICAL PROTEIN A	SIR FOLDBUS VIRUS-LIKE PARTICLE SSVI	7.07	8						L
PV 12K SSVI	HYPOTHETICAL 31 S KU PROILIS	ELA CON CALIF VIRUS-LIKE PARTICLE SSVI	310-276							L
PYIIK MPVAC	INTORIETICAL 11 7 KD PROTEIN	ALTHOUGH APILL CALIFORNICA MUCLEAR POLYHEDAOSIS VIRUS	133-341							L
PY1 SOCAN	IIVPOTIETICAL 117 KD PROTEIN	SOVERAM CHO DEDITIC MOTTLE VIRUS	113.149							
PVIKE SSVI	IN POTIETICAL PROTEIN)	SIN BOL DRING WRUS LIKE PARTICLE SSVI	1.31							
711 SOCAIV	HYPOTHE FICAL SOKO PROTEIN	SOCIETY OF DEDITION THE WAUS	2.3							L
PVISK SSVI	HYPOTHETICAL PROTEIN?	THE CO. CHICK VINCELLINE PARTICLE SSVI	81-139	503-537	346-583	638-780				
PVE SOCAIV	HYPOTIETICAL 85 7 KD PROTEIN	SOUTH AND ADDITION OF THE VIEWS	10-03							1
PVENDS SOUPPLE	Г	SOTEMAN CHANGE A PERSON AND AND AND AND AND AND AND AND AND AN	34.115	164-331						
		CONTRACTOR OF THE PARTY OF THE								

		All Vieures (no beeteriophoges)		187.1	1864.5	VRFA 4	ABEAS	ARIAS	ABEA?	APEAL
Γ	X131000		T	Τ	Γ	Γ		П		
TOWN TOWN			T		Ì					
T					Ī					L
Ī		TOWL FOX VIRUS (1500 ATE 119-414) NUNICIII)	31.6	1	İ					
P. HOT TOWARD			14.17	<u> </u>	1					
N DIO FOWPA			162-253	-	7		T			
Ī			6.47	13.13						1
2			133.163							
77RL3 CBV	I COLETA	HILAPESVIAUS 4)	138.506							
PV (3) 115/13?	0.0	SEPECATOR CANADACCE AND AND AND	147.118							
11 10 10WPI	2002		160.204							
PI GAI HSYNCE			10.00							
PIGAL HSVADI	OPROTEI	Ī	176.31							
VACCV	OPROTEI	US (STRACK MIDS) (MIDS)								
אלניי איניי	INPOTEIR FICAL 31 7 KD HINDHI-C PROTEIN	VACCINIA VIRUS (STRAIN WR)			Ī					
	757	_	76.38	777	T					
		BOS-IJ (HUNIAN HURPESVIRUS 4)		1	Ī	1				
MIN ADE	Majora Carta	THE AND ADENDY IN US TYPE 41	11:11	-						
7) LR.2 EDV	III TO THE FILL ALL TO THOUGHT IN THE PARTY OF THE PARTY	DOS-01 (HUNIAM HERPESVIRUS 4)	64-128							
Pical Coniv	INTOTAL BURY TROISING	CONDICTION VELLOW ALDITLE VIRUS (COTALV)	94.143							1
PLORE CONSIV	HYPOTHE FICAL 23 KD PROJEIN	CONDICTION ACT TOWN MOTTLE VIPUS (COYNIV)	11.11							1
איסמז רונרא	IIYPOTICE TICAL 15 KD PAULEIM	STANDAMENT OF	100-034							
PLORE TIVE	HYPOTHETICAL 21 4 KD PROTEIN	SIGNATURE CENAX VIRIS (STRAIN KRAI) (TIVI)	10.94							
PIONI ADEGI	HYPOTHE HCAL 69 KD PROTEIN	HEARIOTACION ICANO TIMOS TOTAL SOCIAL ADENOVIBLE	70.127							
PAGEA TIVI	HYPOTHE FICAL 31 5 KD PROTEIN	AVIAN ADENDVIRUS GALI (STRAIN MIELTS) (FOR E ADENOTION		-						
12.00	HYPOTHETICAL BIRD PROTEIN	HERMOPROTEUS TEMAX VIRUS I (STRAIN KRAT) (TTVI)				İ				
	STATE OF THE PROPERTY.	THERMIOPROTEUS TEMAX VIAUS & (STRAIN KRAI) (TTVI)	-	201						
	TOTAL STORY	THERESOPROTEUS TENAX VIRUS I (STRAIN KRAI) (TTVI)	18.123							1
Pical, Tivi		THERMOPROTEUS TEMAX VIRUS I (STRAIN KRAI) (TIVI)	\$7-							-
7,080 TV1	HYPOTHETICAL IS I NO TRUITING	THE BANDEOTEUS TENAX VIRUS I (STRAIN KRAI) (TTVI)	1.43							
NUMT TIVE	HYPOHIETICAL 73 KD FROILIN	HERAIDPROTEUS TEMAX VIRUS I (STRAIN KRAI) (TTVI)	4.38	381-315						
F108W 11VI	HYPOTHETICAL 18 7 KD PROTEIN	THE STATE OF THE PARTY WAS IN THE ALITED WITH THE ALITED WAS ALICE								
P1.P13 R10V	IIYPOTHE HCAL 13 + KD PROTEIN	HEADON OF THE STATE OF THE STAT	33.72							
PUPIT RIBVP	HYPOTHETICAL PIS PROTEIN	DE LONGEO BACHELINGOS VIRGO (STE BILL 1991NES)						·		
7) P.14 B10V	HYPOTHETICAL PIT PROTEIN	RUCE TUNCALO BACILLO DIANI VIADO (1304 A 12 7011) TOTAL	101.15	101.151	Ī					
PAPER RTOVP	IIYPOTIETICAL PIA PROTEIN	DICE TUNGRO BACILLIBORAL VIRUS (R. 1847)		151 701						L
Pires BTBV	HYPOTHETICAL PIN PROTEIN	IE FIREIFFINES) IN	20.10							
PYP46 BTBVP	HYPOTHETICAL P44 PROTEIN	NICE TUNGRO BACILLIFORM VIRUS (R.I.B.V.)								
PANTA MOVAC	HYPOTHE TICAL P46 PROTEIN	NCE TUNCAO BACILLIFORM VIRUS (ISOLATE PHILIPPINES) (IL			Î					
100	HYPOTHETICAL PROTEIN IN PS STRECTON	AUTOGRAPHIA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS (1						-
NAME AND A	HYPOTHETICAL PIA PROTEIN	TOBACCO MECROSIS VIRUS (STRAIN A) (TNV)	î							
VMVI IDAY	HYPOTHETICAL 23 6 KD PROTEIN IN PULYHEDRIN	ALTOGRAPHA CALIFORNICA MUCLEAR POL VIEDROSIS VIRUS I								
VO! ANIFPV	HYPOTIETICAL IT S KD PROTEIN	OT VE JASPER								
VOT ANG PV	INPOTHETICAL 16 KD PROTEIN IN TK STECTION	AMSACTA MODRES ENTONOPOXVIRUS (AMEPV)	•	T						ļ
110,40	HYPOTHE INCAL PROTEIN IN THE SEGION	AMSACTA MOOREI ENTONIOPOXVIRUS (AMEPV)	46-1	2						
C770311	INVESTIGATION PROTEIN RET	HERPES SINGLEX VIRUS (TYPE 6/STRAIN GS)	¥2.5							1
	INCOMPRESSION PROTEIN RS)	HENDES SINGLEX VIXUS (TYPE 6 / STRAIN GS)	34-173							1
THE ROLL	730 7330 77 70 77 70 77 70 77 77 77 77 77 77 77	HERPES SINDLEX VIRUS (TYPE 47 STRAIN GS)	252-286	404.42						1
PYRT BY	INTOINE IN ALTHOUGH W.	CHILO INDESCENT VIRUS (CIV) (INSECT INDESCENT VIRUS TV								
PYRI EBY	ALTERNATION OF THE PROPERTY OF	EPSTEIN-BARR VIRUS (STRAIN BOS-8) (INDIAN JERVESVIRUS 4)	P4-130							
PYSRI EBV	NYPOINS IN ALL BIOC I PROTEIN	FPETFIN BABB VIRUS (STRAIN 893-0) MURIAN HERPESVIRUS 4)	41.13							
PYTRI EBV	INTOTAL INC. BSIC I PROTEIN	EPETETA BARR VIRUS (STRAIN DSS-8) (HUMAN HERPESVIRUS 4)	190-424							
PATON COUNTY	INTOTAL BIRGINGIA		935-49	10.10						
אגיעכ געכככ	5		39.43							
PYVAG VACCC	IIIYOTIGIKAL ILAKUTKOTKIN	VACCIDIA VIRUS (STRAIN COPENHAGEN)	1.17							-
PYVAH VACCC	HYPOTHETICAL 9 3 KD PROTEIN	VACCINIA VIRIS (STRAIN COPENIAGEN)	70.112							
PYVAN VACCC	HYPOTHETICAL 14 SKD PROTEIN									

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TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

		All Vigues (so becerfaghages)	V 1 V 20 V	12	AREAL	385.34	ANTAS	10110	SHEA!	1864	SHEAS
			1	1007.1114	103-1169						1
T	CAULTER OF THE PROPERTY OF THE		١					ļ		1	:
┪				1			İ]	İ
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		SECTION NOT TA VIRING INSOLATE AND RICANI	8	i	-						! i
		TANAMENT A VIRILE / SCOL A PE ANY RICAN)	-		-						
WANT HOVE		THE STATE STATE STATE AND AND AND AND AND AND AND AND AND AND	٦	ŝ	į						i
SAMI HOVE	DELTA ANTIGEN	THE ALL PROPERTY OF THE ANNUAL AND AND AND AND AND AND AND AND AND AND	?	1							! !_
Γ	DELTA ANTICEN	MEANING PLEIN VINCENTIAL STATES AND STATES A	106-133					-			!
L		GPATITIS DELTA VIRUS (1504.A.C. A.C. A.C. A.C. A.C. A.C. A.C. A.C	33.106								
T	IN MOVED OG	FOWLPOX VIRUS (ISOLATE ID 4 JULIUNIUM LILL)	Τ		430.432	\$10.625					
Ţ	AN 11 100 100 100 100 100 100 100 100 100	VACCOUL VIBUS (STRAIN W.R.)	Ī],	100	İ					
	M KD A. IYPE DK. LUSIUM PRO	MINE A WHITE	٦	٦							
		VARIOUS TO SEE COMPANY OF SECURITY	304-315							-	!
	ALPHA TRANS DAD FACTOR 78 KD PRO	KENDES SPICIES AND STILLE	306.315				İ	1		-	:
I		HERPES SDOLEX VIRUS (TVPE I / SIRAIN F)								ļ	1
	ALTIN CHANGE STATE	ENIMAL MERPESVIRUS TYPE I ISTRAIN ABAP)		Ī							
PATE HISVED		TANKS DEPARENCED OF TANKS I ASSESSED. A ADAPT	255.280					000	1314.1761		
PATIN HSVEB	ALPIN TRANSPROTEIN		3.4	1.04	176.47	2				-	
Γ	A. TYPE INCLUSION PROTEIN	COWPOX VIXOS	027.50								
T	AND THE AMELACTIVATOR PROTEIN	EFSTEIN-BARR VIRUS (STRAIM BY)-11	ī	117.100							
T	THE PROPERTY OF THE PARTY OF TH	VACCODA VIBUS (STRAIN COPENHAGEN)	ī	113.144							
7	CELL MAY AND SOUTH SECOND SECO	VACCINDA VIRUS (STRAIN W.R.)	ī								
	CELL SURFACE EDMINO PROJECT	VANDA AVEIR	7								
PCAJGH VAILV	CELL SURFACE SENDING PROTEIN	TANADA TANADA SAND	112-339								
THE WAYER	CELL FUSION PROTEIN PRECURSOR	EQUINE RELUES VINOS 1 TE 151%	137.154								
10000	CYCL IN HOMOLOG	HEAPESVIAUS SABAIN (STRAIN 11)	100.1116								
V. C. T. D. X.	The second secon	HAMSTER POLYOMAVIRUS									
PCOAL POWIA	COAT PROTEIN VI	DIENCERICAN DE EINCLINE DISEASE VIRUS	1								
PCOAL BUDY	COAT PROTEDY V73		2 2								į
OWNER POWER	COAT PROTECT VP3	BOVING FOLYOMAVIRUS	100								
	POAT BEATERN VP2	POLYDMAVIAUS JC	20, 00								
KOM POW		L YLCHOTROPIC POLYONAVIRUS		İ					L		
COAL POYLY	COAT PROTEIN VIZ	MOUSE POLYOMAVIRUS (STRAIN KILLIAN)		İ							
KOAJ POVICE	COAT PROTEIN VE	20.11 A VIET 40	174.703								
PCOAL SV40	COAT PROTEIN V72	SELECT A SECONDATED VIBILS 2	120-147								
KON WY	PROBABLE COAT PROTEIN 1	ADENOTISE SELECTION CONTRACTOR CO	1.30	İ							
MOAT TIVE	COAT PROTEIN IPS	INCHAOTICIAN TRACE TO THE PARTY OF THE PARTY	196.321								
2000	COAT PROTECH VPI	ALEUTIAN MINK DISEASE PARTOVIRUS (STRAINT)	1								
	TO A T PROTEIN	BEAN LEAFROLL VIAUS	8	100	197						
Y OY	1000	CALL DIVER MOSAIC VIRUS (STRAIN CH. 1841)							L		
NOVI COMME	CONTROLL	CALL BLOWER MOSAIC VIRUS (STRAIN DAI)									
COAT CAMPE	COALPACIELY	PAIR IN DWEE MOSAIC VILLS (STRAIN BBC)	R.	2							
POONT CALME	COAT PROTEIN	CALL STOWER LANCAIT VIRIA (STRAIN MYRIS)	8:3	2	9						L
PCOAT CAMPA	COAT PROTEDY	TANKE STOCKE STOCKE WILL STRASBOURG	64-91	1 K -23							
POAT CANS	COAT PROTECN	CAULTURES ACCOUNTS	3								
POAT CABLO	COAT PROTEIN	CARATION MOITLE VINOS	1								
1000	MAKOR CAPSID PROTEIN	PANANGERIN BURSALIA CHI ONELLA VIRUS I						L			
	TOTAL PROTEIN	CUCUMOER MECROSIS VIRUS									
5	CONTRACTOR	CHE CALLS STRUCTE MOSAIC VIRUS									
NOAT CAN	COALTROIT	CHOWER YELL OW MOSALC VIRUS	30-200								
PCOAT CTATA	COAL PROTEIN	REI INT CALLCIVINIS (STRAIN CFUSEFIV)	366-600								
PCOAT FCVC	COAT PROTEIN	TELEVISION OF THE PARTY OF THE	516-543	99.35 35.					\downarrow		
PCOAT PCVF4	COAT PROTEIN	TELENC CALCULATION OF THE ACT OF	\$19.546	(09-69)							
SUNT BONE	COAT PROTEIN	FELDRE CALICUMENT (STRAIN TV)	330.243	20.00		L					
	BEOBARI E COAT PROTEIN	FIGWORT MOSAJC VIRUS (STRAIN DAS)	1	1							
COAL PART	TOTAL PROTECT	LILY SMOTOMAESS VIRUS								L	
YOY C	CON TROUBLE	MASCANTHUS STREAK VIDUS									L
PCOAT MOSV	COMPROTEIN	CODMITOGLOSSUM ROKSPOT VIRUS	2								
PCOAT ORSV	COAT PROTECT	HIDAAN PARVOVINUS BIP	3	200				1	1		
PCOAT PAVID	PROBABLE COAT PROTEIN VFI	PARTY AND AND VALLE AISOLATE AICC PV ? !	(F-3)								
PCOAT POPINY	COAT PROTEIN	TUTLAR MUSANE VINDS (1905)	138-163								
PCOAT SOCIAL	COAT PROTEIN	SOYBEAN CIRCUIT MOTILE VINOS	31-48								_
PCOAT TAMV	GENOME POLYPROTEIN	TAMARELO MOSAL VACO	21.50			L					
PCOAT TAV	COAT PROTEIN	TOMATO ASPENAT VIRUS	17.70	3:							
	COAT PROTEIN	FOMATO BUSHY STUNT VILUS (STRAIM BS-1)				L	L				
YOU	POST OFF TAXON	TOMATO BUSHY STUNT VINUS (STRAIN CHERRY)									
PUAL IBATE	LOW FROM										

						-	-	İ		ŀ	
PCGENE		ses (no bacteriophages)	ABFAI	AREAI	AREA J	ARTA	AREAS	AREAS	AREA?	AREAD	AREA .
THE HAME	CROIGIN	VINUS PERGIT CONTRA	35.55			7		Г	Т	Т	
PCOAT 1CV		MOCAIC VIRGIS	2								
COAT TACAIV			200					<u> </u>	_		
PCOAT TAV		174 PE A1	38-133							h	:
MOAT THINGO			3					r			j
COAL INVOA	COALFROIEN		2.5								
PCOAT THVEA		TOBACCO MOSAIC VIBING ASSESSED AND MAN KOKINGED	2.5								-
COAL INCO	COALTROISM	TOWARTO MOSAIC VIRIS (STRAIN DAI)	25								
ACOAT TRACE		TOBACCO MOSAIC VIRUS (STRAIN TOMATOR.)	12.50							<u> </u>	i
2011			8								
COAL BRAN			111.145								
יייייייייייייייייייייייייייייייייייייי			Î								
LOAI INDA	COAL PROPERTY	PERSONAL PARAIT CIPIN	3								
MOAT TOWN			7								
MOAT TRAVA			1.4				-			İ	- !
TOWN ADEG	2		13,1004	1041.1068	-		-			<u>-</u>	ĺ
-1			77							İ	
ار	MAJOR DNA-BENDENG PROTEIN	INDIAN CYTOMECALUVINOS (STRAIN ADIOV)	171	(1).410		T			 		Ī
1			204.418								
_		ALDVIRUS (STRAIM SALITIT)						T		T	
				917 117				T		 	
POSTEL BONC	BINDING PROTEIN	aug.					+	T	l	l	
PORT VACCC		VACCINIA VIRUS (STILAIN COPEMIAGEN)					1	t		T	ĺ
PONLI VACCV		VACCINIA VIRUS (STRAIN W.R.)						Ì	Ì	İ	-
POPEJ VARV		VARIOLA VIRUS		A				1		i	
POPOL ADELL	POLYNGRASE	HUMAN ADEMOVIAUS TYPE 12				Ì	1	Ť	ļ	T	Ī
POPOL CELEV	DHA POLYNŒKASE		-	101-140				1	Ì	\dagger	
POPOL CHANS			336.345			1		1	+	+	
POPOL CHAPI	11	PARAMECIUM BURSAUA CIGORELLA VIRUS I						Ì	†	t	Ī
POPOL TOWAY			?	10.416				1		\dagger	
POPOL HOAVA			201.00				1			i	
rotot, lineide		DUCK NEPATITIS B VIRUS (BROWN SHAMSHAI DUCK 150 LATH. 39)		İ		İ	1	Ì		ļ	
POPOL HORDC							+	Ì		İ	
POPOL MOBDW	DNA FOLTACRASE	ANGILAL DUCK ISAL ATE STI	A.			Ī	1	1	Ì	$\frac{1}{1}$	
POPOL HORGS		IIIS VIRUS				Ì	+	T	\dagger	+	Ī
Perof. Pers	POLYMERASE		A				t	Ť		\dagger	
POPOL IOBVP	DHA FOL YAEAASE	IEPATITIS B VILUS (SUB) TPE ADW / STRAIN THEIT CONTONING				Ī		T	t	t	Ī
POPOL HYBYZ	DNA POLYNGRASE		771.011	110 016				T	T	\dagger	
POPOL HSVI	DHA FOLYNGIASE					Ì		İ		t	
POPOL HSVSA		Ī				Ì	\dagger	T		İ	
POPOL NOVAC		AUTOMOTIVE CALE CHARCA NUCLEAR FOL FREDAUSIS VINUS				T	t	t		t	Ī
FORCE NAMES	COLA PARTORIA	Ī	170.767								
VACCV			130,787								
POPOL VALV	DNA POLYMEJAŠŠ		169.786							1	
POPOL WHY!	DNA POLYNERASE	WOODCHUCK HEPATITIS VINUS I	325-335							1	١
PDPOL WHYSP	DHA POLYNEJASE		290-331							1	
POPOL WHY	DNA POLYMERASE		111.141	390-331							Ī
POPOL WHYS	DNA POLYNGRASE		111.341	206-370			1	1		İ	
PDPOL WHYE		TIS VIRUS 9	22.22	3			1	1	1	†	Ī
POTXEL CORUBE	DUPHTH TOXIN HOMOLOG CRAZZE PREC	COR YNE HAGE BETA	25						1	1	
POTX COLLE	DUHITHERIA TOXON PRECUASOR		23.560				1		1	†	Ī
POTA CORDA	DEPHTHELIA TOXON PRECURSOR		25.2					1		1	
POUT HISVEA	DEOXYU F.TRIPHOSPH MUCHYDROLASE	EQUING HEIDESVIRIUS TYPE 4 (STRAIN 1942)	=				+	1	1	1	
PDUT ISVSA	DECOXTU S-TREMIOSPH MUCHYDROLASE	IERPESVRUS SAIDOU (STILAN II)						1	1	\dagger	Ī
PEIRL ADEO7	EIB PROTEIN, LARGE T-ANTIGEN	HOLLN ADERGYTUS 1778.					1	\dagger	\dagger	t	Ī
PEIN ADEA	EIB PROTEDY, LAUGE T-ANTIGEN	HAMAN ADENOVICOS 1172 4	1				1		\dagger	t	Ī
PEURS ADEIN	EIB PROTEIN, SMALL I.ANIIVER	INDEAN APPROVINCE 14								1]

		1000 4-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	П	T		ANTA	AHFA S. A	ARTAB	AREAT	ABEAL	AREAS
PCGEME	16761784	J. I.	J	3	1				_		
FILEMANE	PROTEIN	AND TABLE AND AND TABLE	2	-		:	į	i !		:	i
PEIBS ADEM!	EIB FROTEIN, SMALL T.ANTIGEN	MOUSE ADDRESS TANKS		Ì	İ	Ì	Ì				
PETIA ADEGA	EARLY EJB 14 KD PROTEIN	INDIAN ADERUCINOS CONTRACTOR	11-12					Ī	Ī		
SELLA APERT	FARLY ED 19 1 KD PROTEIN	HUNGA ADENOVIRUS LITE	35:3	30-100		1	1			T	<u> </u>
PETTO APEDI	EARLY ES 70 I KD GLYCOPHOTER	IGACAN ADEMOVIRUS 1 TC. 3	101-01				İ	Ì		Ī	
1124	EARLY FLY MAIN CALYCOPROTEDY	IRBIAN ADENOVILUS I VPE 13	181:181				į	_	į		
	FAST V 61 36 4 PD CL VCOPROTEIN	HIGHAN ADEMOVIRUS TYPE 15	1	:			_				
PERSONAL PROPERTY.	PART OF THE PART OF MODERN						_				
AUG.	CARL CALL CONTRACTOR	EPSTEIN DARR VIRUS (STRAIN 1111.1)	1		! ! ! ! !	-		-			
PEAR EDV	EARLY ANTREM TRUITING	Pilety & Science	_[1						
PEFTI VARV	EAST Y TRANS FACTOR TO KD SUBURIL	TANGE TO SELECTION OF THE PARTY	130-021	,			1				
PENV AVIRE	ENV POLYPROTEIN	AVIAN RETRUIDENUM INCLUSIO TINOS	63	426.474			Ì			1	
2012	TOTAL CENTREM	AVIAN SPLEEN NECROSIS VIRUS	12		Ī		_				
PENY AVISM	ENV POLITACION	MAINOR EXPOCENCUS VIRUS (STRATIN N.T.)	1		411.404	Ī	Ī				
PENV BAEVIA	ENV POLYPRUIEM	COLUMN TRANSPORTER VIEW VIEWS (1501.ATE 106)	17.44				-				
PENC BIVOL	ENV POLYPROTEIN	BOATILE BETTON OF THE THE THE THE THE	17.44	573-632	660-724						
10000	CAV POR VPROTEIN	BOVINE INMINIODEFICIENCY VINUS FRONT OF 1417	111								
N. T.		BOVING LEUKEMIA VIRUS (ALIERICAN ISOLATE PLK)									
PENV BLVA	ENV POLYPROTELIA	COUNTY TELEVISION WATER CALISTIAN ISOLATE)) OF 3.7								
PENY BLVAU	ENV POL YPROTEIN	BOVING THE THE THE STATE OF THE	36.33	į							
VAV III VAV	ENV POLYPROTEDM	BOVINE LEUKEARA VILLUS (AMENICARI ISCUELI)	111.133								
	SAN TO VERD TRINE	BOVING LEUKENDA VIRUS (BELGIUM ISOLATE LOTT)									
WAY BLVE		BOVDE LEIKEMIA VIRUS (BELGITAI ISOLATE LB19)									
PERV MUNES	ENV POLITICIA	PANAME FIRESAIA VIBIN (JAPANESE ISOLATE BLV-I)	Š								Ĺ
IPENV BLVI	ENV POLYPROTECH	BOOK AND THE STATE WILL WILL CARLES (STANING CO.)	165-192								
DENN PARKE	ENV POLYPROTEIN	CAPURE AN ING IN ENCE	641.712								
1000	END BOA VERDITEIN	EQUAC DO ECTIOUS ANEAUS VINOS (LLOPE 73 1.1)	167 645								
TENY ELA		FOLIDIE MEECTIOUS ANEMIA VIRUS (CLONE P) 3-2)									
PENV ELAVI	ENV POLYTRO I EUR	FRANKE BARETTONIK AMELIJA VIRUS (CLONE P) 3-3)	77.75								
PENV ELAVS	ENV POLYMOTERN	PACHE BACKET THE STATE OF THE BACKET	269-675								
PENT FIAVE	SHV POLYPROTEON	EQUIPE DEECTION AND A VINCE CO.	448.313								
LENA ELVAS	7235045	EQUIPE INTECTIOUS APENIA VIRUS (CLORE 1189)							_		
PENV ELAVO	ENA POLITICION	FORTING INSECTIOUS AVENTA VIRUS (CLONE CL22)									
PENV ELAVO	ENV POLYPROTEIN	PARTIES FARE FARE FARE AND AND AND IS ISTRACT WOUS	646-712								
PENV ELAVA	ENV POLYTROTED	EUCKE STEELINGS STATE STATE WYOMING	666-712								
PENV FLAVY	ENV POLYPROTEDI	EQUIPE DO ECTIONS AVENUE VINOS (1905)	39-66	\$13.546							
INC.	SAV POLYPROTEIN	FELINE ENDOCENOUS VINUS ECET	440.480	122.749							
	SALVE SOLVERS	FEI DE GOADNODEFICIENCY VIRUS (ISOLATE PETALUPIA)		671. 980							
PEN SINE	ENV POLITICISM	I ET INT NAMBIODE FICTENCY VIXUS (ISOLATE SAN DIEGO)		100							L
PENV FIVED	ENV POLITICUEDA	THE TANK THAT THAT IS TO WAY WINDS (ISOLATE TAU)	640-679	121.121							L
PEN INT	ENV POLYPROTEIN	THE PROPERTY OF STREET COME CAREA	501-511								L
PENV FLVCA	ENV POLYPROTEIN	SELINE LAUGHDA PROVINCE COMPANY OF THE PROPERT	490-519								
200	SAV POLYPROTEIN	SELDG LEUKEAGA VIAUS (STRAIN MULASUM)	410-414								
3	ENA POLIVERNIEN	FELING LEUKENDA VIRUS (STRAIN LANGIDA-BI)							_		
AND ALVE	ENV POLITICAL DE LA COMPANION	FFI DOE LEUKENDA VIRUS (STRAIN SAUMA)									L
PERV FLVSA	ENV POL TPROTEGY	INDIAN CHIMARETROVIRUS	3	2	64.00				ļ		
PERV FORM	ENV POLYPROTEIN	THE PARTY CONTINUES AND CARDINER. ARMSTEIN	202								
PENV PSVCA	ENV POLYPROTEDI	FELDE SARLUNG VINOS (SIRVING COCK)	8								
SEATON SEATON	ENV POLYPROTEDN	FELDE SARCOMA VIRUS (STRAIN DA)	167 (91								
	10 and 10	[FELDICE SARCOMA VIRUS (STRAIN SM)									_
PON FSVSA	ENVIOLEN	CIRECTAL APPLIEUX SACA VIDUS	120	5							
PD-V CALV	ENV POLYTHUIEUN	WALLEY OF THE FIRE FAIR VIRUS TYPE I (STRAIN ATK)	342-376								
MENV HILLIA	ENV POLYPROTEDY	THE STATE STATE OF THE PART OF THE ARIBDE AN ISOLATE)	343-376								1
PEN HTLIC	ENV POLYPROTEON	MUNICAL LE LE CONTRACTOR STATE COLOR AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE AND AND LIVE	142.176		L						
11	ENV POLYPROTEDI	INDIAN T CELL LEUKENDA VIRUS I ITE I (1905 AL	114.130								
	Salve box VanAtitible	HUDANN F-CELL LEUKENDA VIRUS TYPE II			100				L		
PENV HILYS	ENV POLITROLEM	INTERN BARANOSFICIENCY VIRUS TYPE I (ARVUSE) ISOLATE)	344-392	200.00					-		L
PENY HVIAL	ENV POLYPROTEDI	THE LABOR BANDER FOR VIEWS TYPE (BILLO ISOLATE)	148-8M	631-683	10-16				4		
PEN HVIBI	ENV POLYPROTEDI	HANAN BOLUMBER RICH : VIPUS CORE PRIN 1601 A 161	\$40.519	676-678	3	Ĺ					
191701	ENV POLYPROTED	PRINCIA BOADWOOEFICENCY VINUS 11TE 1 UNIT 13CLATE)	1	Š	85:58	6.9.0	107.015	L			
	Man New York	INDIAN DOADWOOFFICENCY VIRUS TYPE I (BRAIN 1904 ATE)			1				L		
ACA HAIR	DAY FOLLTROITES	IN INJAN BOARMODE HEIENCY VIRUS TYPE I (BRU ISOLATE)	20,24								L
FOY HAIR	ENV POLYTROIEUM	THE TANK BANDAGE STOREMEN VIRIUS TYPE 1 ICDC-451 ISOLATI:)	383-234	22.408	•	6					L
204 204	ENV POLYPROTED [®]	HUMAN MANAGERICAL VINE 1 (FL) 1504 ATT.	33.78	116-411	345-391	628-620					ļ
PEN INE	DAY POLYPROTED ⁴	HUMAN BENEVICE TO THE STATE OF	345-594	139.159	31.018						1
PENY HYIE	ENV FOL YPROTEDM	TOUR DESCRIPTION OF THE PARTY O	10.00	100	701.01				4		_
DHIVN VICE	ENV POLYPROTEDY	INDIAN DEALINGS IN THE STATE OF	116.133	38.40	149.63	607.03					1
WIND NAME	DAY FOL YPLOTER	MANAN BARACOER CERCT VIROS 1775 (11) 100-11-1	177	433.433	10.01	L					4
A NAME OF THE PARTY OF THE PART	PAN AN VOROTERA	HEBLAN BOADWOODSICIENCY VIRUS TYPE I INCSF ISOLATES	124-141								İ
PER HVID	DO POLITRUIEM										

47.500		At Viscon (an bacterdoshages)						\Box	П	П	
TI P MANIE	PROTEIN	VIRUS		286	ABEA L	┙	A LAND	ABEAS	AREA!	ARTALA	ARA
PENV HVIKE	ENV POLYPROTEIN	HUMAN DOURIODEFICIENCY VIRUS TYPE I (STRAIN KII-1-GP)3)			2		i		<u>;</u>	•	
PENV HVIMA	ENV POLYPROTEIN		7	_	20.00		1	1	1	İ	
PENV HVING	ENV POLYPROTEIN	HEINAM INDAMNODEFICIENCY VIRUS TYPE I (NIFA ISOLATE)	<u> </u>	П	٦			+		1	
PENY HVINGY	ENV POLYPROTEIN		2	25.75	30.23	1	1				Ī
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PENV IIVIND	ENV POLYPROTEIN		R	2	Т		İ	†	T	†	
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PENV HVIPV	ENV POLYPROTEDI		Т	T	Т	100	1			Ì	Ī
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PENY HYING	ENV POLYPROTEIN		┑	_1	┪	113.50	j	1	+	†	
PENV HVIZ3	ENV POLYPROTEIN	HALAN DOGMODEFICIENCY VIRUS TYPE 1122CDC-234150LATE)	Т	2	678-610	20.0	j	1	1	İ	i
PENV HVIZS	ENV POLYPROTEIN		7		ī		1		Ì	1	1
PEN HVIZE	ENV POLYPROTEIN	HIGHAN BOATHODEFICIENCY VIRUS TYPE I (ZAIRE & ISTA ATL)	٦	╗	╗	2	İ		1	-	!
PENY HVIZE	ENV POLYPROTEIN	HUNAN BOARNODEFICIENCY VIRUS TYPE 1 (2.14 ISOLATI)			╗	2	İ			<u>.</u> !	:
L	ENV POLYPROTEIN	HUMAN INDAMPORENCIEMCY VIRUS TYPE I (ZAIRE 14/11) ISUI ATI:)	_	€2.666		j			1	i	i
	ENV POLYPROTEDI		1	135-561		611.697	-	_	-		:
	ENV POLYPROTED		330-595								
١	FAV POLYPROTEON		=======================================	1	i	819.77				_	
	ENV POL VPROTECU	HANDAN BANDODE HOTENCY VIRUS TYPE 2 (1504 ATE GUANA-1)	3	\$24.551	_		(69.57				
L	CAN BOX VEC TREAT	HERAN PARAMONS INCIDENCY VIRING TYPE 2 (150) A FE KIRL 2)	17:19	-	356.383	079.619	67:58			-	i
200	STATES SECTION	MANAGEMENT AND THE STATE OF THE	Ī		ī	ī	İ	Ī	Ï	<u> </u>	i
	LAY FOLTROITIN		١	-	T	441.400	İ	!	-	i	:
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	ENV POLITICISM		611		i		İ			<u> </u>	Ī
	ENV POLYROIEIN	11 12 11 12		Ī	T		i	ļ	<u> </u>	i	
Ĺ	ENV POLYMOTERN	MINK CELL POLUS-FURNING MONTHE LEUKESTA VIAUS (1904ATELT)				Ì	İ		İ	<u>:</u> - 	Ī
	ENA POLYTROIE IN	ALV PRINCIPLE LEGISLANDS	***	Ī		+			1	1	
	ENV POLYTHOTEIN	CAS-BR-E MUNICE LEUNENIA VIAUS			Ì		İ		+	†	Ī
ADIA MENA	ENV POLYPROTEIN			Ì		1	T	t		\dagger	
PEN MENT	ENA POL TPROTEIN	PALEND PROGRES LEGICATION VIACOS (1904.A.) E 78.77)		Ī	\uparrow	1	1		\dagger	\dagger	Ī
TOW ME VIEW	ENV POLITICAL	PARKAD PROMINE LEGINERIA VINOS (130LA SE FYLATI)	95.01	Ī	1	Ť	1	t		\dagger	Ī
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	SAY POLYPROTEIN		Τ	42.50		T	T	t	t	t	Ī
PENY MACTIVE	ENV POLYPROTEDN		Т	262.589	Ī	İ	T		l		Ī
VOIN NOT	DIV POLYPROTED		Г			T					
HENV MISVED	ENV POLYTROTEIN										
PEN CHANS	ENV POLYPROTEDI		69-20	(((:9)	160-607				_		
PENV ENCTV	ENV POLYPROTEDI	IANUSCIERA MONT CELL FOCUS-INDUCING VIRUS	1								
PEN STVI	ENV POLYPROTEDI	SDGAN FOAMY VIRUS (TYPE 1)									
PEN STVIL	ENV POLYPROTEIN	SDGAN FOAMY VIRUS (TYPE 1/STRAIN LK1)	\$ 7		Ē	П					
PEN SIVA!	ENV POLYPROTEIN	SOCIAN DOCUMODES ICIENCY VIRUS (AGMISS ISOLATE)	269. 269.	╗	7	٦	27.734				
PEN SIVAG	DAV POLYPROTEIN		270-301	ī	_		101.130				
PEN SIVA	ENV POLYPROTEIN	SEGAN BARINGOEFICENCY VIRUS (ISOLATE AGM / CLONE GRJ-1)	=	П	3.00	614.708			1		
PEN SIVAT	ENV POLYPROTEDI	SOCIAN DOG/NODEFICENCY VIRUS (TYO-1 ISOLATE)	П	П	7						
PDIV SINCE	ENV POL YPROTEIN	CHING ANZEE DIGATHODEFICIENCY VIRUS	- Ge	ī	34.34	╗	24.5	1	1	1	Ī
PENV SIVCE	ENV POLYPROTECH	SPIGAN DARINGDEFICIENCY VIRUS (ISOLATE GBI)	-1	ī	╗	26.25	÷			1	
PDV SIVAI	ENV POLYPROTEIN	SINGAN DOMINODEFICIENCY VIRUS (NOVINE) ISOLATE)	Т	┪		1	1		+	1	
	ENV POLYPROTEDN	SDAAM DAADOOF/CENCY VIRUS (NDAY) ISOLATE)	Л	37.78			1		1	1	1
PEN SIVNOX	ENV POLYPROTEDI	SDOAN DOCUMORPICIENCY VIRUS (KOW ISOLATE)	337408]	1	1	1	1	1	1]

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П		VINUS	1	ī	107 077 177	601.318				1	
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		MILAN BEAUMODES KIENCE VIALUS (1722-1717) ATEL		25.25		İ	T	-		•]
200 EVE		INIAN BARMODERCENCY VINOS (FRANCE)	400-463	۱	1	T	t				إ
٦		SQUEARL MONIKEY RETROVIRUS (SAUKTIN)	409-411		+	İ	İ	-			
ξ		SPOAN RETROVING SAV-1	23-62	23.68	1	İ		-			ī
EN SAVI		ACMA LEVITYTHUS (STRAIN 1914)	1142	100.00	-	1	1	1	-	l	
VIV VIO	ENV POLYTHOIEM	WINNE LENTIVENUS (STRAIN) 1514/ CLONE LVI-16.31	Γ	182.609	-	1	1		1	T	
		ASSESS FORTIVE IS TRAIN (5) 4 / CLONE LVI-1852)	1				1	1	+	Ì	
		CONTROL VIELE /STEADIFF!)	Т	440.000	28.583				1	T	
	٦	TOTAL OF THE PREADNIKASZA)	Т	T					1	T	١
T		CHOCK FURNISH A CONCLUSION OF THE PROPERTY AND THE PROPER	٦		+	Ī			-	ا	
1		VACCINIA VILUS (SI ILAIN LOCALISA)		ī	1	Ī	Ī				,
٦	THE PROPERTY OF THE PROPERTY O	VACCINIA VIRUS (STRAIN WR.)	66-03	7	70.00		ĺ	-	<u>.</u>	 :	
	Γ	VACCINIA VIRUS (STIVAIN COPEMIAGEN)	Γ	134.210	101:101			İ	İ	Ī	
	T	VASIVA WILL	1						Ì	Ī	
Γ	CIONIS	CONTRACTOR CIBILS (STRAIN DUMAS)			-					1	
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I		INDIAN ADENOVICO I TRE SO	178-216								
		HISKAN ADENOVICUS TYPE 41	300-333					İ			
	4) 4 KD FIREA PROJECT	KI BAAN ADENOVITUS TYPE 2	134.381	146-173				1	t		
SERVE ADEOL	FUEL PROTEIN	SECTION AND AND AND ADDRESS OF THE PARTY OF		387.177					1	Ī	١
Ī	THER PROTECT	MUNICIPALITY AND AL							1		
Į	MATCH BEOTHER	HUMAN ALEMANTE	2								١
١		BOVING ADEMONIAUS TYPE 2	125.305	125-157							
1	DES PROFES	MOUSE ADENOVARUS TYPE I	138-169		j			İ			
SCREW ADEM!	FIBER PROTEIN	COMPANY OSTE OSARCOMA VIRUS	14.143					1	İ		
	V-FOSTOX TRANSFORMONG PROTEIN	THE PROPERTY AND P						1	1		
Ţ	PALVIDOS TRANSFORMANO PROTEIN	AVIAN REINOVINOS PROPINS									
I	THE VIEW TRANSPORMING PROTEIN	FBJ MUSIUM USI EUSTANIA	330-337								
١	Separate Management	A VIAM SPLEEN NECKONS VICTORIS AND AND WITHOUT	144-171								
١	GAUTOLICA	EOUNG DESCHOUS ANEMIA VIRUS (1900.01)	121-129								
POAG ELAVY	GAG FOLTFRUIE	HIMAN SPUNALE TROVIRUS	394-442	447.474							
ľ	GAG POLYPROTEUR	CINDON APELEUREADA VIRUS							T		
	GAG FOL YPROTEDY	INDIAN DEADMODE FILENCY VIAUS TYPE I (ARVDST 2 ISOLATE)									
	GAG FOLYPROTEIN	THE TANK AND THE PROPERTY OF THE 1 (BI) ISOLATE)							1		١
T	CAG POLYPROTEIN	HUMON THE STANSFILMENTY WALLE TYPE I (AM ISOLATE)									
Ī,	AAA BOL VPADTEDA	DUBLAND BOOK OF THE STATE BOOK ATE BOOK								1	
	A SA VIEW CONTROL	INDIAN PERSONAL PROPERTY COMES AND ATTEMPTS	2			1					
١	UAUTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	HOLAN BARDOOCI KURACT VIROS 117E 117E 117. 3	811.93								
١	GAG FOLYFRUITES	HEBLAN BOARNOOF HOTENCY VINUS TYPE & U.S.C.		L							
	GAG POLYMOIE LA	HADLAN BOADWOOD SCHOCKY VINUS TYTE 2 (BUCANE 21)	19.80	L							
	GAB FOL YPROTED			101.04	\$57.516						
POLO DRIA											
1		PACCES MINISTERIAL A.PABTETE	2		Ī						
	REFUNDAMINE LES ATED GAG FOL YPROTE		16-131								
	A COUNTY OF THE PARTY OF THE PA	MOUSE MANORARY TURNAR VICTOR (STRONG	84-116								
POAD MATTY	CAUTALITA	LICOUSE MANDINALY TURKOR VIRUS (STRAIR C.M.)	3	136-107							L
POAD MANTING	GAG FOL TYRU LEW	LOGICE MANDALARY TURIOR VIRUS (STRAIN OR)	333.346								L
POAG MATIVO	GAG POLYPROTEUM	PRINTAN LASON PIZER VIRUS (NOWY)		434.451							1
OAG LONGY	GAO POLYPROTEDA	TO THE PERMITTE VINIS L.A					L				1
A 6000	LAJOR COAT PROTED	SACCONE CANONING AND ATE AGM / CLONE GRU!)	2.42								
	CAST APPOSITED	SOCIAL BEALDINGS CONTRACTOR (CONTRACTOR ATE)	18-115					-			
TOAO MYA	STATE STATE OF THE PARTY AND ADDRESS OF THE PA	Spake Boardon R. Err. 1 vinos (no. 1 vinos)	11:32								L
AO SIMBA	GAUTE TRACTER	SDOAN DOCKNOSTICIENCY VIRUS (SIM ISOLATE)	11.11	L							<u> </u>
POAG SIVAS	GAG FOLTENIEN	SUCIAN DOMONOES ICIENCY VIRUS (F1965ARIA 1300-A 12)	1	L							ļ
POAD SIVE	GAG POLYPROTEDA	SECTAN BEACHOOFFICIENCY VIRUS (POMCI) ISOLATE)		-	-	L	Ц				1
POAG SIVSP	GAG POLYPROTEIN	CELTAN SARCOMA VINUS		-		L					ļ
POAD SMSAV	GAG POLYPROTED	Chan LE PROVIDUS SRV-1		121.348			 -				ļ
POAG SAVI	GAÖ POL YPROTEDA	ENTERS WELLS VINES TYPE I (STRAIN ABAP)					L				1
ANTI MENTIL	PROBABLE HELICASE	CANADA IN CANADA (STRAIN 11)				L	ļ	L			4
THE PARTY	PROBABLE HELICASE	THE STATE OF THE VALUE OF THE OWNERS	2	7	1						4
A 10 10 10 10 10 10 10 10 10 10 10 10 10			201-143					-			
2424	THE STREET OF THE STREET PRECURSOR	OR BOVER COLOMAVEUS IS HAM TO	206-343	_				-			L
HEMA CVII	٦	OF BOYPE CORORA YOUS (STIANS LT -!!!)	\$6.343	L							
PHENA CVELY	HEMACOLUTBOLES I EMARE THE SECOND	EXCENSIVE AND A VIBING (STRAIN) (STRAIN)									

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PORON	BOVDOR CORONAVIRUS (STRAIN QUEBEC)	П						<u> </u>
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5	DOT LEDGA A VIRUS (STRAIN AROUNEMEW MARKETHA)	F	M-221	161-151				
5		19-36	122.70	100.457				-
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PCCENE	2551044	VIRIS	36452								
TOTAL TOTAL	HENACO IN NON PRECURSOR	RELUENZA A VIEUS (STANIA MEQUINO IL MONTO IL MON	186-455								
MENA IANIE	HENACAT INTONIN PRECURSOR	DOLUENZA A VINUS (STEAM ACCOUNT OF 1721A VINA)	106-452							•	-
SIELLA IALEM	INTERIOR PRECINSOR	DOCUMENTA A VIEW (STEAM ALLANDAMANS)	196-111								
HIEVA IAIAP	INTRACOLUTION PRECURSOR	INCLUENCE A VICTOR OF THE VICT	20.58								
MELLA LAKIE	REMAGGIUTINEN PRECURSOR	DELUEYCA A VIANA (STRAMA AA FARACAAA) (1)	× 0.								
HEMA MEN	HEMACOLUTINEN PRECURSOR	DOLUMENCA A VINOS (STRAMILANDIASTRAKITANDANDI)	300								
HENT INNA	BELLAGGE UTDYDY PRECURSOR	INCLUENCE CONTRACTOR AND ANIAL LABOVASTRAKHANOGIAN	33.43								
SELVA IAMAB	HEMAGGLUTBON PRECURSOR	DOLUENZA A VIKUS (SIEVAN ANIALI ABDANTIV YORKABIAM)	387-453	1		1					
OVINT IVE	HIEMAGGLUTHAN PRECURSOR	INFLUENCE A VIRUS (STRAIN ASSESSMENT)	40.63				1				
MENT INTE	HEMAGGLUTININ PRECURSOR	INCLUENZA A VIXUS (STRAIN ANTENIALIZADA)	40-47	3							
THE PART OF THE PA	IGMAGGLUTININ PRECURSOR	INFLUENZA A VIZUS (STEAM AMERICANA)	14-31	3			1	1			L
1 March	HELLA COLUMNIA PRECURSOR	DELUENZA A VIRUS (STRAIN AMERICANS)	5:1	162-441				1			
HENA WAGE		INGILIENZA A VIRUS (STRAIN AMININO WELLENZA)	3				:	:	:		
PIESTA INDIA	HEMACKEL INCH PRECIBION	INGLIENZA A VINUS (STRAIN ANTMONA)	3								1
HEMA LANTE	IGMACKAU I IMIN FACTORSON	DATI LENZA A VIRUS (STRAIN APILOT WILALIZATA)		100							
HEMA LAPIL	BIEMAGGLUT ININ PRECUASOR	CATTERNS A WHITE PERADA APURATO RICOVINA	200								
HIGHER LAPUE	HEMAGGLUTININ PRECURSOR	INCLUENCE A VINCE (CLOAN AND VINO)	٦		1	1	1				
WITH IACO	HENLAGGLUTANN PRECURSOR	THE CAPACITY OF THE ART AND TOWNSTONE MILE SE YATHEST	ï						L		
Cievi Treis	HATTA COLUTION PRECUMSOR	DOLUBACA A VIACO (STRAINS AND ALACTACHUSETTS) (NA.)				1	+			_	L
200	HISTORY LITTORN PAECURSON	DELUENZA A VIRUS (SI INCHESTA MARCHATES) A LICTRAL (A.12)	20.55	160-187	200			-			L
1	INC. ACCES INTOINED PRECUASOR	DELLENZA A VICUS (SILLAIM ADMENANCE CONTACTOR (ACTION ACTI	115-166	384-443				1			Ļ
PIEMA IANG	TOS WILLIAMS SECTIONS	DELLENZA A VIRUS (STRAIN A/STAILING ST. TURING	3.5		_						
MEMA MSTA	TEMACCE CONTRACTOR CON	INTELEMENT A VIRUS (STRAIN ANTAIWANING)									1
PIEMA LATA	HEMACOLUTINA PIECUASON	PAGE 15 NZA A VIRUS (STRAIN AN URKEYARELAND/1717)					_				
PHEMA LATE	HEMACCIUTININ PLECUESUR	THE LIBERT A VIRING ASTRAIN ANDRIE VARIANES OF AND 1/10)						1			
HENA WITH	Г	ANTITEMENT A VIRILIS (STRAIN ATURKE YONTARIO 1711/44)		9						_	
ELLA LATRO	Г	STATE OF STATE AND AN URKEYON ANDWINES	X Y			-		-			_
MEMA LATRE		AND SENSE A VIETE ISTRAIN ANDRES YORE CONTIN				-	1	_			
GLA LATER	1	THE THE A CHAIN OF TAKE AND AND THE TAKES CONSINUMS	\$	2000	-	+					
MEMA LATEN	١.	THE COUNTY A COMPACT AND ANTERNATIONAL INCOMO. 13)	2-5			1	1		Ļ		
PREMA LATRA	JENACCI UTBON PRECURSOR	INTERPRETATION AND STRAIN AUDORNION?	8		1	1	-	L	L		
EMA IAUDO		ANTITEMP A VIETS (STEADY ANSSEADOT)	2					L	_		
EMA MUSS		PART TREATA A VIRIUS (\$18A DI AVIC TORUN) (1)			<u> </u>	1	-				
PHENA LAVIT	HENVOOR DADON PRECURSOR	THE LEAST A VIETS (STRAIN AND SON-SMITH)		1	-	+	-	_	L		
HEELA LAWIL	INDIANCE UTDAN PRECURSOR	THE THE A TANK ATTO AND	2		1	-		-	-		
HEM WAY	HENAGGLUTDEN PRECURSOR	CHIEFTA A VIBIN CITATA ASWINGEOUGHADOUNTS	9		1	1	-	-	_		
HETAL LAZCO	HEMAGGLUTENEN PARCURSON	THE LUCKEN A CASE OF THE ANALYSING ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED TO BE ASSESSED.	17		-	$\frac{1}{1}$	+				
MENTA LAZAD	HENAGOLUTOWN PRECURSOR	TO LOCKEY A CHAIR ASSESSMENT ON A SWINE A LONG KONG (13642)	331-43			-	1				L
HENLY LABID	HEMACALITHON PRECURSOR	LINE LUCK A NAME OF BANK ASWINGTON AND AND AND AND AND AND AND AND AND AN	418-478	Š		1	1	+	ļ	_	_
MENT INTER	HELLACCE UTDOM PRECURSOR	INCLUDES A STATE OF THE PARTY OF THE SECTION OF THE	417	\$06.540			1	+	-	-	L
HELLA LAND	INDIANGLUTINON PRECURSOR	DOLUMENTA A VINCE (STORT A A WANTANKEL) (MA)	387-451				-	+	-		L
ABS A LABOR	SEMAGE UTBON PRECIDISON	DELUCIA A VICE STATE AND AND INCLUSES	100-431	- 2 2	1	1	1	1	1	-	-
ACTUAL BORDER	HELLAGOLUTION PRECUISOR	INCLUDIO STRUCTURE AND	10041			1	+	+	-	L	L
HENT BOBO	Γ	THE COURT A VALUE OF THE ATM BEINGLAND 72.2/2)	¥.	Т		+	+	-	-	L	
PEDA PREM	Γ	LICELACIONE CONTRACTOR DATE DATE DATE DATE DATE DATE DATE DATE	39.418	╗		+	+			L	
PIESTA DESC	Ī	DATE DESCRIPTION OF THE PARTY O	207	\neg	1	+	1	1	-		_
HELLA DOLLE	Ī	THE CONTRACT OF THE PAINT AND	27-54	7		+	+		-	L	_
AFFAY DANAGE	۲	INTURKA B VICOS (SI PORT PROPERTY)	193-424			1	1	+	+	-	-
	۳	DOLLENCA B VILLS (STRAIN PRESENTATION)	196429	437.481		_	1	+	1	+	+
	٣	BOLLENZA B VILLS (STEAM BOLLENAS CO.)	47.86				-	1	+	-	+
	T	DOLLED ZA B VIRUS (STIAM BOUNDS CHEET	11-161	\$ T T T			-	1	1	1	
	T	Detucate a vaus (STIAM Bussings)	707-161	433-476	_			1	1	-	1
DENT PROM	T	DELUENCA & VEUS (STIAM EVYC.)	157 009	3.45	_	_		4	1	1	+
1	T	DOLUENZA B VBLUS (STRADN BIVICTORIA 2007)	165-767			L		-	-	+	$\frac{1}{1}$
MEN WEN	T	DOLLENZA C VIDUS (STRAIN O'CALIFOUNIA)	41.559			_		4	-	1	+
100 A	Ť	DATLIENZA C VIDUS (STRAIN CENCLANDISTURE)	41.339		<u> </u>		H	-	+	+	+
A VICE	T	BUT LENZA C VRUS (STLAIN COREA) LALENTING	401.131		L	L			1	+	+
TO YOU	1	DELLEGIZA C VRUS (STRAIN CAMOGORIA)			-	F		_		_	-
						-			l		

	107,17814	AR Virusa (no bocteriophoges)			12.00	ARTA	ANEAS	AREA 6 ARE	AREA? AREA!	\Box	AREAL
FILE HAME	PROTEIN	YARUS	Т	4		_	Т			Г	
Τ	HEMAGGLUTININ PRECURSOR	INFLUENZA C VIRUS (STRAIN CX YOTOMINI)						-			
PARMA BECM	HEMACGLUT DADY PRECURSOR	INGLUENZA C VIRUS (STRAIN CALISSISSIPPUSO)					T			-	Ī
T	WEALANGE UT DAIN PRECITESOR	INGLUENCA C YOU'S (STRAIN CANARATI)	25.23				t		T		T
T	HELY COLL INTERNA PRECIMENT	DELLENZA C VIDUS (STRAIN CALGELIING/10/11)	63.53				1	+	1	ł	Į
Ī	INMAGES LITIDEN PRECUMBOR	DELLENZA C VIXIIS (STRADI CAICDEIIING/115/11)	66.536				İ		<u> </u>	1	
Ī	HEMACKE LITISAN PRECURSOR	DWILLENZA C VIRUS (STRAIN CPICOEUMCA19412)	\$				1	T	<u> </u>	T	į,
T	HE MACCALITIDAN PRECURSOR	BELLENZA C VIRUS (STRAIN C/TAYLOW/17)1/41)	63 - 53				İ			t	1
PHEMA DACYA	HEMACOL LITIDIDA PRECUMSOR	INFLUENZA C VIRUS (STRAIN CYANIAGATA/1041)	2				İ	<u> </u>	<u> </u>	1	
NACH VINE	HEMACKS IN THIN ME IN AMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA))	16.3						1	\dagger	Ī
	HEMACACH ITT DAMANE INCAMINADASE	INEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	3						+	+	Ī
The state of	HEMACATA LITERALIZE LITERALIZADA SE	INEWCASTLE DESEASE VIRUS (STRAIN DISCUS)	<u> </u>					1	+	\dagger	Ī
The strain	AFWACCT INTRADUCTOR IN AMOUNTASE	NEWCASTLE DISEASE VIRUS (STRAIN BI-MITCINERAT)	2					1	<u> </u>	<u> </u>	1
	INTACATOR IN DOMESTIC ANDREDACE	INEWCASTI E DISEASE VIRUS (STRAIN ITALIENAS)	64.91						<u> </u> 	:	
THE PERSON NAMED IN	THE STATE OF THE PARTY OF THE P	NEWCASTLE DISEASE VIRUS (STRAD) MIYADERANI)	16-19					1	1	1	
THE MAY POWE	TELEVISION INTERPREDICTION OF THE PARTIT	THE WEATH E DISEASE VIETS (STRAM) CUPENSLANDS	16-53						1	+	Ī
	MENA COLUMNIA METRA AMBRIDA CO	INFWEATH REPARENTE VIRUS (STRAIN TEXAS G B /48)	16-19					+		1	
	THE PARTY OF THE P	INTERCASTLE DISEASE VIRUS (STRAIN OF STERVA)	16.79						+	\dagger	
AND VOICE	TENANCE OF THE PROPERTY OF THE PARTY OF THE	PHYCOG DISTRAPER VIRUS	39-66	44-73					<u> </u> 	1	
MENA PRODV	I DATE OF THE WAY WE IN A LANGE OF	INTERNATIONAL LENZA I VIRUS (STRAIN WASHINGTOWINST)	¥-110	144-393				-	<u> </u>	<u> </u>	
MENA VIINW		BANKE BABANS IRMA I VIRIS	(6-33						-	1	
PIGENTA PUB	IEMANCALUI IMINIMEDIA MARINIDA SE	CHAINE DAS AND LIEUZA I VIBILE (STEAIN NIH 47885)	37-41							+	
PIEMA PUM		HANDER STRAINS THEN A STRAIN AUSTRAIN	27-61							1	
MEA TOTA	I EMAGGLUI PUN PEUIAMINASE	THE PARTY OF THE PERTY A 1 VIBILATED IN THE VISASSINGS	37-75							1	
PIEMA PISHT	HEMACCLUT BOW-NEUTAMINDANE	TOTAL STREET STREET A CORP. OF THE STREET, STR	11.70			L					
MENT MINE	HEMACCUTINGN-NEURAMINIDASE	HUNCAN FACTOR LIGHT A VIOLET FOR THE VIOLET AND THE	37.4								
PIEMA PUHY	HEMAGGLUT DIDY-NEUTAMINIDASE	INDIANA CALANTA LACACA A USAGA GENALIA MACINALIZED	37.4								
PIEMA PIJIW	HEMADOLUT DON-NEUTAMBRIDASE	HUNGAN FACTOR LUCATA A UNIO (SECONDA MARINELLO)	37.41								
NEMA PUHX	HEMA GOLUT DVDN. NEURAARNIDASE	HUMAN PAKUN LUCKA A VINCE SERVIN MASINEES	116.2114	336.213				_			
HEMA MACH	HEMAGGELTINON PRECURSOR	CALLOLING TO VIEWS	79.106								
PENA SEROS	HEMAGGLUT BYDY VE UNAMINUA'SE	PENDANT CARLO (STROME AND STROME)	79.10								
PIEMA SENDE	HEMAGGLUT DON-HEUTANDANE	SECOND VIEWS (STRAIN POSTER)	20-16								
HEAT SECTI	IEMARCE DI MIN-MEURAMINIDASE	SECURAL UPING ACTA AND INCOME.	7.18								
MEMA SENOI	DEMACKALUI MIN-TEURANIMANA	GENDAL VIEWS (STRADA Z)	20.5								
PIEMA SENDE	SEMAGELUI PRINCIPE IN COMPANIA SE	CINAL VIBILE AL	11:53	194-421		L					
MEDA SV4	TEMACRED I DUM TREUM TREUM	VACABLIA URI IS ISTRADA COPENDIAGENO	115-146	175-202	216-243						
MENA VACE	HEMACAL CITY THE CORPORATION	VACCOBA VILLIS (STRAD) B.D.D.	201-461	113.302	216-243						
MENT WAS	LICENTAL CONTINUES PRECINATION	VACCIDED VILLS (STRAIN TIAN TAN)	119-146	119.202	216.243					1	
PIENA VACCV	HISTAGE LITTER PRECURSOR	VACCOULA VOLUS (STRAIN WR)	371-60	175-202	22.52				+	†	T
PIEMA VARV	HEMACCAUTININ PRECUISOR	VALIOLA VIDUS			2			1	\dagger	†	Ī
PIEXO ADEOL	HEXON-ASSOCIATED PROTEIN	HUMAN ADENOVIALIS TYPE 2	Š						+	\dagger	Ī
PHEX9 ADEOS	HEXON-ASSOCIATED PROTEIN	INDIAN ADENOVIRUS TYPE S	8					1	\dagger	\dagger	T
MEXO ADEO?	INCOM-ASSOCIATED PROTEIN	HIDAM ADENOVIALS TYPES 1 and 7	97.127					+	+	\dagger	
HEX ADEOS	HEXON PROTEON	HENGAN ADENOVICUS TYPE 2		2	8			1	+	\dagger	T
MEX ADEOS	HEXON PROTEDA	HEDAAN ADENOVEUS TYPE 5							\dagger	\dagger	Ī
MEX ADE40	HEXON PROTEIN	HUMAN ADENOVORUS TYPE 40							╁	l	Ī
PIEX ADERS	HEXON PROTEDY	-							+	t	
NEUS CONTX	IEMOKRHAGE-DYDUCDYG 18 KD PROTEDY	-	20.00					1	+	t	Ī
PICE COWPX	HOST RANGE PROTEDY	COWPOX YOU'S	A					+	+		Ī
FIN ASTRI	LATE PROTEIN 1194L	AFRICAN SWORE FEVER VIXUS (STRAIN BATIV)	7						+	ł	T
PULTS ASPB)	LATE PROTEIN 12268.	AFIRCAN SWING FEVER VILLE (STILLIN BATTY)						-		\dagger	
PONO CANVA	INCLUSION BODY MATRIX PROTEIN	CAULDIOWER MOSAIC VIRUS (STILAUM DA)							\dagger	\mid	T
ABIN COLVE	DICLUSION BODY MATRUX PROTEDA	CAULDIOWER MOTAIC VOIUS (STILAIN DW)						1	1	\dagger	Ī
PER CUM	DACLUSION BODY MATRIX PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN PVIAT)	200					+	$\frac{1}{1}$	\dagger	Ī
PERSON CERV	DACLUSION BODY MATRIX PROTEIN	CALMATION ETCHED RING VULUS	100					\mid	+	t	Ī
PONC FAND	INCLUSION BODY MATTLY PROTEIN	FIGWORT MOSALC VICUS (STRAIN DAS)		111.14					-	l	
VOICE SOCIAL	DICTUSION BODY MATRIX PROTEIN	SOURCE CHANGE IN MOTITED VINOS	711.7						\mid		Γ
PICIO HCNVA	PROB PROC & TRANSPORT PRO ULS	HUMAN CT UMBUNEVINOS (2000) TETTT									

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	7	All Virgos (se becortophige)	AREA! A	AREA J	2 4 2 1 V	4864	TO TO	4	9	ī	:
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PUEAS HAVII			29.00	j							
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	HTTO THE LAND TO SELLEN THE PARTY OF THE PAR	MELLAN POTONIS CAL DITALES (STRATIN AD169)		Ì							
PIRES HOLIVA			•	-		!	!	•	:		
Ī		ADAMI CYTOMETONICO ISSUE	97-120	_					!		
AND HEAVY	TENDER			!							
PKFES PSVOA	3		116-22								
2000	3		127.343								1
KICK PAVOR	ě	REI THE BALCOMA VIRUS (STRAIN NICDONOUCID	Ť						į		
LINE ISNO	į		22.5								
Lead Sales	TVENCEDE KOLASE TRANSF PROTEDUTES		***				1				
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ICHIE ALEN		A STATE OF THE A PART A PART OF THE			-			:			
Times de la constante	HANNERS KONAUL		140.384				:	•	i	•	•
TIM CO.	87:32	İ			!						į
ALTER MOVIN	THYNCOON KUNAN	CLIENT STRAIN THURSE COLD	36.36							1	
The second second	TAVALIED MEN K DIA SE	DE ECHOUS LANDON CONTRACTOR	15.18								
Alin Civi		ATALIBID KEAPES VIAUS 1									
HEND HEND	CENE 14 PROTEIN RIPASE	Control of the American Action (Control of C									
TARE UNITED	THE PROTECTION ROLLS WOLLD CO.	VACUUMA VIMOS ISTEMITY CONTRACTOR	191-101								
- Aug.	THE REPORT OF THE PARKET WAS AND THE	VACCORA VIDUS (STRAIN WIL)									
YEAR! YACKY	10 KD TRUICLY RICHARD INCHES	CARTAN WEIN COTTANN COPENIAGEN		Ī							
WEST VALLE	POSTUDIE PROTECT KINASE BIZ	VACLUM VIII I	27.72								
	CONTRACT BANKER PRIATE BILL	VACCODA VINUS (STILADY WA)						4			
ALLES VACEV	POSSELL PRUIEM ALVANA	MANAGEMENT TO BE A TO CONTINUE TO BE A STATE OF THE ACT						L			
WART VACOR	POSSIBLE PROTEDS KINASE F10	William was in the second of t	2.5								i
	CASCINE & BEAVERS IN TRACE \$ 10	YARIOLA VIRUS									İ
KED! VAIV	POSSIBLE PROTEIN ALMANDE	AND AND DESCRIPTION OF STRAIN OF STR									
PERCE AVISU	ROS TYROSDIE KINASE TILANSI PROTEIN	A VIAN SALVENIA BATINA	3-49								
	THE PRINTER THANKS PROTEIN RYK	AVIAN RETROVINUS INLIN	100.333								
PERVE AVEC	TROSER ROME TO THE PROPERTY OF C	AMAN SARCOMA VIRUS (STRAIN Y?))						L	-		
PEVEL AVISY	TYROSDA KDASE TRANSF PROTEIN TES	AVIAN SOUTH STATE OF THE STATE									
1	A THE LIES IND PROTEDI	MAKAN ADENOVIKUS 117E J	384-413								
T. I've Anders	TES AND SEATON	HIGAN ADENOVIRUS TYPE 3					_				
PLICE ADEM	LATE 100 AD TRUIT	MANAN AMPROVIEUS TYPE 40		Ī			1		L		
H 100 ADEAD	LATE 100 KD PROTEIN	A PROPERTY OF THE ASSESSMENT ASSESSMENT OF THE A	Ē								
100	A THE 100 KID PROTEDN	HOACA ALEXA VIACO	146-175	ı							
	1. A DECAY LAKAMBA AND PROTEON I	EPSTEIN-BALL VIRUS (STRAIN BYSS)					_				İ
V	CALCAL PERSONAL PROPERTY	FERTHEN BALL VICUS (STRAIN CAO)									
ALC: EBYC	LATENT MEMORIANE PROJECT	PERFECT BARB MALLE ACTUALITY BASIS	1								
MAGI BAVA	LATENT MENDIANAE PROTEIN I		- III								
		=	٢	289-316	163.534	612.4%					
	THE PARTY OF THE P		Ţ		410.411						
5	MINA CAMPA LAK I'M. LANCE 1000		٦								
MATER VACOL	LONA CAPPIO DOTTOR, LALUE SUBUR			291-318	630-631						
L	KIND PAPPORT DIE YNG. LAKER SUBUNI	_		291-318	630-633						
-1	THE PROPERTY OF LANCE SIGNATURE	-	T					L			
	MOUNT CATTURE LANGE IN THE STATE OF THE STAT	-	111								L
1937	LANA CAPPIO DATAG	AMAN STATES TO STATES ON STRAIN WILLIAM	1170-193								
ı.	SOURCE OF THE OWNERS OF THE OW	CUCLAMER GREEN MOTITE MOSAM, VINUS (WATER COLLEGE AND THE PARTY AND THE MOSAM, VINUS (WATER COLLEGE AND THE PARTY									
PACOVI CANO		THE RAMES CREEN MOTHE MOSAIC VIRUS (WATERMELLOW STRAIN SHIP							Ļ	_	
PLADOVP CCACVW	-	THE PERSON STREET STREET STREET	ŝ							L	
75 AL AL AL	f	DOOM IOACUS AND	96-10		_						
	TANKS AND DECITEDA	TOWATO MOSALC VIRIAL LINA					_	_			
PACON ICHAM		TOUGHT MOSAIC VIDUS (STRAIN LII)				ļ	L		-		
PAROVE TOWN	MOVEMENT PROJECT	A. 72 M. 67 A. 184 B. 1	143-176	47.47					-		L
MALC: OWN	MODERCATION METHYLASE CVIDS	COCCEPTATION AND THE COLUMN CO	16-31	130.173							
	TANAMA THOS LOCTION ASE CYIAL	PALAMECTUM BUXXANA LIMEDIELA VIACO	775 555	136.403		_	_	_			
DIAM DIAM		A VIAN INTELOCYTOMATOSIS VIRUS CHILI				-	ļ		L		_
MAYE AVBA	MYC TILANS GILDERIC TICULES	THE PROPERTY OF PARTY WALLS INCOME.	207:267	376-403					-		L
PACY C AVEAC	LANC TRANSFORMEND PROTEIN	A VAC PUT LANGE COMPANY AND A VACABLE AND A	1315.363	116-403							1
	LANCE TO AMERICA MONDA PROTECT	AVIAN INTELOCYTOMATONIS VIAUS PIDI	930 346	131.404		L					
TATE AVE	Carlotte Carlotte	AVIAN RETROVIRUS MODEZ!					-	_	L		
PAC AVER	MYC INAMA COMPANIA	STATE OF IS	227-281	10.13			-		-		L
PLAY AVIOR	MYC TRANSFORMOND PROTEIN	AVIANTE	393-420						\downarrow		
A LANGE	MYC TRANSFORMOND PROTEIN	FELDE LEGALMAN VINOS	2776								
	LANCE TO A MASS CORNOR OF PROTECTS	FELDS LEUKEARA PROVINCE FT	3	31.05		L		_			
	The same and the s	BERNEL VIDUS						L	L		
3	NOTICE STATE OF THE PARTY OF TH	PLINYAVBUS LA CROSSE	-						L		_
TICS PAGE		Taxable Avenue and the Court of Labor.	2								L
PACAB MARK	Г		46-15	169-330			-				
VALUE OF STREET	MICHECAPSID PROTEIN	BUNYAKWEKA VIRUS					1				
THE PLANT	7										

PCGDE	10721784	uses [as besterlephages]		7 1 7 1 1 7	AREAL	AREA AR	AREA! AREA!	ABEAL	SHEAF	48.64.2
FILEHAME	PROTEIN		Т			7		г	_	
PHCAP COSTV	MUCLEOCAPSID PROTEDY	11	1			<u> </u> 				
MICAP COVO	MUCL EOCAPSID PROTEIN	ND: KS IET COK I J		Ī		<u> </u> 		L		
PHCAP CHAV	MUCLEOCAPSID PROTEIN	CHANDIPULA VIRUS (STRAIN 1033)14)	101	Ì						
PNCAP CVCAE	MUCL EOCAPSID PROTEIN	CANDE ENTERIOR CONCHANTACION (STANIA)		Ī	<u> </u>	<u> </u>				<u>.</u>
PNCAP CVPPU	MUCL EOCAPSID PROTEIN	PORCEON INCREMENTATION OF THE REPORT OF THE PROPERTY OF THE PR		Ī						
PICA CVE	MUCL EOCAPSID PROTEIN	TOTAL PROPERTY OF CONCAVING AND	101.337							٦
	MUCLEUCAPSID PROFEIN	MINE COLUMN	235.263	Ī						
	National Property	FEET DOE INTECTIOUS PERITONITIS VIAUS (STRAIN 79-1144)	13.709					1		
178 771	MAIN BOCAPED PROTEIN	HAZARA VIRUS (1SOLATE IC189)	£13				1			Ī
IN STATE	MAIN ENCANTION PROTEIN	IAL VIRUS (SUBGROUP B / STRAIN 18537)	€1 1	74.100	=======================================					
PACAS INCVA	MILLI FOCAPSID PROTEIN						1			
27.1	MAICH EOCAPSID PROTEDI	(LASSA VIRIUS (STRADI GAUSI)		27.	1	1				
111111111111111111111111111111111111111	MAKE EDCAPSID PROTEIN	LASSA VIRUS (STRADH IOSIAM)		Ž.	1	1		$\frac{1}{1}$!
PHCAL LYCVA	INDCLEOCAPSID PROTEIN	LYAPHOCYTIC CHORUCHENINGITIS VIRUS (STRAIN ARAISTRONG)	٦			1				
PHCAP MAGV	MUCLEOCAPSID PROTEIN	ALACTIAN VIRUS	7	63:216		1	+	 -		Ī
PHCAP MOPE!	MUCLEOCAPSID PROTEIN	MOPELA VIRUS				+				
PHCAP PEINC	MUCLEOCAPS DIROTEIN	HIBAAN PARADGELENZA I VIRUS (STRAIN C)9)	Т			1	 	-		
THE WILLY	NUCLEOCAPSID PROTEIN	HENCH PARADELLENZA I VIRUS (STRAIN WASHINGTON/1937)	Т		\dagger	$\frac{1}{1}$				
THESE PURE	MUCLEOCAPSED PROTEIN	HUMAN PARAING LUENZA 3 VIRUS (STRAIN NIN 1978)S	Î Î		1	<u> </u>	<u> </u>	-		
THE PIP	NUCLEOCAPSID PROTEIN	PUNTA TORO PREEDOVIRUS	R	Ì		+	<u> </u>	+		
PHICA PURE	MUCLEOCAPSID PROTEIN	PURDALA VIRUS (STRAIN HALLINAS DI)			1	$\frac{1}{1}$				
PHCAP PUUMS	NUCLEOCAPSID PROTEIN	PUTDAALA VIRUS (STRAIN SOTKANIO)	4.47	Ì		+				
PICE IVE	NUCLEOCAPSID PROTEIN	PNEUMONIA VIRUS OF MICE			†	-		-		
PHCAP BABVA	NUCL ECCAPSIO PROTEIN	RABUES VIRUS (STRADY AVOI)		Ì		+		+		
PHCAD BABVE	NUCL EOCAPSID PROTEIN	RABLES VIBUS (STRAIN PV)		Ì	1	<u> </u>	<u> </u>			ĺ
PHCAP EABVS	MUCLEOCAPSID PROTEIN	RABIES VIRUS (STRAM SAD BI9)			1	1	<u> </u> 	<u> </u>		
PHCAL SENS	MUCL EGGAPSID PROTEIN	SENDAL VIRUS (STRAIN Z / HOST MUTANTS)				+	<u> </u>			
PHCAL SENDE	MACLEOCAPSID PROTEIN	SEMBAI VILLAIR ENDEAS)	141.404	Ì		ł				
PHCAP SENDZ	MUCL FOCAPSID PROTEIN	SEROAL VIEWS (STRAIN VIEWS	-	Ī	1					
32	RUCEUCATS PROTEIN	SAME IN THE SECOND STATE OF THE SECOND STATE O	50.534	Ī						
WC2 5V	NOTION SIDE MOTERN	TACABLE CHIR	20.23			_				
PRCA TACY	NUCLEUCATION PROJECT	POCCANA VIOLE	13							
35	MACLE CONTROL OF THE PROPERTY OF THE PERTY O	I STATE OF THE STA	46.162	Ī						
	MULTIPOLITIES OF PROPERTY	VILLE TOWNSHAGE SEPTICEMIA VIRUS (STRAIN 07.71)	314.314							
CANADA STATE	NAMES OF A PROPERTY	VIRAL HEMORIPHACIC SEPTICEMIA VIRUS (STRAIN MAKAM)	105-176	284-314						
PACAS VEVAG	NUCLEOCAPSID PROTEDY	VESICUEAR STONATITIS VIRUS (SEROTYPE INDIANA / STRAIN GLASCOW						-		
PHCAD VSVIO	NUCL EOCAPSID PROTEDY	VESICIEAR STONATITIS VINUS (SEROTYPE NEW JERSEY / STRAIN OCIDEN		2	1	1	1	-		
PHCAP VSVS	NUCLEOCAPSED PROTEIN	VESICULAR STORATITIS VIDUS (STRAIN SAN TUAN)		Ī	Ì	+	1	-		
THEFT HYIEL	NEGATIVE FACTOR	HONGAN BOACHOOFFICENCY VIRUS 177E I (ELITISOLATE)		Ì	+		1	-		
PLET HYIND	NEGATIVE FACTOR	HAMAN BOARNOOF ICENCY VINUS 177B I (MUK ISOLATE)				1	+	+		
PHEF HY1ZA	NEOA TIVE FACTOR	HUMAN DANGMONT FUENCY VINOS 1172 (LAME V 1354.4)		Ī				-		
TANK TANK	NEUM IVE FALTOR	MATISTICA A VIRUS (STRAIN AREACK DUCKAUSTRALIA/102/11)	43.81			-				
TANK TANK	NETH ALMORDA SE	DOLUMETA A VIRUS (STRAIN ACAMELMONGOLIANS	7							
PARAM IAGIS	NEURANDASE	DOLLEDZA A VIKUS (STIADA ACHILE/1/1))	1791	-						
PARAM MADAI	NEIDANDODASE	DELLENZA A VIRUS (STRAIN ADUCK/ALBERTA/1974)	<u></u>							
PRICE INDGE	NEURALEMEDASE	DELUBICA A VIIUS (STRAIN ADUCKIGERMANY/49)	7	1		+		+		
PHILAM LATTW	NEURANDADASE	INGI (IENZA A VINUS (STRAIN AFOWL PLAGUE VIRUS/WEYBRUDGE)	Į	T	27.75	\dagger	$\frac{1}{1}$			Ī
PRICE LANCO	NEURALDMEDASE	INFLUDICA A VILUS (STRAIM ALQUIMEA UNIVER)			764.400	\dagger		+		Ī
PHONE LANK!	NECTAL ENGINESS	INTLUDICA A VINUS (STRAIN ARQUINDAR FOLLA VIVE)		T	3	+		+		
PRAM WKIE	MELIEANDASE	INCLUDAÇÃA A VICIOS (STIAZATIA ANE MINICIPARIA)	,	Ì	Ì	+	<u> </u>			
MANN INEN	NEURANDASE	DOLUBERA A VINCE IS INCLINED AND AND INCLINED AND AND AND AND AND AND AND AND AND AN		9	Ť	+	+	-		
PRINAM WAGE	VEURANDASE	INCLUSION A VIDER (STRAIN APAROTAL STEW))	3	= 2	T					
TOWN WAS	Necessary and American	INSTITUTOR A VIRUS (STEATH A/PUERTO FUCORDA)	Ī							
That were	INC DINOMETER COLOR									

		ERSEYMONIS	3					-		
		۱		İ	Ī		•			-
		Г	28.6	Ì			T	+	_	
		DOLLERCA A VINUS (STRAIN AT ENCADO)	19.00					+	<u> </u>	
		RELUENZA A VINUS (STILATIN ANDSSENTE)	19.68				T	1	<u> </u>	
		DOLLENZA VIALS (STACITY AND CONCRITIVE)	16.0					-		
		DELLENZA A VIEWS (STRAIN A PERSON	53					-		
		DOLUGACA B VIACO (SINCE)	33, 310							
Ш	PRO PRECUMSOR	BOLD TA DEMOCRAÇÃO VALIA	\$ 2					-		
П		BOADYX DENGRACLE COR VINCE (CTRAIN NL -07)	اء	ŀ					<u> </u> -	_
1	ACOL STRUCTURAL PROTEIN	DOATION PECHOLIC STOLENGY AND LONG ATE (PRILIAIR AL)	i	- F	1		. ::	<u>:</u> :		1
Ī	AND CTRICTIONAL PROTEIN	IONATO SPOTTED WILL VIAUS (INAV. II. II. II. II. II. III. III. III. I	133	į					<u> </u>	<u> </u>
Ī	COST CHARLEST IN PROTEIN	TOMATO SPOTTED WILL VIRUS (STRAIN C.)	\$ 0.0					Ì	1	<u> </u>
1	TOTAL PROPERTY OF THE PARTY OF	ANSACTA MOGREI ENTONICHOXVIRUS	3	10.00	326-551				1	H
	MUCLEUSIUS (MUTICIONIS) A CE I	CHORISTONEURA BIENAIS ENTORIOPOXVIRUS	٣	394.42	15.5				1	+
HITPI CHEPY K	AICLEOSIDE TRIPMOSTIALASE	CAPTERIA VIBILIS ISTRAIN COPENIAGEN)	T	197	115.513					1
Γ	MUCLEOSIDE TRUMOSPHAIASE	CAPTINIA VIRILE ISTRAIN WR.)	Ţ.		446.401					1
Ī	MUCLEOSIDE TRIPMOSPILATASE	The second secon	Ţ			110.012				-
Ī	MIXI EOSIDE TRUMIOSMIATASE I	VALUE AND	8	1						
	MAINE ANTIGERIC STRUCTL PROFEIN	PEUPES SUPPLEA VINCE STATES OF ANY	11111							<u> </u>
T	SAN BOAT CATALYTIC SUBUNIT	VACCINA VIRUS (STRAIN CUPENIACEN)	86-113							<u> </u>
T	TO PATE VIEW CONTROL	VACCINIA VIRUS (STRAIN WR)	511							
	THE PART OF THE PRINCIPLE	VARIOLA VIRUS	118-165							1
	POLY(A) POL CA I AL TITAL	CAPRIDOXYDUS (STRAIN KS-1)	77 11							+
PPADI CAPYK	OLY(A) FOL REG SUBURIL	Sour Box VIIII					L		_	1
Ī	FOCY(A) FOL REG SUBLINGT	ALTOCA ABILA CALIFORNICA NUCLEAR POLYIE DROSIS VIRUS	6							-
74/67	13 1 KD PROTEIN IN PE STECTON	AUTOMORITO CALLE AND TICABLID POR MIEDROSIS VIRUS	61-93			1				
T	11 5 KD PROTEDI IN P26 STREGION	ORCYTA PERMUISMENT MICE TAN POLYTIFOROSIS VINUS	204.348							
T		AUTOGRAPHA CALIFORNIA NICE EAR POR VIIEDROSIS VIRUS	6 .3	=			1		-	-
200	AS TO IN PERSON INTERCENTOR REGION	AUTOCRAPHA CALIPURARA POCLESA FOC			_		1			-
T	PENTON PROTEIN	AVIAN ABENOVEUS GALIGIS INCHA SAST	2	1775-1807	36.36			1		\mid
1	CALCALATE IN VINCOITE IN	BALLEY YELLOW MOSAIC VIRUS (CEMENTAL SOCIAL)	1374-1801	1134-1261						l
TOL BATH	CONCRETE CONTROL I	BAALEY YELLOW MOSALC VIRUS (IAPANESE SURVIN III.II		1909-1941					1	1
7	CENCHE POLITICAL	HUNDALIAN GRAPEVING CHRONE MOSAIC VINUS	Т	616-677	938-883	1161-1195	5		1	+
٦	MAI FOLITAGE IN	GRAPEVINE FAMEAF VINUS	15		L	_				+
	ENA! POLYPRUIEUM	TOWATO BLACK RING VIRUS (STRAIN S)		841.838		L	L			1
	RHAI POLYPROTEDA	BARE BY YELLOW MOSAIC VIRUS (CERUMAN ISOLATE)				-				1
PPOL 1 BAYING	CENCIPE POLYPROTEIN I	STATES TOWN LANGAL VIELDS (I APANESE STRAIN (I-1)	2007							
TANKS S	CENOMIC POLYPROTEIN 2	BALLET TELLOW MONEY CONTRACTOR VIRUS	11-38			-	1			-
22.50	RNAS POLYMOTEDA	HUNGALLAN GRATEVING	25-576							-
	SUAN BON VOROTEDA	CAAPEVDE FANCEA VICUS	943-1009		_					\mid
215	The Sales of the S	TOWATO IDMOSPOT VINUS (ISOLATE MASTREMAT)	7	1030-1057		12			-	+
PPOLJ TASYA	WALLES CO. CO. CO. CO.	BOVINE EXTEROVINUS (STRAIN VG-5-23)	670.46		3 1301 1310	1022-0101	14 2476-2503	12609-2636	3613-3642	+
PPOLO BOVEV	GENOME FOLLTROSEE	INVINE VIRAL DIABILIEA VIRUS (ISOLATE NADL)				16 2102-28	351.155		-	+
PPOLD BYDYN	GENORGE POLYPROTECH	PONTAL MARRIES VINUS (STRAIN SD-1)	100		-					_
PROLIGIBITIONS	CENDAL FOLYPROTEIN	TOTAL LOCATION VIBILS	2			301	1			
VANA O 10mm	GENOVAL FOL YPROTEON	SECOND CONTRACTOR AND CORP.	:		2				-	-
STANK VICE	GENOLO POLYPROTEDI	CONSTITUTE OF STATE O	1040-1076				-	1		-
WAY WAY	CENOLEI FOL YPROTEDI	COXSACREVADO	645-473	141.04	1021-1037					
10000	CENTRAL VPROTED	COXSACKEYBUS BI	1034-1040	101-100					1	\dagger
	PENCHAL BON VORDITEDA	COXSACKLE VIDIUS B1	44441		-	_				+
100000	CANCEL CALLED THE	COXSACKE VIDIUS BA	1010.1040	_		-				1
11010 COXIA	CENOME POLITICAL	CONTACKIE VIEWS BS			1					1
Froto coors	GENOME FOR THEOREM	CLOVER YELLOW VERN VIRUS		21 02 000	1000 101					
POLO CYW	CENCRE POLYPROTEDI	DELICATE CARINE TYPE 1 (STRAIN SINGAPORE \$115/40)	2		-	100	113.114			
PHOLD DENIS	CENONA POLYPROTEDI	DEVICE A LIMIT TYPE 3 (CTAIN 1641)	1304-1571		_	_	_	A		
170L0 DEATS	GENOME FOLYPROTEIN	CELESTIC CASTA TYPE 5 (CTRADY 1841 PDK)1)	2		_	-		-		
FOLO DENS!	GENERAL PAROTER	DEFICIE CARLIE TYPE 1/4 TAXIAICA)	1544-1571		-		_	2 1141.1170		H
Non Pro-	GENOME FOLYPROTEIN	DENGUE VINUS I TTE STRUKEN TO THE STRUKEN THE STRUKEN TO THE STRUKEN THE	1844-1931	1830-1885	1 2005-2012	11 107.301	_	-		+
200	CENOME FOR VPROTEDY	DENCIAL VOIUS TYPE 3 13 HAND THE STATE OF TH	1134-1161	1448-14	7.5				1	+
	COUNTY FOR VPROTEDA	DESCRIPTION OF STRAIN TOPICA 1971	134.00	1502-1560		1657-1684 3494-3531	331 7960-3014	14 1345-1372		†
Maro Devis	CHICAGO VEROTEDI	DENOIS VILLS TYPE 3	265.7930	1101-1101	11 1141-1160	100				†
MOTO DO	CONCESS TO STATE OF THE PARTY O	INDIVIDUATIVE A	20.116		-					1
POLO DES	CDOOR FOLTMUTEUM	PETUNYALIK II STEATH GALCORY)			1					

		Att Vicence (no begin families)		l		-	-	L	-	_	
T.C.C.T.	20/11/010	Value of the second of the sec	AREAL		AREAL	AREA4 A	AREA 5 A	AREA 6 AREA 7	A1 AREAR	P ARCAS	4
2000	CENTRAL POLICE IN	ENCEPHALOMYOCARDITIS VIRUS	Ī	į	1322-1343						
EN-241	CENTAGE POR VEROTERA	INVESTIGATION YOCARDITIS VIRUS (STRAIN ENC. B NONDIABET OCENIC)	20.00	486-1570	1334-1565					_	
	CENTRAL PARTIES	ENCENNATION/YOCARDITIS VIRUS (STRADN ENC.D DIABETOCENIC)	Ī		1534-1565			L		L	
THE PARTY	Church for Who ten	AND SACTORIAL DAINOCARDITIS VIRUS (STRAIN 17A)	70-168			-					١.
CONTRACTOR OF THE PERSON	CENTRAL POLITICAL	AGENCIA ENCEPHAL DALYDCAADITIS VIRUS	-								,
Prot o Provi	CENCRE POLYPROTEIN	FLOT. AND MOUTH DISEASE VIRUS (STRAIN A10-61)	207.130	1119-1146							Ī
	GENOME POLYPROTEDI	FOOT-AND MOUTH DISEASE WIRUS (STRAIN A12)	301-328	1119-1146							
F.	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIB) SI	1116-1146				<u> </u> 	-		-	Ì
F	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN CL.SANTA PAUTC-SA)	10 10 10 10 10 10 10 10 10 10 10 10 10 1							+	Ī
П	GENORGE POLYPROFEIN	HEPATITIS CYIRUS (ISOLATE I)	20.12	_	-		100	211	1	1	Ī
	CENCHE POLYPROTEIN	HOG CHOLERA VIRUS (STRAIN ALFORT)	27.						1	 	Ī
	GENOME FOLYPROTEIN	HOG CHOLERA VIRUS (STRAIN BRESCIA)	2	2	6	100-1440	27.77	!	<u>:</u> !	:	:
¥	GENOME POLYPROTERN	NEPATITIS CVIRUS (ISOLATE BA)	2	100				_		_	
PROLID HEWI	CREMONAL POLYPROTEIN	14-7-A 11515 C VIRTIS (1518-A 16: 11)		78.4				_	_	_	
	CENCING POLYPRUTEIN	INFATITIS C'VIRUS (IXILATI: IN: IN)		3 5	İ			-		<u> </u>	!
ı	GENOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE HC.18)	2	200.5		-		1		1	Ī
L	GENOME FOLYPROTEIN	HEPATITIS C VILUS (ISOCATE JAPANESE)	╛	2.72	0 F	-	1			1	Ī
Ì	GENORGE FOL YPROTEIN	HEPATHIS C VIRUS (ISOLATE MC·IT)		1045-1073			_ <u>'</u> 			_ <u>i</u>	i
PPOLO HEVTW	GENOME POLYPROTEIN	INEPATITIS C VIRUS (ISOLATE TAIWAN)		_	_		 	-		_	-
ı	GENOME POLYPROTEIN	HEPATITIS A VIRUS (STEAM 24A)	103-237		_	1454.6481					-
ı	CENONE POLYPROTEIN	HEPATITIS A VIAUS (STRAIN 4)C)		_	_	1434-1481					ij
ļ	GENOME FOLVPROTEIN	HEPATIFIS A VIRUS (STRAIN IOF)	201-233	1071.1048	- E	1434-1481	<u> </u>	-			
L	GENOME FOR YPROTEIN	HEPATITIS A VIRUS (STRAIN CRUSO)	112-101	İ			<u>-</u>			<u> </u>	
L	CENTAGE BOL VPROTE DA	HEPATIFIS A VIRUS (STRAIN GA76)	183.216			<u> </u> 	-		<u> </u> -	_	
1	Chanks hat vegative	ILEPATITIES A VIELS (STEATH IDA. 195)	100.00	021.104	101	İ	<u>!</u> 			-	
П	COOLS FOLVED TEN	HEPATTHS A VIRUS (STRADA LA)	201-201	8701.180	110)-1149		<u> </u>			L	ì
	CENTAL FOLYPROTEIN	INCPATITIS A VALUS (STRADA ACAB)	105.005		103.1	H	-			-	Γ
.1	GENOME FOR YPROTEDY	SOCIAN IGPATITIS A VIBUS (STRAIN ACAN-22)	Ī	_	2011-5111	<u> </u> 				<u> </u>	
Ł	GENOME FOLYPROTEIN	SOULAN HEPATITIS A VIBUS (STRAIN CY-143)	101.111	1	•						
1	GENORGI POLYPROTEIN	FRIDACAN BUDNOVIBLUS 14		_	621 670	1.18					
1	CENCING POLYPROTEIN	HEDLAN BEDNOVINUS I B		1835-116:			_				
ı	CENORAL FOLYPROTEIN	HEBRAN REGNOVIRUS 2	Н	_	_						
POLD ICEVIS	GENOMAL POLYPROTEIN	HIPLAN REGNOVIRUS 69		141.14	1366-1607	1862-1889					
PICTO MEN	GENORGI POL YPROTEIN	HUMAN ENTEROVITUS TO (STRAIN MION!)	174-910					_			
Proto movo	STRUCTURAL POLYPROTEIN	AVIAN BRECTIOUS BURSAL DISEASE VIRUS (STRAIN ON)		_						H	Ī
L	CENCING FOLYPROTEIN	INPANESE EXCEPTALITIS VIRUS (STRAIN SA-14)		_	1796-2023						
L	CENONG FOR YPROTED	JAPANESE ENCEPHALITIS VIRUS (STRAIN SA(V))	П	_	2 Prof. 2823					Н	
	GENOME FOLVPROTEIN	INTEREST ENCEMENTING VIRUS (STRAIN INDARSTIL)		911-1010	2794-2823						1
	CENTRAL PROTEDY	INFANESE ENCEMBALITIS VIRUS (STRAIN MAKAYANA)		911-938							1
	CENOME POLYPROTEIN	KUNIN VIIIS (STAIN NOUNIC)	I			1		1	4	+	Ī
MOLD LAWY	CENCING POLYPROTEIN		7	3		1	1	1	1	+	Ī
PROLIG LANY	GENOME FOR THROTEIN	LAIN YEL AMI SEV)	S S		1		1	+	1	+	Ī
200	GENOME FOLYPROTEIN	LOUPING BLL VIBUS	3	1	1	\dagger	†			+	Ī
THUE OF THE	COUNTY TO THE OWNER.	LUCKERO LLA VIACO (SILAMIN SO MA)	Ť	1000 3001	411 1411	Ì	\dagger			+	Ī
A CALL	CENTRAL POLYMOISIN	INTERIOR DIVINA BELLEVICATION	Ť		2000		\dagger		1	+	Ī
2007	CANONIA POLITICA	LOBBAY VALUE PROFESSION VIRIUS		Ì	1		+	-	ŀ	+	Ī
	CONTRACT PROTEIN	DENTIFICAL IN MOSAIC VILLIS	Ť	10.44		Ť	t				Γ
PROTO PERVIC	CENTRAL POLYPROTEIN	PEPPER MOTTE VIRUS (CALIFORNIA ISOLATE)	Ī,	Т	88:15	100-627	167.1201	405-1312 1767	1767-1814 2433-246-		Ī
PRO DE LIV	GENOME POLYPROTEIN	POLIOVIDUS TYPE I (STRAIN MAJONEY)	18	1=	Τ	1	-	-	•	-	Ī
Proto Potis	GENOME FOLYPLOTERY	POLIDOVIDUS TYPE I (STEAM SABIN)	_	- -	1603-1933	r	\mid	-		L	
FOLD FOLK	GENOME POLYPROTED ¹	POLIDIVALUS TYPE 1 (STRAIN LANSING)		1001-1001				-		_	
PHOLD POLYW	CENOME POLYPROTEEN	POLIDVBUS TYPE 2 (STRAIN W-2)		1681-1061				-		L	
PPOLO POLI	GENOME POLYPROTEIN	POLIOVIDUS TYPE 3 (STRAIN 2)123)		0(61-0061							
POLO POLIL	GENOME FOLYPROTERN	POLIOVIRUS TYPE 3 (STRAINS PIA EOM)? AND PIA EON 124(19)	ij	900-1930							П
PHOLO PHYD	ODIONE POLYPROTEDI	PLUM POX POTYVIRUS (STEADN D)		1001.1535	2771-2794					\downarrow	1
PROLID HYVEA	CENDAGE POLYPROTERM	PLUM POX POTYVIRLIS (STRAIN EL AMAR)	114-1163					Н		+	٦

			П			Т	т		6.444	4874	ARFAS
PCCUR	107417844	As Virginia (ne bacteropasgri)	П	1920	7	7	रकार	1900	Т	ī	
FILKNAME	PROTEIN	ATE NAT)	П						1	:	
PPOLO PPYNIA	GENOME POLYPROTEIN	OVICI	7	27.132	10-11		-	:	:	:	:
PROLA HVIA	GENOME FOLYPROTEIN	LIT MAN	56.53							ŀ	
IN ME DIVE	GENORAL POLYPROTEIN		31:41								!
CV 104 C 104	CENOALE POLYPROTEIN	MOINT IN CASE	110.516							1	٩
	CONTACT AND VORONTEIN		Т	111.111	1110-1117						
3	THE PARTY OF THE P	AIN OPO!)	Т	101							٠
Proto Park	CENTRE INCIDENT		Т		150	1131.300	1111.000				
Proto Pryc	GENORE FOR TPROJECT	TAX SECURITY OF THE ABOUT OF TH	_	201-100			_		:		
PROLA PAYIN	CENCIAL POLYPROTEIN		433.460	20:32 20:02	1486-1517		<u>:</u>	!	:	: :	:
No.	GENOME POLYPROTEIN		-	Tol. 735							
2	THE PART WHEN THE PARTY IN		1								
POLO PVVO	CENCRE FOLVERIN		2	1101.171							
PROLO PYTY!	CENDRE POLYPROTEIN	PADAL TELLOW COMP. TO SEC.	16.33								
100	CENTRAL POL YPROTEDY		1024-1060			L					
	STATE OF VERNIEN	(6)						L			
HOLD SVOVI	CENTRAL FOR 17801 ELV	1	٦								
Proces two	GENOME FOLYPROTEIN	TANK PARPERSON OF THE CHAIN CASH AND SCHOOL	2.5	114-177	1613-1061	1203-177					
PROLID TREV	GENOME POLYPROTEIN	TREACHER ENCETTAINS TREET TO THE CORP.	1433-1659								
AND MARKET	CENTRAL FOL YPROTEIN	VIRUS (WESTERM SOUTHE)	667	1146.1175	1416-1443	1773-1800					
	CENTRAL IN VERNITEIN	Ī		1		_					
PICTO TEV	CENTRE FOR IT AND EAST	1314)	2					ŀ			L
PROLO THEY	GENOME POLYPROTEIN		- - -	20.23							
١_	GENOME POLYPROTEIN	THE RESERVE OF THE PARTY OF THE	100	100-111							
ı	CELEVACE BOX VOLUMEDI			111.800		L					
_1	CANAL TO SERVICE AND ADDRESS OF THE PARKS OF				170				L		
	CENCRE FOL VPRUIEIN	ONG VIRUS	404-433	670.704	7.107.7						
VAVI O POPP	GENOME POLYPROTEIN		302-329								
The second	CENTAGE POLYPROTEIN	WATERMELON MOSAIC VIRUS II	20, 416	1104.141.7							
2	TO SECOND TO THE PERSON										
PPOLO WIN	CENCHE INCIDENT										
PROLO YEFVI	GENORE FOLTFRUIEN	COLL SOLD SECURE COOLIN STATE OF SECURE 17D 2041	136-46)								
PPOLO YEAV	GENORGE POL VPROTEIN		90-69								
VANA D POST	GENOME FOL YPROTEIN	ZUCCHIMI YELLOW MUSHIC VINUS	1007-1101	1903-1933							
THE PARTY OF	GENOME FOLYPROTEIN	POLIDIVILIS TYPE I (STRUM PLANMET)	1403.1467	164-1931							
The second	NOWSTRUCTURAL POLYPROTEDY	VENEZUELAN EQUAT DICEPILALITIS VIRUS (3) INCHES INCHES	25.77				L				
	ACCESSION IN THE ACT WAS VAROUED.	FELDIG CALICIVIDIS (STRAIN CFUSIFIV)							L		
	MALURA IV. I THE TAIL AND ADDRESS OF	IFFE INE CALICIVALIS (STRAIN F9)									L
	MON-SIEUCIONO POR LINGUISE	THE SAME OF WHITE AND BURNAN	219-246	346.376					\downarrow		
PROCES IN VIEW	NON-STRUCTURAL POLYTROJEIN	THE STATE OF WASHINGTON AND AND AND AND AND AND AND AND AND AN	219-346	16.18				1			
PPOLICE INVO	Г		219.344	149-176							
A VANA	Т	ICPATITISE VIEWS (STRAIN MY ANNIAM)	914.944	141.131		L		_			
	Т	HEPATITIS E VIDUS (STRAIN PAKISTAN)							L		
	Ť	Lamber Butto Valus	233-105					-			L
	POPULIOUAL PALIFFORM	CANADAL LANGE OF THE ADM CUT. U)	2453-2480								
PHOLIN CHRING	MONSTRUCTURAL FOLVERS I ELM	S. CHILLS LINE LAND IN CAP PACE ACE VIRING	113-347	1631-166	-						
VOLUMBIO!	NON-STRUCTURAL POLYPROTEIN		1037-1004	1435.1304	2410.1445	_					
7	MONSTRUCTURAL POLYPROTEIN	ROSS RIVER VICUS (STRAW RESMY)	181 271						_		
	ANALOGICATION AT BOX YPROTEDY	ROSS RIVER VIRUS (STRAIN T48)		-		ļ		_	L		
	MONOTON TO THE WAY OF THE PARTY	TIPETIA VILLE (STRAIN THE RIEM)	2000								
PIOUS RUBY	POPULION FOR THE STATE OF THE S	TOBLE PET TOBER T VINUS	1134-1111					-	-		
7	HONOTHUCTURAL POLITICAL	CALIFORNIA CONTRACTOR OF FEBRUARY EDSDYN 12-5)	976-978								
PIOCH EDGD	HOMSTRUCTURAL FOLYTROTEIN	Michael Vision (active active	4.11	L							
A STATE OF THE PARTY OF THE PAR	MONETHER TURAL POLYPROTER	WESTERN EQUIPME ENGINEERING	100	L		L		_	_		
	September 1 has venoted	AVIAN DOECTIOUS BURSAL DISEASE VIRUS (STRAIN 32/10)				\downarrow			L	L	L
200	SIRUCIONA PARTICIONA	AND AND DESTRIBUTE BUREAL DISEASE VIRUS (STRAIN AUSTRALIAN 001-7)	1111-158						1		
PICOLS DIDYA	STRUCTURAL FOLITHOLES	CONTRACTOR BUILDIAN PAGE ACE VIRGIN (STRAIN (U.1)	231-324				_				
PICE S BOYC	STRUCTURAL POLYPROTEIN	A VAN DE CLINE ALLES A CASE ARE UNITE ACT AIN EN	131.388								
PACE S POR	STRUCTURAL POLYPROTEIN	AVIAN DOLCTRUS BUILDAL USEASE VINOS (STRAIN E)	315.916				L	_	_		
	STRIPPING ALL WARDIED	AVIAN DEECTIOUS BURGAL DISEASE VIRUS (STRAIN FOUND				-		-			
	STANCTON OF THE PARTY OF THE PA	AVIAN HEF CHICUS BURSAL DISEASE VIRUS (STRAIN STC)						1	-		
Profs BOV	STRUCTURAL POLITICISM	CONSTRUCTION OF ITS ASSESSED OF UN	124-101					1	-		
PIOLS GROND	STRUCTURAL POLYMOIRIN	10 TO 10 TO	1919-913	L		_					
NATE S TOAK	STRUCTURAL POLYPROTED	ROSS MVEA VIBUS (STRAM MEXA)	616.033			_	L	L			
1	REPRIETIGAL FOLVPROTED	ROSS RIVER VOLUS (STRAIP 1 ct)					-	L	L		
	STATE OF THE ACT AND VALUE OF	SOCIETY VINUS (SUBTYPE OCKELBO / STRAIN EDSOYN 17:3)					-	-	-		L
100	STATE OF COUNTY OF	SINDBIS VIRUS (STILADIS HILSP AND HOLP)				\downarrow	-	-	-		L
ADG TOL	SIRUCIONAL PACIFICA	WASTITUM EXCEPT ENCEPTION VINUS	928-943						+	l	
ATT NEED	STRUCTURAL POLITICALITY	TAX EXCEL BELLEVISION OF US (\$19A) MIT	475-704	715-742		4	$\frac{1}{4}$				
PPOL BALVA	FOL POLYPROTEIN	Bypoon Times		ŀ							

		An Victor Las Lacterises here!	П	П	-	П	1	1 1 1 1 1 1 1	, , , , , ,	10.00	
THE HAME	PROTEIN		J	4864	7		_		Т	_	
STORY CARNE	POL POLYPROTEIN	CE ARTHUTIS ENCEPHALITIS VIRUS (STRATH CORK)			1011 1101	11 36.1301	in in			l	Ī
PPOL COYMY	PUTATIVE POLYPROTEIN		Т				+		+		Ī
PPOL ELAVO	POL POLYPROTEDI	EQUING DIFFECTIOUS ANEADA VIRIUS (CLONE 1984)	200		T	T		T	-	•	
POL ELAVO	POL POLYPROTEIN	EQUING SAFECTIOUS ANEAGA VIRUS (CLONE CL22)	Т						\mid	1	<u> </u>
PPOL ELAW	POL POLYPROTED ⁴	EQUINE BUTCHOUS ANEMIA VIRUS (ISOLATE WYDAIING)	T	37.44	İ	T	T		-	-	
POL IDWI	POL POLYPROTED	FELDAT ENDOCEDIOUS VALUE ECE!	Т							-	٠
PIOL FIVE	NOT POLYPROTEIN	FEINE BOARDOE RUNNE VINUE (BOLATE TELALOPIA)	97.109			İ			-		
PPOL PAYD	ENZYMATIC POLYPROTEIN		ī	10, 301				:	:	·	
POL GALV	POL POLYMOTEIN		Т			İ					
POL HTLIA	POL POLYPROTEIN	MUMAN T-CELL LEUKEMA VIKUS I VPE I (SIKAIM AIN)				T	T		_		
PPOL HTLIC	POL POLYPROTEDM	HUMAN I CELL LEUKENIA VIKUS ITTE I (CARIBUEAN INOLATE)	Ţ	4 70 44.1							
PPOL HVIA3	POL POLYPROTEDI	HEMILAN DOCUMENTER TO THE STATE STATES TO A SOUCH IT	Т	11411		İ					
PPOL HVIBI	POL POLYPROTED ⁴	HEBLAN BOACHOOF RELEACT VIX.03 1 TPE 1 (BITTO 1300-715)	T.	117.117		İ				<u> </u>	
FOL HVIBS	POL POLYPROTEIN	HUBAN DOCOCOCENCY VIRUS TYPE I (HII)	•		1	1	-	!	<u> </u>	.	· !
POC HVIBE	POL POLYPROTEIN	INDIAN BERUNDDEFICIENCY VINUS TYPE I (IIINU ISOLATE)	Т			Ť				-	
PPOL HVIEL	POL POLYTROTEIN	HAMAN BOMINGOEFICIENCY VIRUS TYPE I (ELLISOLATE)	Т	77.54	031.00	Ì	İ	1	-		
PPOL HVIND	POL POLYPROTEIN	INDIANA BOADWOOEFICENCY VIRUS TYPE I (IIXD2 ISOLATE)		777		T			-	f	
PFOL HVIR	POL POLYPROTEIN	INDIAN DOMINODEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	Т		977	İ		T	-	T	
PPOL HVIMA	POL POLYPROTEIN	HIDAM DOADNODEFICIENCY VIAUS TYPE I (MAL ISOLATE)	T	916-310		Ť		Ť	1	!	į
POL HVIDA	POL POLYPROTEIN	HUMAN INDAUNICE FICIENCY VIRUS TYPE I (MN ISOLATE)	Т			Ì	1	\dagger		t	
SMIAN TOAK	POL POLYPROTEIN	HERAN DOLDHODE HEENCY VIRUS TYPE I (NEW YORK'S ISOLATE)	٦			1	1	1		t	
ONIAN TORK	POL POLYPROTEDY	INDIAN DOLUMODE ICIENCY VIRUS TYPE I (NOK ISOLATE)	Т	24				t		t	Ī
AU NO	POR POR YPROTEIN	HUNLAN INDAUMODEFICIENCY VIRUS TYPE I (OVI ISOLATE)	٦	2000		1	+	1	$\frac{1}{1}$	\dagger	
70177	POS CARA VARIOUS INC.	HIBIAN DAGRADDEFICIENCY VIRUS TYPE I (PV22 ISOLATE)	130-257	63.633		1	1	1		†	Ī
	TOLINGIEM	IN BAAN BAGGAODE FICTENCY VIRUS TYPE ((BJAIAT ISOLATE)	117.144	119-460						1	
TAC HAIRS	THE TOTAL STATE OF THE PARTY OF	IN BAAN BAARMOOFFICE NEW VIRUS TYPE I ISTRAIN UGANDAN / ISOLATE U	211.344	513-540	099-619						
MAIN MAIN	TOL TOTAL	LENALLY WANTED SPECIFICATIVE TYPE I (ZACDC-214 ISOLATE)	207-244	619-440							
POL HVIZI	POL POL VPROTEIN	LABORAL BARBANGER CENTRAL STATE OF STATE DENI	101-101								
WINE HATEL	POLICE STRUCTURE	TOWNS IN THE PROPERTY VIEWS TYPE 2 (150LATE CAM2)	431-543								
POL HVICA	POL POLTFROIEIN	INDIANA HAMANAGEICHENTY VIBIG TYPE 2 (1904 ATE D194)	89468								
E MAD	POL POL VAROTEIN	HENNEY PARTICIPATION OF VIRING TYPE 2 (ISOLATE D205.2)	35.								
MOTO NATION	POL POLITICISM	INDIAN PARAMETER VIEW VIEW TYPE 3 (ICOL A 15 CHANA.)	471-562					-			
POL HV201	POL POL YPEDIEIN	CHARLE MANAGEMENT VIEW TYPE 3 1150 A 25 MILES	631.528								
POL HYZINZ	POL TOTAL	CHANAL WANTED COLOR VIEW TYPE 3 HOLD AT BODS	472.543							r	
POL HVID	POL POLYPROTEIN	HOWAY BEAUTION FIRM I VINDS THE A GOOD IN AND AND AND AND AND AND AND AND AND AN	13.562			T				r	
PPOL HVISB	FOL FOLTFROTEIN	MINISTER PROPERTY VIEWS TYPE 2 (ISOLATE ST)	691-582								
THOU HYES	TOUR TOUR TOUR UNA CASE OF	HALLETTE BUTTACISTERNAL A.PARTICLE	100-127	10.25	667-197						
	AND ALLY BOAT DOLLAND TEN	MONISE DITTACTS TERMAL A PARTICLE	Т	107-339	400-473			Н			
	SECTION OF VERNIEN	MOUSE DITTACISTERNAL A-PARTICLE	130-157	111.24							
2	TANDALE OF COLUMN	SWEEP PULLACHARY ADENCHATOSIS VIRUS	20-23 20-23								
PROFESSION VAL	POL POL VPROTEIN	AKR MURUME LEUKEMAN VIRUS	453-480						1	1	
PPOL MEVAV	POL POLYMOTEDA	AKV HUNDVE LEUKENÖA VIRUS	20-632				1	1	\dagger	†	
PPOL LA VILD	POL POLYPROTEDA	RADIATION MURDIE LEUKEAGA VIRUS	10.00	20-61			\dagger	t		+	
PPOL MEVICK	POL POLYPROTED	RADIATION MULINE LEUKEMIA VIRUS (STRAIN KAPLAN)	201					T	$\frac{1}{1}$	T	
PPOL MONAY	POL POLYPROTEIN	SDECAN MASON PFIZER VIRUS	210-215	100	8		Ť	t		t	Ī
PPOL COUNTS	POL POLYPROTEIN	OVDE LENTIVILUS (STIAIN SA-OMVV)	71.0	411-303	34.1		†			T	
PPOL BSVP	POL POLYPROTEIN	ROUS SARCOMA VILLE (STRAIN PRACUE C)		10.00	100,761	203.330	410.41	11 247.434	1622.1046	t	
PPOL BTBV	POLYPROTEDI	RICE TENGRO BACILLE ON VIRUS		10.00	Т	Т	Т	Ť	023.1049	t	
PPOL RTBVP	POLYPROTEIN	RICE TUNCKO BACILLIFORM VIKUS (ISOLATE PHILIPPINES)			Т	Т	Τ	Ť		t	Ī
POL SFVI	POL POLYPROTEIN	SDIGAN FOAMY VILUS (1778-1)		101 671	113.615	1	t	T		t	Ī
PPOL SIVAI	POL POLYPROTED ⁴	SOUGH BOOLEGE FLENCE VIRUS (ACHIES INCLAIR)				Ī	T	T			
PPOL SIVAL	POL POLYPROTEIN	SUGAN BUILDING FUERC I VINUS (ACHIEV 1905 AFE)						T			
PPOL SIVAS	POL POLYPROTEIN	SOCIAN DOMINIONE REPORT VINOS (AUMINIONES)	710	417.416	944.54		Ť	T	I		
PPOL SIVAG	POL POLYPROTEDI	SURLANDORONO PLENCT VIANO (ACM) 1904 X E.	411.4116					T		ŀ	
PPOL SIVAL	POL POLYTROTED	AND THE PROPERTY OF THE PARTY O	187 (89			Ī	İ	T		T	
POL SIVAT	POLITICISM	CHALLE A NOTE TO BEALD ACTION OF VIRIOS (SIVICED)	L	620-65							
TAGE SING	TOL FOLTEROIEUM										

477	7	All Viewers (no bacteriophoges)	AREAL		ABEAL	ANEA	2	9			
		VIRGO	Ť	2					Ī		
Γ		SHIPAN INDAMENDER CULTURE AND AND ISOLATES	3								
PPCK SIVIAL		SOUND TO THE PROPERTY VIEWS (KAW ISOLATE)	3		Ī						
Γ		SDUAN BOURNOOF THE TO VIEW VIEW AND	44-33								۲
		SOUTH PRODUCE THE STATE OF THE	7								
SIME TO		SACRET LANGE OF THE CARRIED (SARV.H)	401-438								٠
	POL POLYPROTEDN	STANDARD MANUEL	I	1							
		SUTERAT CIT. CALL OF THE STATE	170-612	630-697							
Ī		SMIAN RETROVERS SAV:	eno-534	111.919							
Ī		VISNA LENTIVIRUS (STRAIM 1919)	1110	490-534	111-919						
		VISMA LEMTIVIAUS (STRADM 1914 / CLUMB LV 1-18.31)	Ī,	816-181		_					
	TOT TOTAL STATE OF THE STATE OF	VISIA LENTIVIZUS (STIADIV 1514/ CLONG LVI-1KS2)	Т								
١		ACCITED MALALARY TURGOR VIRUS (STRATIV BRA)	,								
PPATT MACTIVE		CALLES LIANDALA TURIOR VIRUS (STRAIN CIVI)									
PRIN LOUTVE		CONTRACTOR VIRIAL STRADE OF	2.5		:	1	!	•	_		
PPR73 MOSTIVO		POUS PROPERTY OF THE PROPERTY VINIS	11.11				ļ				
MINO GIVE	POLYHEDRIN PRECURSOR	DONOTA MONICE CONTRACTOR OF THE PARK VIEWS	11.43								
74797		AUTOGRAPHA CALLI ORDER A PACIFICA	14.48	201.328			-	1	1	: 1	!
2011	POR VICEOBRA	AGROTIS SEGETUM MUCLEAR POLYICEDROSIS VIRUS	13.51								
VA.M.		BOMBYX MORI MUCHEAR FOL VIICUROSIS VIRUS				L	i				
PAND WAY	POL THE LINE	BITTITA SUPPRESSANA NUCLEAR POLYHEDROSIS VIRUS						L			
D Neves	POLYNEDRIN	HYPHANTRIA CLINEA MUCLEAR POLYHEDROSIS VINUS	?								
D NEVIC	POLYNEDRIN	SYLANTIA PHEBAR MAIL TICAPSID MUCLEAR POLYTIEDROSIS VIRUS	7				1				
PYID WALD	POLYNEDRIN	THE PARTY OF THE PARTY OF WEDINGS STATE	77				1				
BYN BYNG	POLYIEDADA	MANUEL STREET STREET STREET STREET POR VIII DROSIS VIRUS	(*:							-	<u>i</u>
PONEN	POLYNEDAD!	ORGYTA PARUDOLISMA I A MICE IN THE INCHES A POR VIII THE DISTORATION	10.40								İ
AND TOWN	POLYMEDADA	DRGYIA PSEUDOISUCATA SIMULE CARROLOS CONTRACTOR VIEUS	1								
	PCK VIG DR.DK	PANOLIS PLANALA MALIPILE NULLEULA PUR POLITICIO POLITICIO PER POLITICIO PER PER PER PER PER PER PER PER PER PER	14.43								
	LOS CALCADANA	SPODOPTELA EXIGUA MUCLEAR POLYIEURONO VIRGINATIONIO				L					
	The little has been a second	SPODOPTEDA PRUGIPERDA MUCLEAR POLYIGERROSIS VIRUS									
2	TOT UNEXPEND	SOUND BOADNOOFFICENCY WIRUS (TVO-1 ISOLATE)									
PREV STVAT	MAY PROJECT	VISNA I EMTIVAGOS (STRAIN 1514)			19		<u> </u>				
MEV WEV	REV PROITE								_		
PRINI ASTAG	MORAL CONTRACTOR AND					-					
1	RECONCEDENCIAL MEDICAL LANCE CHE	EXILEM LESDES VISITS TYPE 1 (STRAIN ABAP)	29:183				-				L
	ABORAC DONORM NEWS I CANCELLO		134-131								L
	LEGALIC DEMOSMINEDUCT LANGE CITA		167-401								
	RECONDED BY BEDICK LANCE CHA	VACCING VICTORIANI VICTORIAN VICTORIAN VICTORIAN VICTORIA VICTORIAN VICTORIAN VICTORIA VICTORIAN VICTORIAN VICTORIAN VICTORIAN VICTORIAN VICTORIA	167-401								
HHI VACEV	MERCHALL DOHOSPH REDUCT LANGE CHA	VACEBOA VINOS (STINAIN TR)	107 (91								
ı	THE MALE BOHOSPH REDUCT LANGE CHA	VALOLA VAUS	110.146								
	A HOLE IN THE MANDE OF A PEDICT LANCE CHA										_
2	THE PROPERTY OF THE PROPERTY O			53.11	1	-					
MON HOVE	THE PERSON NAMED IN COLUMN				1				L	L	
PRIM VACCV	DA FOLLANDE INC.	CARLY A VIETR	2			7	-	-			L
VAAV	ANA-POLASSOC TRAPS SPECTAL TOR	VACCINIA VINITA VINITANI COPENIAGEM	337-364	1		7			1		L
POI VACE	DHA DO ECTED IDA POL 147 EU	THE CONTRACTOR AND MEN	11:36	317-616		┪	7				ļ
PLINE VACEV	DWA-DARKTED BUA POK. 107 KD		133.264	383-416	10-13	W-172					l
MINDI VARV	DAIA-BURETED RIVA POL 147 KD	VALUE VALUE	19.65	114-155							
GENT CAPVE	DNA DELECTED LIVA POL. 133 KD	CAMBOTVEUS (STRAIN RS-1)	1211.341	<u> </u>							
X CHUCK CHIEF	DAY DEFETED THE FOL 131 KD	COWPOX VIXUS	111.341	8	L	L	L				
	TAMA PAREPER BNA POL 131 KD	VACCEDIA VIRUS (STRAIN WR)		85			-				
	THE PARK BUT DO 112 KD	VALIGIA VIAUS					-	-	L	-	
WARV	DIVATORE TELEVISION IN TO	CAMPOXYBUS (STRAM KS-I)	1		-	1	1				
	THE PERSON OF THE PARTY OF THE	VAPCEDALA VIRUS (STRAIN WR)	6			1	1	-			L
U) VACEV	UNA-UNIO LES ENTE DO 10 ES	VALIDIA VIDUS	R		1	+					L
PLPO) VARV	DNA-DBLELLED MAA FOL 17 NO.	LELYSTAD VIRUS	1333-1380	_	1	1		1	-		
PEPOA LELV	ANA DESCRED LINA FOLTMENAN	CALENCE ARTERITIES	201-915	1639-1673		4	1		1		
PEPOL EAV	ANA-BOLECTED BNA POL TACANSE	COUNTY AND A UNITE COT AND ANCION AND ANCIONAL	175-402						1		1
) MEGR	INA-DOLECTED INVA POL SUB 71	UNICOLOGICAL A CASTA COTO A CANA ABRADAMAS	119-146						1		1
A IN IAAIO	ANA DESCRED ANA POL SUB PI	DATIONA A VICIO (STRAIN AND AND AND AND AND AND AND AND AND AN	110.100				L				4
DATA TABLE	THA DOLECTED LINA POL SUB P2	DELLENZA A VILLO (STRAIN ALIONAMINAMINAMINAMINAMINAMINAMINAMINAMINAMI	110.10	-	L		_				4
	ALC: L-SAMER BUT BAN COM BY	BELIEFEA A VINUS (STRAIN ANOWL PLACOR VINUS NOTICE !!		1	1			-			
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PROTEIN	WRUS	Т	7	<u> </u>	7	:-	,	Т		
ANA DIRECTED ANA POL SUB PI		951-61					! :		; ; 	:
HAN-DAKE TED ANA POL 300 F2		19-146						Ì		
NA SUBSTITUTE BUY BOL SIGN PO		119-146					1		T	Ī
NAM - DIRECTED RNA POL SUB P3		91-6						İ	Ī	
ANA-DIRECTED ANA POL SUB PI	678)	2					Ī	İ		
NA-DIRECTED ENA POL BING PI	DOLLENZA A VRUS (STRAIN ANT/KOKE)			T				İ	Ī	$\left \cdot \right $
NA-DIRECTED RNA POL SUB PI							ľ	!	: 	1
INA-DIRECTED RNA POL SUB P2	1							İ		
ANA-DIRECTED RNA POL SUB P2	MEMETA IERSETATION				Ī			Ī		
LECTED RINA POL SUB P1			Ī					Ī		
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KNA-DOLECTED KNA FOL. SUB P2		₹			Ī					
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BHA-MERCIFD BNA POLICIO PE		110-146		i			1			
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ACCIDED MAN PAC SUR IN		19:146								١
DA-DURECTED ANA POL BUR PA	nevin	118-146								
DNA-DOBECTED ANA POL. SUB 72	THE COURT IS COME AND A COME AND	157.194								
LECTED RIVA FOL. SUB P3	INCLUDICAL WINDS (STEAM) OF ANY AND COUNTY OF AN	1	Ī							
ANA-DIRECTED RNA POL SUB PR	Ī				:	i	:			
ANA-DIRECTED BAY POL SUB PI		27-14		-	1	111	1	İ		į
RMA DARECTED ANA POL SUB PS	KAIIXVIIII	337-567								
SECTED BY CITE PI		П								
CALL PROPERTY BUY IN COME ST		331.361	480-507							
STATES AND THE STATES OF THE S	3	487-514								
MANAGEMENT BASE OF STREET		16.2	477-506							
ELIED BAA POL SUB FI	HART RAPA & CHAIR COR AND MANNA ARRORATING INTO TYPE	3	472.309							
INA CORECTED RIPA FOR SUB P	T	20.60								
INA URELIED INA PAL SUE VI		20,30								
RECTED RIVA FOL. SUB 71		T	154.101							
RNA-DIRECTED INVA POL SUS 73		ī	124-751	1971.2008	1711.3011					
INA DERECTED RNA POLYNERASE	PUDDATA CONCERNATION CONT.	Т	134.4161							
INA-DIRECTED INA POLYMERASE		Т								
ANA-DOLECTED ANA POLYNORASE		T	337-384	20.1						
WA BOLECTED ENA POLYNGRASE		7	22.12							
INA-BOLECTED RIVA POLYNGUASE		202-015	139-1170							
RNA-DOBECTED BNA POLYMERASE	IS CORONAVIRUS (STRAM FS772		353-380							
NA DREFTED BNA POLYNGBASE	116)	J	3294-2331	3547-3374						
NA DOBETTED BNA POLYNGRASE			-							
NA DANGCTED RWA POLYNGRASE		1032-1059			-					
NA POLYMERASE		100	117.330	1602-1161	1007-1919					
BANA BOI VARBACE RETA SUBLINIT	DRUS (STRATH ONDERSTEPOORT)	16-51								
NA POLVACE ASS		((1-10)	461-510	364-391	136.765	905.946	1993-2020			
NA POLYACEBACE BETA SUBURIT	L VIRUS (STRAIN AJ)	103-192	110-111	147.494		_	1007-1034 1118-1163	163)-1480	176-1203	102-101
BNA PARETTED BNA POLYNORASE		9101-166	143.1370	1490-1524	1011-1839	1029-1067	1216-2766			
BMA DAMECTED BMA FOL YAGBASE		1101-166	1490-1524	_						
RMA POR YNGRASE BETA SUBLOST		121-56	196-223	2121-214						
NA POS VACEDAÇE RETA SUMIDOT		111-143	710-10)	1603-1413						
ENA POLIVACERASE BETA SIZEIDAT	(TEC43)	110-364	117.304	1030-3013						
DALL BY WASHAGE BETA CIPATED	MEDIAM PARAMELLENCA 1 VIRUS (SPLAIM TOSHIDA)	132.346	1544-1501		_	_				
NA BOT WARE A CE BETA CITAISAT	HENGAN PARADICLENZA) VIRUS (STILATIN MIH 47885)	97-86	136-163	111-101	1661-1133	1894-2016	3115-31143			
BUT THE FIRST BUT DO VICE ASE		20 4 ES	337-381	21.32	_	150-928	1948-1971	194.2025		
AND THE PROPERTY OF THE PARTY	PARITY VIRUS (STRADA PV)	10 m	603-633	2066-2123		L				
NA box water a ce meya summari	BABIES VIDUS (STIAM SAD 819)	104-231	605-411	2068-2123						
NA TOUR MEAN BOX YOUR ASE	ALCE DWARF VINUS	137.01								
NA DOPETTED BWA POLYNGRASE	LYRUS (STRAIN ZIL 948 MIZ)	1374-1363	1453-1607							
And the same and t										
		1	Ŝ			_				

PCGUNE TILE NAME PRINE SPIOÈ	PROTEIN COLUMNITY AND INCOME.	VIRUS SENTAL VIRUS (STRAIN Z)		1001	36.136	3145-2180					
	PROTEIN		1								۱
_				-	331.758	\$05.932	_				
	ANA POLYMERASE BEIN SUBSTITION	SECOND CORPORATION IN THE SECOND IN THE SECO		1:		1130.2143					
	ANA DIRECTED RNA POLYNGIASE	SECURITY CONTRACTOR OF THE PROPERTY OF THE PRO	ᅱ				1010			ŀ	
Γ	RHA FOL YACRASE BETA SUBUNIT	SIMILA VIRUS S (SI INALIF ALIONI TILI)	835-050	•	1490-1570		1000		10071	1007.1004	204 16 31 10
T	RHA POLYMORACE BETA SUBUMT	SONCIAL CONTRACTOR OF THE CONTRACTOR OF CONTRACTOR			2 - 2	1193-1279	100		-		
ACTION ASSESSMENT	BWA DIRECTED LIKA POLYNGRASE	TOWATO SPOTTED WILL VINUS (BRAZILIAN ISOLATE	2164-31912	3334-3368	1771-1798						ŀ
T				101.100	1304-1131						1
Wall 1225	BUT BO WASHASE	COKIDATE OF THE ST	1510-155	1009-1016							
	SUA BOLVAGE ALE BETA SUBLOGI	VESICILAR STOMATITIS VIRUS (SENOITTE NEW JERSEY STRAIN OCHEN)	100.1313	1809-1136							
	BUT BOY VACEBACK BETA SUBSECT	VESICIL AR STOMATITES VIRUS (SEROITYE NEW PRASE) (31 NATIONAL DESIGNATION OF THE SERVICE OF THE	1500.154)	194-1791							
200	THE PART OF A SECOND ASSESSED AS SECOND SECO	VESICULAR STOMATITIS VIRUS (STRAIN SAN IUAN)	136.361	165.55							
744	MAN POLITICAL STATE OF THE AREA	APPLE CHEOROTIC LEAF SPOT VIRUS	Т								
PILIDO ACLSV	DAY-DOLECTED BAY FOR THE MAN	BEEF WEETERN VELLOWS VIRUS (ISOLATE FL-1)									
PATA BUTY	PUTATIVE BUA-DOL BUA FOL	TELEVISION OF THE PROPERTY OF THE NAV. PS.)	773.77	١							
PRESON NYOVE	PUTATIVE RNA-DIR RNA POL	BALLET TELLOW DWAY AND AND AND AND AND	731.78						Ī	1	
2000	SAME AND THE BANK POL	BABLEY YELLOW DWALF VIRUS (1900A) E A.	111.700								
	101 A 101 A 101 A 101 A 101	TAKEL BY YELLOW DWALE VIRUS (ISOLATE P.PAV)	Т	2	707.67/						
PRING BYDYR	PUINIVE ANY WAR SON ! SO	PARKATION MOTTLE MAUS	7	Ī							
TABLO CANAV	PUTATIVE RNA-DIR RNA FOL	STATE OF THE MOTHER MOSAIC VIRUS (WATERNELON STRAIN SIE	7	90 180							
PRING COLINS	PUTATIVE BNA DIR RNA POL	CUCUMOEN CALLED AND A CALLED AND A CALLED A CALL	334-363	192-419							
PARTY WILL	PHITATIVE RNA-DIR RNA POL	AVIAN INTECTIOUS BUILDAY DISEASE VINCE AND ANGER ALL AND CO. 731	194-195	117.744							l
TOTAL PROVE	HITATIVE BMA-DIE BMA POL	AVIAN DOECTIONS BURSAL DISEASE VINOS (STRAINS AND STREET)	31.600								
	ALTO A STATE BALA BOTH BALA BOTH	INGECTIOUS PANCAEATIC NECHOSIS VIRUS (SEKULTYE 1437 E.M.)	80			L	Ļ				
PRING DRVI	PUINITE BOARDON WAY	INTECTIONS PANCEEATIC NECROSIS VIAUS (SEROTYPE SP)		0.07							
PRINO LPHYS	PUTATIVE BYA-DIR RWA FOL	THE STATE OF THE WAS NOTED VIBLIS (STRAIN ARMSTRONG)	94-156	037-107							
PLEPO LYCVA	ANA POLYNGRASE	LYNCHOLT IN COMMENT OF THE COMMENT O	401-419	308.738	200						
PANA PROPERTY	PITTATIVE RNA-DIR RNA POL	PEPPER POLICE VINCE CONTRACTOR	1								
	ALL PROCESS BUY BOX VALUE LASE	REOVINUS (TYPE 3/ STRADI DEARING)		١							
PRING REDVO	KAN-DIELE MAN TOUR BACK	RECOVIEUS (TYPE 1/STRAIN LANG)	T	1	100						
PRINC REOVE	MA DIRECTED IN THE THE	BOODER BOTA VIBUS (STRAD) 85)	1			1					
PREPO ROTER	ANA DOR RNA POL SUBURGI VPI	THE PERSON NAMED IN COLUMN TWO IS NOT THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED IN THE PERSON NAMED	65-95	310-245		3					
PRESO ROTBU	RMA-DER RNA POL SUBLINIT VPI	BOVING MAIN (COCKE CATANA COMDEN)		79-103	2	20.20					L
PREPOROTRC	RMA DUR RMA POL SUBURGE VPI	PORCING ROLL AVENUE (CONCO) CO STATE OF THE PROPERTY OF THE PR	\$6-59	102-130	19-130	93)-180					
DATO BOTH	RNA-DER RNA POL SUBURIT VP1	PORCEME MOTAVALLE (STRAIN COLLEGE)	65.63	701-819	975-1002						
PAUL EARES	INA DER ENA POL SUBURGE VPI	SDDAN 11 ROTAWAUS (STRAIN SATI)	147.163								
	BHA. DIRECTED BNA POLYNERASE	SACOMANDE CENEVISIAE VIXUS L'A	Г	24:12	1103.1134	1971.2004					
2	AND DOLLARS ACIE	TACABLE VOIUS	Τ	1717	•	-		L			
MINO INC	ALIES SHAPE BUY INCH BUY BOX	TOBACCO MILD CALEN MOSAIC VIRUS (TMV STRAIN UZ)						L			
PREPO TACARY	PULATIVE IOCA-CIR. PULATIVE PERSONAL	INCOME EXPERIENCE SYNCYTIAL VIRUS (STRAIN AS1901)									L
PRRPP BBLYA	ANA POLYMERANE ALPINA SUBURIO	TAXABLE TAXABLES VIBILIS (STILAD) ONDERSTEPOORT)	315.370					1			
PLEAT COVO	RNA POLYMERASE ALPHA SUBURUL	CANAMA USI BACTA VINCO (VINCO VINCO	121-46								
VERN SERV	IRNA POLYNGRASE ALPHA SUBURIT	MUNICAL PROPERTY STATES OF THE PROPERTY OF THE	199-141								ļ
Penne tankvi	INNA POLYNGRASE ALMIA SUBUNIT	HOUSE REPUBLICATION OF THE CARLO AND	99-141								1
AVIET SEEVA	INA POLYNERASE ALPHA SUBURET	HABLAN REPORTIONE STALLING VINCE AS INCHASE A STREET IN TORICE	198-141								1
	SAIN BOY VACOR ALPHA SUBUNIT	HUBLAN RESPONATORY STRUCTION VINUS ISUBORON AS STRUCT	114.120			L		_			
	TOTAL BOLL WAS A SET AT BULL SIBILBRIT	MEASUES VIRUS (STRAIN EDMONSTON)						L			
THE PERSON	THE SALE WAS A CONTRACT OF THE STREET	MEASUES VIRUS (STRAM P. J.C.A)							L		
-	THE PARTY OF THE ATTEMPT STREET	MEASUES VIRUS (STRAIN YANGATA-!)		77.		-	-		L		
THE PERSON	THE PARTY OF THE P	HEIDGAN PARADINE (BENZA I VIRUS (STRAIN C35)				-					
	PACK TO THE PACK THE AT BOLD OF SHIP STATE	HABBARN PARADOFLUENZA I VIRUS (STRAIN C19)				-	-	ļ			L
NAT MIKE	MA PALTMERANG ALTIM SCHOOL	HENDAN PARABOLLIENZA I VIRUS (STRAIN CI-S/1)	=			-		1			L
PLIN THE	ANA POLTME LASSE ALLTIA SUSCIENTE	HAMANDA BANGE HENCA I VIRUS (STRAIN CI-1441)	-			1	1	ļ			L
PLAYP MIKE	RNA POLYNERASE ALPIA SUBURIL	CHAPTEL STATE OF THE WAY A STATE OF	163-194	22.22							L
PERSON PURSON	RNA POLYNGRASE ALPHA SUBUNIT	STUDION CALCALLE SERVICE STATE OF THE SET BATH THE STATE OF THE SET BATH THE SET BA	167-191	223-236							1
THE STREET	DNA POLYNERASE ALPHA SUBURUT	HOMAN PALACTOR & VAND (21700)	16.57	135-203	285-314						1
STEE STEE	INA POLYMERASE ALPHA SUBURIT	BOYDG PAIADIPLUACA J VINOS	14.14	20.45							1
HILL CARRO	ANA POLYNGRASS ALMIA SUBURGE	MINCH PARADELLENCA) VINUS (STICALIF MAY 4182)	10.3		Ĺ	L		Ц			1
1177	BMA NOT WASHALE AL PHA SUBURIT	PUBLISH PARAPHELIENZA 4A VIRUS (STRAIN LUSHIBA)	01.137			-	L				
200	BNA WATERASS ALPHA SUBUMIT	AABIES VILUS (STRADY PV)	100	25.20		-		L			
1	THE STATE OF STREET STREET	SENDAL VILLE (STRAIN 2 / HOST MUTANTS)			1	-	ļ	Ŀ			Ц
5	TOTAL STATE AND AND STREET	SENDAL VIBLIS (STRADN 6PM)			ļ	-	-	L	-	L	
	TOWN TO SERVICE A COLOMA COMPANY	SENDAL VIEUS (STRAD) FUSIONS)			1	-	-		_	L	
200	THE POST OF THE PARTY AND AND AND AND AND AND AND AND AND AND	SENDAL VIRUS (STRAM HARRUS)			1	1		-	-		L
PLANT SEPON	ANA POLTIMENASO ALCINA SOSSILI	GENERAL VIRING (STRAIN 2)	200	3442		-					ļ

THE KAME	04/4010						г		Г	
		VIRUS	4	3	3	ORFA ORFA	7	<u>ا</u>	9	
PLL 7 5V5	_	SDGLAN VIRUS S (STRADN W2)	203-202	136-783					t	Ī
PLONE VACEV	OTER	VACCINIA VIRLIS (STRAIN WR)	72.99						1	Ī
ALTER UASV	OTEN	VALIDLA VIRUS	72.99		٦					Ī
VONE ANGRA		AASACTA MOOREI ENTOMOPOXVIRUS	91:10	160-161	2	06.780			1	1
PSPII MYXVI.	SEAPONI	MYXONA YOU'S (STIADY LAUSANNE)	1			1	1		†	4
PSP13 VACCV	SEADE PROTEDIASE DRIBITOR 2	VACCINEA VIRUS (STRAIN WIL)	3			1				Ī
PEPLA VACCE	SEXECT PROTEASE DON 2 HOMOLOG	VACCORIA VINUS (STRAD) COPENDIAGEN)	≘	Ì		1			t	4
rtica dimi	TYPE II RESTRICTION ENZYMIS CVIAII	PANAMECTUM BUTCACUA CILLORELLA VIRUS I	3			-	: : :	:		
PIAA3 VACCV	TRANS. ACTIVATOR PROTEIN AS	VACCINIA VIAUS	2			1			\dagger	Ī
PTAGE FOWPY	TRANS.ACTIVATOR PROTEIN FPO	FOWLPOX VIAUS	₹			1	1			1
PTAGE VACCV	THANS ACTIVATOR PROTEDICKS	VACCINIA VIBUS	90				1		T	
PTACE VARV	TILANS. ACTIVATOR PROTEIN CK!	VANOLA VIAUS	2				+		t	
PTALA BFDV	LARGE T ANTIGEN	BUDGERUGAL FLEDGLING DISEASE VIRUS	291-318						j	Ī
PTALA POVBO	LANGE T ANTIGEN	BOVING POLYOMAVIRUS	55.53		•	:		•	_	
PYALA POVILA	LARGE T ANTIGEN	IIIAMSTER POLYOMAVIRUS	317-631							
PTALA MOVI Y	LARGE T ANTIGEN	LYNGHOTROPIC POLYONA VIRUS	224-258	116-614				1	1	
PTAL A BOWLI	I ABOUT ANTICIEN	MOCKE POLYGMAVIRUS (STRADA 3)	913-540						1	
A VIVIA	A ARCH T ANTIGEN	MOUSE POLYOMAVIRUS (STRAIN A2)	311 538							
1000	A ABOR & ANTROEM	MOUSE FOLYOMAVIRUS (STRAIN CRAWFORD SMALL-PLAQUE)	306-333						1	
PAYER MOVA	THAME AFT TRANS BEG PROTEIN	AUTOCALIFIA CALIFORNICA MUCLEAN POLYMEDADSIS VINUS	407-434	(15-68)	\$11.559					
7147	TEACH AND TO AND BELLEDIN	BONDAY MOST MICE BAR POLYNEDROSIS VIRUS	412-439	494-528	337.564					
TATA PARTY	TO A LIE A THE A PART BECT PORTED	ORGYNA PSELEDOTSUCATA MULTICAPSID POLYHEDROSIS VIRUS	512-154							
ON A IN A	A A DOS TROM BOOK PROTEIN	EPSTEIN-BARR VIXUS (STRAIN 1993-1)	145-171	1215-1242	1344-1371	1836-1903				
	MACANA BE A A B OF THE CHARGE TO BE OF FIN	HOBEAN CYTOMETAL OVIRUS (STRAIN AD169)	1251-1211	2101-1229						Ī
THE PERSON NAMED IN		LIGHTER COAN BY WALK ITYER 1/ STRAIN 171	467.699	1473.1710						
PIECE DIVE	I ARGE TECHNORINE PROTEIN	HERPES SINDLEX VIRUS (TYPE 6/ STRAIN CS)	101.134	238-362	119(9)	963.093 1094	1008-1181 1661-1688	1884-1011		
	TABLE PERIMENT DECISION	FORTING MEDPESVIRIS TYPE 1 (STRAIN ADAP)	226-256	264-50)	\$					
PTECH MAYSA	PROBABLE LANGE TEGINGENT PROTEIN	HERPESVALIS SAIMEN (STEAM II)	334-403	673-700	177.614	986-676 368-978	101-044 996	1467-1497	201.20	
PIECU VZVD	LARCE TECHNOLISM PROTEIN	VALICELLA ZOSTER VIRUS (STRAIN DUNIAS)	1131-1130	1579-1609					1	
PTELM ADEO!	DNA TERMINAL PROTECU	KIDAAN ADENOVIRUS TYPE ?	3						1	Ī
PTAW AVISA	TRANSFORKEDIG PROTEIN MAS	AVIAN MUSCULOAPONEUROTIC FIBROSARCONIA VIRUS AS12	200							1
PTOPI SPYKA	DIVA TOPOISONGUASE I	SHOPE PIBROMA VIRUS (STRAIN KASZA)	2	92.176			+		Ì	Ī
PTOP1 VACCV	DNA TOPOISOMEJASE I	VACCINIA VIRUS					1	1	t	
PTOPI VARV	DRA TOPOISOMERASE I	VARIOLA VILUS				1			1	
HOM ASTAB	DNA TOPOISOAEMASE II	AFRICAN SWINE FEVER WRUS (ISOLATE MALAW) LIL. 201)	4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1						t	
PTYSY HSVAT	THYMEDYLATE SYNTHASE	PEACE STATES				1				Ī
PTYSY HSVSA	THEN STATES STATINGS	PENTLY WALLS SAMMED (STRAIN 11)		111.140	(4). (6)					Ī
A	VINCE PROTECTION AND A	WEBER CHANGE VICTOR 1 CONTRACTOR 121	1771						T	Ī
TOTAL STATE	VINDER PROJECT US	ECHANG MARKET TVOE I CITE AND	190.667						T	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VIEW CENTER AT PROTECT	HELPESYBUS SADOU (STRAIN !!)	2	303.338	107-191					
MEDI HOLVA	HYPOTHETICAL PROTEDY U.L.O	HEBLAN CYTOMEGALOVIRUS (STRAIN AD169)	Ī							
PULL EDV	HYPOTHETICAL PROTEIN BALF!	EPSTEIN-BANK VIRUS (STRAIN BV)-1)	13-43							
PUR IN HOUVA	INYOTHERICAL PROTEDY ULI)	HUNGAN CYTOMEGALOVIAUS (STRAIN AD169)	2						1	
PULL HEVER	HYPOTHETICAL GENE 44 PLOTED ⁴	EQUING MEMPESVIRUS TYPE I (STRAIN ABAP)	2			1	-		1	
בינון אבאם	INPOTIBITICAL GENE 44 PROFEIN	VANCELLA-20STER YBUS (STRAIN DURIAS)	2						1	
PUL 16 HOAVA	INPOTHETICAL PROTEDY UL 16	HUMANI CYTOMEGAL OVINUS (STRAM AD169)							1	Ī
PULSE HOAVA	HYPOTH PRO ULTO PRECURSOR	HUNCH CYTOMECALOVIAUS (STRAIN AD149)	=				+		Í	
PULLI HEVEB	CENE 40 PROTEIN	EQUING MERPESYDUIS TYPE I (STRAIN ABAP)	-				1		1	
מעצא ונשט	CENTE 18 PROTEIN	VALCELLA-ZOSTER VIRUS (STRAIN DUNIAS)	9						†	
PULIS HISVEA	VILLON GENE 19 PROTEIN	HEAPES VILUS SABATA (STRAIN II)	2		2				1	Ī
MUJI HOWA		HUMAN CYTOMEGALOVINUS (STRAIN AD169)	9	2						
PULLY HISVES	MAJOR ENVELOPE GLYCOPROTEIN 100	EQUACE IGRAFES VIDUS TYPE I							†	Ï
וואפו זכווי	VINION PROTEIN ULDA	HERPES SOOTEX VINUS (TYPE 1/STRAIN 17)							1	Ī
PULJ4 HSVSA	GENE 4) PROTEIN	(JEDNES VINCE) SABORU (STRAIN II)				1			†	Ī
75.7 VZVD	VINDA CENE 14 PROTEIN	VALCELLA-LUSTER VIRUS (STRAIN COMAS)							\dagger	
MR.19 HOWA	INFORETICAL PROTEIN ULSS	HUMAN CYTOMECALUVIRUS (STRAIM ADJUST)	377-784			1	$\left\{ \right.$	1	1	

		VINUS CONTRACTOR OF COR 1 / CTRAIN 12)			•	_	-	7			
			۲		1						
			1		T						
		EQUAL TELOCIA VINCE	Т	7	310.346	1001-110			•		
	CENE (1) PROTEIN	CALLE VALUE (STIAN DIALAS)	107.00	Т	Т						4
		CONTRACT & SACRED VIELDS (STRAD) DUBANS)									
	ON PROTEIN	TERMS SIGH BY VALUE ITYPE I / STANIN !!)		976					i	:	•
		WASHINGTON OF THE WALLS GIRAIN DURIAS)	7		1	150-708	İ				
	SKANE PROTEIN	HALLE PYTOMETAL DVINUS (STRAIN AD) (4)	Т								
		WEBEL GLOST EX VIELS (TYPE 1/STRAIN 17)	200								
		LEADER CHAPTER VILLS ITYPE 1 / STRAIN !)									
	VILLON PROTEIN ULA!	SAN THE PROPERTY IN TAKE 4									
	ILANS INDUCINO PRO	SELECTION OF STRAIN AD 149)		710.64		1			į	:	:
		CONTRACT AND VIELDS (STRAIN 89)-8)	1		-	į	į				
Ī		EXAMPLE THE EVENT RAPE LIST RAIN AUST	Т								
		ECONG TEACHER FOR AND III	S S								
T		HOLDEN THE STATE OF THE PARTY O	301-337						L		
٢		VALK ELLA COSTEA (STRAIN ADIM)	76-601								
Į		THE TANK THE PARTY OF PARTY AND LAST	24-6						L		
T	PROS DAIA REP PROTEDI UL 10	HADAN CT CONTRACT ON THE ATTACK AD (49)	F.						L		
Γ	ULTS CLYCOPROTEIN PRECURSOR	PUREAU CT COMMENT AFTER AND 113									
Γ	HYPOTHETICAL GENEE SU PROTEDY	HELDER TO THE PARTY OF THE ACTION AD 169)	2,1					L			1
	TYPOTISTICAL PROTEIN UL.74	CANADA AND WALLE STRADE 095-4)		176. 272			L				
T	HYPOTHETICAL PROTECH B(C)*31	COLUMN TANKE EN VIEIS (TYPE 6/ SIRAIN UGANDA-1102)	2				L				
	HYPOTHETICAL PROTEIN SR	PENCES SOME SEA BATTLE	383.40						L		
	HYPOTHETICAL CENE 24 PROTEIN	WELCHEN WALLS CHANGE OF THE BOS 4)	107-104	2	1						
Γ	HYPOTHETICAL PROTEIN BOLY	CONTRACTOR OF STRAIN (STRAIN 13)				ļ	L	L			
Ī	HYPOTHETICAL GENE 11 PROTEIN	IN THE PARTY OF THE PARTY STRAIN ADIMS									1
	PROTEIN UR.93	HELLAN CYTOMEGAL OVIRUS (STRAIN ADIM)		104.674						\downarrow	1
	HYPOTHETICAL PROTEIN ULY	HE ENER SELECT EN VIELES (TYPE 6/STEATM UCANDA-1102)				L					1
PULES HIS VOU	HYPOTHETICAL PROJESIN 12A	HUMAN CYTCHEGALOVIRUS (STRAIN AD169)								1	1
PULAS HOSYA	VIRGON FILLS OF THE STATE OF TH	HIBLAN CYTOMEDALOVIBUS (STRAIN AD109)	1	L					4	1	1
AN HOWA	MYPOTHETICAL PROTECTION OF THE	HUBLAN CYTOMOGALOWALIS (STRAIN AD169)							-	1	1
ا۔	INTOTAL CANADA A SE	HELDESVINUS SAIMED (STINAIN !!)					Ц		1	1	1
١	CHACLE THE THE VOICE OF LASE	SHOPE FEBRUALA VIBILS (STRADA KASZA)	13.116	20150				1	4	1	+
١	STATE THE PROSPERSE	VACCINE VILUS (STRAIN COPERMAGEN)	18118	134-136			4	1	1	1	-
MINO VACE	THE THE NAME OF VOOS PLASS	VACCORA VINUS (STRAIN WR)					1	$\frac{1}{4}$	1	1	ļ
П	THE LOS THAN OF VOOSTLASS	VABOLA VRUS	į				4	4	1	+	1
1	GOOD HOUSE MOTERNINGS	HENCH CYTOMEONLOVICES (STRAIN ACTIV)	177.300				1	4	+	1	-
.1	LOWERTH PLOTEN HW.F4	HOLAN CYTOMEGALDVING (3) IAAM ADIM	118:161				1	1	-	1	L
	CANADA NAM PROTECT HALLS	KIDALNI CYTOMEGALOVIZIUS (STIANITY ACITY)	8.7					1	1	1	1
PUSIT HEAVY	i is ist. I profess	AFLICAN SWING FEVER VILLES (STRAIN LAST)	57.55 5.73				1	1	\downarrow	1	+
200	135 EN PROTEIN	ALFALFA BOSANC WILLS (STRAIN 425) 1500A 1 C.	27	L			1	4	-	1	+
TANK CINA	KI 119 PROTEDA	AFRICAN SWINE FEVER VICES (2110APT LIST)	77-65				-	1	1	1	1
	ILKED PROFEDA	TOBACCO RATTLE VILLS (STICKLY PAR POR VHEDROSIS VIRUS	096-360	945-973		1	1	\downarrow	-	-	L
VIVE TOOLS	HELICASI	AUTOUNATIV CALE OFFICE AND PACE	38-113		7	-	1	1	-	L	lack
NOT LEVEL	14 KD PROTED	TORACOURATILE VILLE (SINATURE)	13.5K	110-111		7	1	1	1	-	L
PART VIN	IA PROTEDI	BROAD BEAN MULLE VIKUS	13-50	36411	3	2	1	1	1	-	ļ
A BEA	A PROTED	BROME MOAL VINOS	349-376		1	1	1	\downarrow	1	-	L
A STATE OF THE STA	IA PROTEDA	COWNEA CHACKEL MAIL CONTINUES OF THE PROPERTY	11-38	П	-	+	\downarrow	1	1	-	
MIN AIN	IIA PROTEDI	COCCUPATION OF THE ARM OF	2 2	20.	-	1	\downarrow	-	-		H
WIA CAMO	IA PROTEIN	COULDER LACKIC VALID (STIAM O)	11.38		\downarrow	\downarrow	-	ļ	L		
VIA CAVO	IA PROTEIN	SALANT CHIRCH VINIS AS TO AND	7	2	70.	73	1	ļ	-		Н
PVIA PEVI	IA PROTEDI	FRANTO ASPERAT VIRUS	-		Т	Т	-	-	L	H	
PVIA TAV	IA PROTEIN	ATTENDED PAR CALEGRACA FUCLEAR FOLTHEDROSIS VIRUS	7	$\frac{1}{1}$	1	-	-	-			
PV2SK NEVAC	25 KD PROTEDA	SEA HARLY REDWINDS VIEWS		+	+	+	-	H	-		-
VIN PEBV	29 I KD PROTEDI	TATE AND THE VIEWS		1	1	1					

PCCENE	10/11/11/01				YOUNG						
П	PROTEIN	VIRUS	Т	Г			-			_	
PV29K TRVTC	29 KD PROTEIN	TOBACCO PATILLE VIRUS (STANIS)	20.10			_			: -	<u>:</u> :	
V2A DEMV	2A PROTEIN	BROAD DEAN MOTILE VINTA	. S	:	:	<u> </u>				- 1	١
PVZA COMV	2A PROTEIN	COMPEA CILOMOTIC: VIROS	017.00						_		1
PV2A CHOFIN	2A PROTEIN	CULUMBER MUSAM, VINUS (STRAIN TRY)	Т	187.511					-		╡
PVZA_PSVJ	2A PROTEIN	PEAKUI SIUMI VAUS (SIMAIM)	1	72.7%						1	١
VZA TAV	2A PROTEDY	TOWATO ASSERT VINOS	Т							-	-
PV30K HCMVE	30 KD MAJOR EARLY PROTEIN	HUMAN CT LONGOALD MALE COLORS	130-160					:		_	
VJOK TRVTC	29.1 KD PROTEIN	TOBACCO LATTLE VIRUS (3 FRAIN 10 A)	3		!					-	
PV33P ADEAL	33 KD MIOSMIOPROTEIN	HIUMAN ADENOVIRUS TYPE 41	16.163				İ	-			
PVX42 ASFB?	K'362 PROTEIN	AFALCAN SWINE PEVER VIRUS (STRAIN BATTL)	T	13.100				-	_	-	
PVIAL ASPRI	D'363 PRÔTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)	T						-		
VIA MV	1A PROTED	BRONE MOSALC VINUS		T			T		-	I	1
MAY ANN	1A PROTEIN	CUCLAMBER MOSANC VIRUS (STRAIN FNY)								Ė	i
200	TA DECISION	CUCUAMER MOSAIC VIRUS (STRAIN NI)	252.612	Ī		İ		+	1	-	!
W. C.	14 MOUREN	CUCUMBER MOSAIC VIRUS (STRAIN O)	222-253				1	+	1	t	
200	700000	CUCUMBER MOSAUC VIRUS (STRAIN Y)	222-253						+	t	
WIA CANY	A TROIGH	AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN HEALTH.)	25-57					1		\dagger	l
PVJA UVB	JA PROJECT	AVIAN BEPCTIONS BRONCHITIS VIRUS (STRAIN UNIT 1666)	29.56					+	1	†	İ
WIA DWUS	JA MOIEN	IAVIAN DEFECTIONS BRONCHITIS VIRUS (STRAIN DEACHETTE)	6-33							t	
773 DVB	Ja PROTECT	PARTERY VELLOW DWARF VIRUS (ISOLATE PAV)	110-146						1	i	į
WOK BYDY	NO KID PROTECTI	ACCT WERPEN VELLOWS VILLIS (ISOLATE P.L.1)	113-147	150-020							i
VSIK BUTVE	SI KD PROTELIN	DECEMBERSEN VEHION'S VIRIES (ISOLATE GRI)	113-147	134.451						†	ı
VSIK BWYVG	SI KD PROTEDV	POCE TENEDO VIBIL (STRAIN)	124-151	438-472						+	İ
VSAK PLAVI	SE KED PROTEIN	CANDAMAN AND A STREET OF THE PARTY OF THE PA	124-151	438.477						1	١
WALK PLAW	SE KD PROTEIN	POINT DE LEAST AND LANGE OF THE PROPERTY OF TH	128-155								
WASH MSWV	SO KO PROTEDA	BALLEY STUTE MOSAK VIROS	10.140								Ì
VYDK MAN	# 7 KD PROTEIN	TOTAL CARROLL WELL CITALIN WACRINGEN	110-140							1	١
YYDK PLAW	49 7 KD PROTEIN	ALTAIN LANGAR VINITE (CTRAIN 425 / ISOLATE LEIDEN)	107.134							1	
PVICK ANVLE	SO KD PROTEDY	VACCEDA GABIN COM AN COMMAGEN	157.216	150-277	263-310	314-355				1	ł
VACCT	PROTEIN AS	VACCINIA VIBIS (STRAIN WIL)	156-215	346.376	282.309	313-354			+	1	١
VAGS VACEV	FROTEIN AB	VARIOLA VIRIUS	157.216	250-277	283-310	216-355				+	١
TVAUS VARV	PROTEIN AS	VACCINIA VIRUS (STRAIN COPENHAGEN)	176-206					1	+	t	
7000	PROTEIN AS	VALUOLA VIRUS	176-206					+		T	
7000	PROJECT AS	VALUELA VIRUS	\$6.00							t	
TANK VALVE	PROTEIN ALL	VACCINIA VIRUS (STRAIN COPENHAGEN)	219-283							†	
	PROTEIN A11	VALIDLA VIRUS	220-284					1		t	1
7411	SA P.O. ABOR TIVE I ATE PROTEIN	VANOLA VIXUS	440-467					†	+	T	1
AVA STAN	MOTEN A10	VACCINIA VIDUS (STRAIN COPENHAGEN)	3	200					1	†	1
אלים אינריר	THOUSEN AND	VARIORA VIRUS	8-67	330-357					$\frac{1}{1}$	†	
PVALO VALV	PROJEIN ACO	VACCINIA VIRUS (STIVAIN COPENHAGEN)	45-33							1	ļ
אירור אירור	PROJECT ALS	VARIOLA VIRUS	%-E3							†	
	BEATEN AN	VACCINIA VIRUIS (STRAIN COPENHAGEN)	25.							†	١
- AAC	BEATEN ASS	VARIOLA VIRUS	95-144						+	1	I
1 AVA	PROTEIN AS	VACCINIA VIRUS (STRAIN WR)	22-49							1	
AVE AVEC	TACIFET AS	VARIOLA VIRUS	22-49						+	Ì	١
- NA.	A VICTOR	VACCINIA VIRUS (STRAIN WR)	12.55						+	1	Ì
A NAME OF THE PARTY OF THE PART	PROTEIN A11	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-13						1	†	١
774	Security And	VARIOLA VIRUS	88-122						+	T	1
אאון אאנא	SECULED AS	VACCINGA VIXUS (STIVAIN COPENHAGEN)	17.114							1	
NAME AND THE PROPERTY OF THE P	PROTECT AND	VACCIDIA VIRUS (STRAIN WR)	17.114						$\frac{1}{1}$	1	١
7877	PROTEGN AND	VALIDLA VIDUS	<u> </u>						+	T	
7777	PROTEIN A14 PRECURSOR	VACCINIA VIRUS (STRAIN WR)	20-130						+	T	Ì
200	PROPERI A14 PRECIESOR	VARIOLA VIDUS	<u> </u>						+	T	
JULY NAME	PROTEIN A31	VACCINIA VIRUS (STRAIN COPENHAGEN)	20.2						+	T	١
AVVII VACO	PROTEIN A38	VACCINIA VIRUS (STRAIM WR.)	7		\downarrow		1			T	
WAN VARV	PROTEIN A38	VARIOLA VIDUS	44-91							1	١
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PROTEIN A19 VI	VACCIBAL VIRUS (STRAIN WR) VACCIBAL VIRUS (STRAIN CORENIAGEN) VACCIBAL VIRUS (STRAIN CORENIAGEN) VACCIBAL VIRUS (STRAIN COPENIAGEN) VACCIBAL VIRUS (STRAIN COPENIAGEN) VACCIBAL VIRUS (STRAIN COPENIAGEN) VACCIBAL VIRUS (STRAIN COPENIAGEN) VACCIBAL VIRUS (STRAIN WR) VACCIBAL VIRUS (STRAIN WR) VACCIBAL VIRUS (STRAIN WR) VACCIBAL VIRUS (STRAIN WR)		193-220						
C. MOTERN A.9 V. V. MOTERN A.9 V. V. V. MOTERN B.9 V. V. V. V. MOTERN B.9 V. V. V. V. V. MOTERN B.9 V. V. V. V. V. MOTERN B.9 V. V. V. V. V. V. V. V. V. V. V. V. V.	ACCENTA VIRUS (STRAIN WIN) ACCENTA VIRUS (STRAIN COPENIAGEN) ACCENTA VIRUS (STRAIN COPENIAGEN) ACCENTA VIRUS (STRAIN COPENIAGEN) ACCENTA VIRUS (STRAIN WIN) ACCENTA VIRUS (STRAIN WIN) ACCENTA VIRUS ACCENTA VIRU						$\frac{\parallel}{\parallel}$		
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PROTEBLA ANT PROTEBLA BIT PROTE	AGENTA VILUS (STRAIN WR) AALOA VILUS (STRAIN COPENIAGEN) ACCINAL VILUS (STRAIN COPENIAGEN) AACCINAL VILUS (STRAIN COPENIAGEN) AACCINAL VILUS (STRAIN COPENIAGEN)	143.184 61.91 61.91 15.82					-		
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MATERN ALS ALI PROTEIN ALI PR	ACCOUNTY VALUE (STEADER WA)		П	70-67	†				
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AND TAANSAGSSON PROTEIN AND TA	CAULD LOWER MOSAIC VIXUS (STRAIN CHILLY)	33.30							
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APID TANSMASSION FROTEIN APID TANSMASSION FROTEIN APID TANSMASSION FROTEIN APID TANSMASSION FROTEIN FORTEN BI FROTEIN BI		22-70	27.72			+		-	L
APHOTEN BY PACTE	CALA HELOWER MOSALC VIRUS (STRAIN W260)	7 - 70				1			L
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PAGTEN BY PAGTEN	VACCINIA VIDUS (STRAIN WA)	21:23	112-211	216-313	134-361				
PROTEIN BY PROTEIN BY	VACCINIA VIAUS (STRAIN CUPENHAGEN)	161.191	112.211	286-313	124.361				
HOTEN BY HOTEN BY HAGTEN BY HAGGE SIZE / HOST LANGE PRO PREC HAGGE SIZE / HOST LANGE PRO PREC HAGGE SIZE / HOST LANGE PRO PREC HAGGE SIZE / HOST LANGE PRO PREC HAGGE SIZE / HOST LANGE PRO PREC HAGGE SIZE / HOST LANGE PRO PREC HAGGE SIZE / HOST LANGE PRO PREC HAGGE SIZE / HOST LANGE PRO PREC HAGGEN BY HAGTEN BY HAGTEN BY SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR SUP AGE ANTIGEN S PRECURSOR HAGTEN BLI PROTEIN BLI PROTEIN BLI PROTEIN BLI PROTEIN	VACCINIA VINUS (STILADIA WR.)	10.133	112:211	286-313	324-361				
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HAQUESTEE I HOST PANGE PRO PREC PARQUESTEE I HOST PANGE PRO PREC PRAGUESTEE I HOST PANGE PRO PREC PARQUESTEE I HOST PANGE PRO PREC PROTEIN BY PRECURSOR PROTEIN BY PRECURSOR PROTEIN BY PRECURSOR PROTEIN BY PRECURSOR PROTEIN BY PROTE	VACCINIA VIRUS (STRAIM LL 1944U)	254.284							
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PROTEIN BIT PROTEIN BIT PROTEIN BIT PROTEIN BIT PROTEIN BIT SUPFACE ANTICEN S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PRECUESOR SUPFACE S PREC	VACCINIA VIRUS (STRAIN WR.)	111 111		ļ			-		
MOTEN BIL PROTEN BIL PROTEN BIL SURFACE ANTIGEN SPECURSOR SURFACE ANTIGEN SPECURSOR SURFACE ANTIGEN SPECURSOR SURFACE ANTIGEN SPECURSOR PROTEIN BIL BLI PROTEIN BLI PROTEIN BLI PROTEIN	VACCINIA VIRUS (STIVAIN COPENHAGEN)		-	L					
PROTEIN BIT FROTEIN BIT STUP ACE ANTIGEN S PRECURSOR STUP ACE ANTIGEN S PRECURSOR STUP ACE ANTIGEN S PRECURSOR STUP ACE ANTIGEN S PRECURSOR PROTEIN BIT BIT PROTEIN BIT PROTEIN BIT PROTEIN	VACCIMIA VIRUS (STRAIN WR)							-	L
SUIP EAR SITE ANTICEN S PRECURSOR SUIP ACE ANTICEN S PRECURSOR SUIP ACE ANTICEN S PRECURSOR SUIP ACE ANTICEN S PRECURSOR SUIP ACE ANTICEN S PRECURSOR PROTEIN B31 B41 PROTEIN C41 PROTEIN	VARIOLA VIRUS	37.76			-			-	L
SUP ACE ANTIGEN S PRECURSOR SUPFACE ANTIGEN S PRECURSOR SUPFACE ANTIGEN S PRECURSOR SUPFACE ANTIGEN S PRECURSOR PROTEIN BIT BLI PROTEIN BLI PROTEIN	VACCENTA VIRUS (STRAIN COPENHAGEN)	162-213						-	ļ
SUID ACE ANTICENS S PLECUISOR SUID ACE ANTICENS S PLECUISOR SUID ACE ANTICENS S PLECUISOR PROTEIN BID PROTEIN BID BIT PROTEIN BIT PROTEIN	VACCOUR WITH ATTE ATT ATTE AND THE EN IN	160-210						+	1
SURFACE ANTIGEN S PLECUISOR SURFACE ANTIGEN S PLECUISOR FROTEIN BJ1 BLI PROTEIN BLI PROTEIN	VACUAL VINITA (STRAIN VE)	110-210					-	1	1
SUPFACE ANTICEN S PLECIASOR PROTEIN B11 B11 PROTEIN B11 PROTEIN B11 PROTEIN	VALUMA VINO (3 INVIII "K)	180-210						$\frac{1}{1}$	1
PROTEIN B20 PROTEIN B21 B41 PROTEIN B41 PROTEIN B41 PROTEIN B41 PROTEIN	VARIOLA VIXUS	44.42	-						_
PADTEN 831 BAI PAOTEN BAI PAOTEN	VACCINIA VINUS (STRAIN CUPENTAUEN)	19.77							
BLI MOTEIN BLI MOTEIN	VACCINIA VIRUS (STRAIN WR)		31.		ļ		-	L	L
BLI PROTEIN	BEAN COLDEN MOSAIC VIRUS	120-14	Т	\downarrow			-	-	L
BLIFMUELM	CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 844)	-10							L
	CASSAVA LATENT VIRUS (STRAIN NIGERIAN)	118-143		1					ļ
BLITTOILE	INTATO VELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	130-147	4	1			-		ļ
BLI MOTEIN	VARTHUM VIBILIA (STRAIN COPENIAGEN)	405-432					1	-	ļ
MOTERIC	CA CAPATA VIDER (CTB ATA GRE)	41.31	405-432						1
PROTEDNC	VACUATA VINOS (3 1 mm								

	PROTEIN PROTEIN CA PRO	VIBLS STOCKED VALUE (STRAIN RASZA) STOCKED VALUE (STRAIN COPENIAGEN) VACCINIA VALUE (STRAIN VA) VALUELA VALUE (STRAIN VA) VALUELA VALUE (STRAIN VA) VALUELA VALUE (STRAIN KASZA) STOCKE STRAIN VALUE (STRAIN KASZA)	209-236 12-46 13-46	\$ 23						
	OTEM CA OTEM C	SHOPE TRACEN VIRGINIA STRUCK NASZA) VACCENIA VERUS (STRAEN VA) VALCEN VERUS (STRAEN VA) VALCEN VERUS SHOPE TRACEN VERUS (STRAEN KASZA) SHOPE TRACEN VERUS STRAEN	П							
	OTEM CA OTEM C	VACCINA VIDUS (STADIN COPERIONERS) VACCINAL VIDUS (STADIN VIA) VALEDIA VIDUS SHOPE FIBLIOLIN (STADIN KASEA) VATERIA VIDUS (STADIN KASEA)	13.46							
	OTEN CO OTE	VACCINIA VIRUS (STAAIN WA) VALIGIA YIRUS SHOPE FIBIDIAA VIRUS (STAAIN KASZA)						_		
	OTEN CA PERIOLIA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA OTEN CA AND MOREN	YALIGU, VRUS SHOVET BIDOM VRUS (STAADN KASZA) TATTERIA VRUS (STAAD GOPENAGEN)								
	POTENCY O	SHOPE FIRMOMA VIDUS (STRAD) KASZA) VARYGRA VIDUS (STRAD) COPENHAGEN)	7							-
	OTEN CS OTEN C	LAPPRING (STRAIN COPENHAGEN)		22.172				-	 	1
	OTEN CO OTEN CO OTEN CO OTEN CO OTEN CO OTEN CO OTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO OTEN COTEN CO		38-65							ŀ
	OTEN CO OTE	VACCINIA VIRUS (STRAIN WIR)	38-65						1	1
	OTEM CO OTEM CO OTEM CO OTEM CO OTEM CO OTEM CO OTEM CO OTEM CIPAS OTE	VANIA A VIETS	36-66						-	i
	OTEN CT OTEN CT OTEN CT OTEN CTO OTEN C	CANCELLA VIDIR (CTB AIM WE)	111-08						_	
	OTEN CO OTEN CO OTEN CO OTEN CO OTEN CO OTEN CIA OTEN CIANA OTEN CIANA OTEN CIANA OTEN CIANA COTEN	CALCANA WALK	11.08							
	OTEN CO OTEN CO OTEN CO OTEN CO OTEN CO OTEN COTEN CO OTEN COTEN COTEN OTEN COTEN COTEN COTEN COURT	CONTRACTOR OF THE PARENTIA CENT	43.69	911-00	Г	152-279		\$75.60\$		
	OTEN CO OTEN CIO OTEN CIO OTEN CIO OTEN CI ASSA OTEN CI ASSA OTEN CI ASSA OTEN CI ASSA ACTOR CI ASSA A	VACUATA VINUS (STRAIN OF CATANOCA)	Ī	2:416	176-205	352-279	289-333	\$75-605		
	OTEN CIO OTEN CIO OTEN CIO OTEN CINAS OTEN CINAS OTEN CINAS OTEN CINAS ACTEN CIONAS ACTEN CIONAS ACTEN CIONAS ACTEN CIONAS MONOLOG	VACCINGA VIRUS (STRAIN WR)	Ī		Т			-	L	L
	OTEN CIO OTEN CIO OTEN CI A33 OTEN CI A33 OTEN CI A33 (OTEN CI A33 COTEN CI A33 KOTEN CI A33 HOMOLOO KOTEN CI A53 HOMOLOO	VACCINIA VIRUS (STRAIN CUPENHAGEN)							<u> </u> 	<u> </u>
	OTEN C10 OTEN C13 OTEN C13 OTEN C1834 OTEN C1834 OTEN C1834 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831 OTEN C1831	VACCINIA VIRUS (STRAIN WR)			:		:	•	:	_
$\Pi\Pi$	OTEN CID OTEN CIPAD OTEN CIPAD (OTEN CIPAD O		136-163		7					ļ
П	OTEN C1/823 (OTEN C1/824 (OTEN C1/824 (OTEN C2/822 (OTEN C2/821 (OTEN	SHOPE FIRECOMA VIRUS (STRAIN KASZA)	3.30	986	227	200			1	-
T	OTEN CIVISA OTEN CIVIS OTEN CIVISA KOTEN CIVISI HOMOLOO KAOR CANSO MOTEN	VACCINIA VIRUS (STRAIN COPENHACEN)	2				I			ļ
	OTEN CIP LOTEN CIVELS HOMOLOG LAKEN CAYES PROTEIN ACKET PRETEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	40-74							\downarrow
T	IOTEM C19814 IOTEM C19814 IOTEM C19819 HOMOLOG CAPED PROTEIN	SHOPE FIREOMA VIRUS (STRAIN KASZA)	26-97						<u> </u>	į
T	OTEN CITED HOWOLOG AND EAST MOTEN TO THE PROPERTY OF THE PRO	VACCERIA VIRUS (STRAIN COPENIACIEN)	72.99							-
	AJOR CAPSID PROTEIN	VANCENCE A VANCE	299-326							
	AJOR CAPSID PROTEIN	TANCELL BARB MOTE AND BOLD	147.874							
٦		LATER CONTRACTOR OF THE CASE OF THE AREST TO A STATE OF THE AREA O	136-170	355-382						
PVCAP HSV6U INC	WAR WE OWN THUS been	MENUTE SINGLES VANCA (1 11% of second control of	148.100							
	MAJOR CAPSID PROTEIN	HEILPESVIRUS SAMULU (STRAIN II)	***	376.000	I			-		L
Γ	DNA-BRODRIG PROTEIN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIKUS	201-102						-	L
	MINOR CORE PROTEIN	HUDGAN ADEMOVIRUS TYPE 2	100						\ 	-
T	MINOR CORE PROTEIN	HUMAN ADENOVIRUS TYPE S	87-114							-
Γ	P2.6 KD PROTED ^I	FOWLPOX VIRUS (STRAIN FP.1)	Ç.		351:-146				-	-
T	PROTEIN DS	VACCINIA VIRUS (STRAIN COPENHACEN)	240-267	335.360						-
T	PROTEIN DS	VACCINIA VIRUS (STRAIN WR)	240-267							1
Days of the	as Arten Int	VARIOLA VIRUS	240-267							1
T	PROTEIN DA	VACCINIA VIRUS (STRAIN COPENHAGEN)	123-150						1	
Т	Mitta Dr	VACCINIA VIBIS (STRAIN WR)	123-150							
PVD09 VACEV	TROIEU DE	VARIOUS A VIBILE	123-166							
	PROTEIN DF	STATES WITH CHECK ACT A LACK A.	16.53							
	PROTEIN DIG	CARACTER TENEDRAL VIEW CITE CONTROL OF THE CONTROL	\$2							
٦	DAA-BINDING PROTEIN	CAMPACA MARINE	287.322							
	PROTEIN ES	VACCA VIEWS	411.4	417.464						L
	PROTEIN EA	VACURA VIND (3) MAN CONTINUES?	1	737.467						-
,	PROTEIN ES	VALLANDA VALUE (STANDA WA)	80.116	167,104	417.464					L
PVEOS VARV	PROTEIN E6	INDICA VICE	60-87							L
1	EI PROTEIN	CHRISTIAN PARAMETER TOPO SA	12.							L
	EI PROTEIN	TORONA PARTICIPANA VANCO 1172 27	160,203							_
	EI PROTEIN	NUMBER OF STATE OF ST	000.00							
	EI PROTEIN	IN IN AND BART I THAN VINIS TYPE 41	23.19							Ц
	EI PROIEM	LANGE AND I CALANTISTYPE 42	25.59							
	EL FAUI EM	Na natali paper 1 change 17 TYPE 47	146-173							
	EI TROTEIN	COMPANY OF THE CONTRACT TYPE 63	31.48							L
	EI PROTEIN	RUPAN PARLUMANING 1176.37								-
	EARLY 25.9 KD PROTEIN	AUTOCIANTIA CALIFORNICA NOCLESIA POETINESSIS VINOS					L			L
	PROBABLE E2 PROTEDY	COLICAI ACEMI (SHOTS) PACILLORA VINCE (SHOTS)								L
PVE2 HPV05	PROBABLE E2 PROTEIN	HUMAN PAPILLUMA VIAUS 1 T.E. S	70.63	146.141		-				ļ
PVE2 HPVI)	E1 PROTEDI	HUMAN PAPILLOMAVIRUS I TPE 13							-	l
PVEZ HPV16	E2 PROTEIN	MUNICAN PAPELLOMAVIRUS TYPE 16	61:10			1	1		<u> </u>	1
	E2 PROTEIN	HIDAAN PAPILLOMAVIRUS TYPE IS	200			\downarrow				\downarrow
	E3 PROTEIN	HEDRAM PAPEL CHAVURUS TYPE IA	30-120	\downarrow				+	-	+
PVE2 HPV2A	EJ PROTEIN	INDIAN PAPILLOMAVIBUS TYPE JA	139-193		1	1	\downarrow	+	+	+
Γ	E2 PROTEIN	HUMAN PAPALOMAVIRUS TYPE 33	5							

	E PROTEIN H H H H H H H H H H H H H H H H H H H	VIRUA RIDAM PAPELDAAVRUS TYPE 33 RIDAM PAPELDAAVRUS TYPE 34 RIDAM PAPELDAAVRUS TYPE 34 RIDAM PAPELDAAVRUS TYPE 34 RIDAM PAPELDAAVRUS TYPE 34 RIDAM PAPELDAAVRUS TYPE 34 RIDAM PAPELDAAVRUS TYPE 34 RIDAM PAPELDAAVRUS TYPE 34 RIDAM PAPELDAAVRUS TYPE 14 RIDAM PAPELDAAVRUS TYPE 14 RIDAM PAPELDAAVRUS TYPE 14 RIDAM PAPELDAAVRUS TYPE 14 RIDAM PAPELDAAVRUS TYPE 14 RIDAM PAPELDAAVRUS TYPE 14 RIDAM PAPELDAAVRUS TYPE 16 RIDAM PAPELDAAVRUS TYPE 17 RIDAM PAPELDAAVRUS TYPE 17 RIDAM PAPELDAAVRUS TYPE 18 RIDAM PAPELDAAV		337-341 (44-13) 106-316 337-341	276-303		+++++	 	+++++	
	E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN E SPROTEIN	NAPELOMANIUS TYPE 39 11 12 13 14 15 15 15 15 15 15 15			106.301		+++++		$\frac{1}{1}$	
77 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	E PROTEIN E PROTEIN				<u>76-101</u>				 	
	ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN ES PROTEIN	IRUS TYPE 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2					+++++		 	
	E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E PROTEIN E S PROTEIN	IRUS TYPE 1 22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		37.361						
	EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE EPROTEIN HE HE PROTEIN H	INUSTYPE 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		11.101	 					
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	E MOTEN E MOTEN	INUS TYPE 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	T 	13.361		$\ $	\parallel			
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	E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E A MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN E MOTEIN	IRUS TYPE 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2								_
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		INVESTMENT	1-108 6-69 6-69 6-69 15-102 15-103 15-103 15-103 15-103 15-103 11-103 11-103			+			_	H
	- 4 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	66-93 15-16 15-102 15-103 15-103 10-10 10-10 11-41 11-41 11-103 11-103			+	†	-	-	L
		INUSTYPE I	15-102 11-97 11-97 101-139 101-00 10-00 11-41 11-41 11-40 11-140			+	1			-
	Z.E.Z.	CRUS TYPE I	15-102 13-51 10-52 10-50 10-60 10-60 11-61 11-61 11-14 11-14 11-14 11-14 11-14			1	1	+	-	ŀ
	Z Z Z	INUSTYPE I	13-91 102-129 10-40 10-40 10-40 11-14 11-146 11-146 11-146				1	1		+
	Z Z Z	TANS TYPE I	102-129 10-60 10-60 10-60 11-41 11-41 11-146 11-146 11-146						-	· ·
	x x x	IRUS TVTE I	10-10 10-10 10-10 11-11 11-10 11-10 11-10				Ī			_
	x x x	// // // // // // // // // // // // //	10-60 10-60 11-41 11-41 11-10 11-10 11-10		1					
	772	/RUS TYPE I	13-60 13-61 13-61 13-61 13-62 13-63 13-103 13-103			Ť	T			
	7.7	IRUS TYTE I	27.54 11.41 15.63 15.63 17.103 11.103		_ :	:		:		_
	2	INUS TYPE I	27.54 11.41 15.63 75.102 66.96 71.102		<u> </u>			-		<u> </u>
$\Pi\Pi\Pi$		IRUS TYPE I	11-41 75-102 66-96 71-102					1		+
$\Pi\Pi\Pi$		iaus Tyre I	13-61 75-103 71-103 11-103				j	 	<u> </u>	<u> </u>
		INUS TYPE I	73-102					_	1	+
П			71-102							
			71-103		†		Ī	-		_
			119:146		1	-	İ		<u> </u> -	
PART HEATS			119-146					-		
Γ			107			-	1	-		<u>i</u>
ENEX LIPUZI			301.6					+		<u>l</u>
Ī			73.90					+		1
Ī			71.102					+		-
		POS VIGEDROSIS VIRUS	620-647			1	1	1	+	+
	П		111-11		1	1		1		\mid
	Т.	TALENCE LANGUA (ATTACAM INDIANAL) (1961)	310-366		†	1		-		-
Γ	ENVELOPE OLYCOPROTEIN PRECURSOR		30.14		†			+		+
Γ	Т.		113.347		1			+		1
		THOSE OF THE ANY COPENHAGEN	11.110	? ?						H
	PROTEDVIA	VACUATA VALIS (STRAN VII)		2.5 2.5 2.5				1		+
r			13-60					+		+
Γ	NA NE MAJOR MENDIALME PRO PRECURSO		13.40					1	-	$\frac{1}{1}$
Ī			101			1		+		+
Ī	PROTEIN F4	VAUCA VIEWS	174-321					$\Big $		\dagger
	PROTEDVIVI	VACCING VIEW COLUMN COL	270-317					$\frac{1}{2}$	+	+
Ī	PROTEDUFIL	VACCINIA VINUS (31) MAIN L-1 V.C.)	134-321							t
T	PROTEIN FIL	VALIOLA VILUS	10.37	113:140	1854-581					\dagger
	PROTEDY #12	VACCINIA VILUS (SI INJIN CUTENTACET)	150	113-140	186-981				1	\dagger
T	PROTEIN FIZ	VACURIA VIAUS (31 MAIN 12:17)	10-33	302-208	554-581				+	\dagger
	PROTEDY F12	VAUGA VICO	35-62	152-179					1	\dagger
T	PROTEDUPIS	VACCORA VIRUS (STIMM COTENANCE)	35.62	152.179					+	†
PROFESSION PROFESSION	PLOTEDI F14	VACCINIA VIRUS (31 KAIN L-1 VT)	<u>×</u>	149-179						\dagger
T	PROTEIN FIG	VANOLA VIDUS	24-13							\dagger
,	PROTEIN FP4	FOWLYOX VIRUS	25	L						+
T	IS KIN PIKTON PROTEDY	ORS VIRUS (STRAIN MZZ)	13.61							+
Ī	A KD FISION PROTEDI	VACCERTA VIRUS (STRAIN COPENNAGEN)	136						+	+
T	KO FISSON PROTEDN	VACCINTA VIDUS (STRAIN WR)	235.232	301-335						+
T	SECTION OF	VACCINIA VINUS (STIAM) COPENHAGEN)	164.19	240-374						+
TOWN TOWN	PROTEIN GI	VACCIMIA VIRUS (STIVAIN WR)	235.353	30.33						1
T	PROTEING	VALIOLA VIRUS	121	-					1	†
Т	REATTHE TSC DEP PROTEIN	VACCINIA VINUS (STRAIN WR)	2	1						1
PVCIII VACE	TO THE PROPERTY OF	VARIOLA VIRUS								

POCEME	1107367814	All Viruses (no becervophages)	П	т	_					
FILENAME	PROTEIN		╗	ABEAL	AKEA L	<u> </u>	ABEAS ABEAS	A ABLAZ	7	
PVOOJ HSVED	GENE 3 PROTEIN	EQUINE HERPESVIAUS TYPE: I (STRAIN ABAP)	2		-	-	:	:	:	:
PVG03 IISVEK	GENE 3 PROTEIN	EQUING HEADESVIAUS TYPE I (STRAIN KIENTUCKY A)	Т	7	T	9				
PVG63 VACCC	PROTEIN GS	S (STRAIN COPENHAGEN)	T	Т	T	201.561			Ī	
PVGOS VARV	PROTEIN GS		T	101-17		11		-	Ţ	Ţ
PVCO) HSVII	HYPOTH GENE 7 MEMB PRO	ICTALIAND HEAPESVIRUS I	M-1		1	+		+		T
PVGOP VACCC	PROTEIN FI	VACCINIA (STRAIN COPEMIAGEN)			-	! :				
PYGOS VACEV	PROTEIN	VACCINIA VIRIIS (STRAIN WR)	101.33		-		-			
PVOCE VARV	PROTEIN FI	VARIOUA VIRUS	2	Ī		İ	-			
MOID STAIR	GENE IZ PROTEIN		200							
PVOID HSVII	HYPOTAETICAL GENE 17 PROTEIN		34.36	T	T			L		
PVOIS HOVE	HYPOTHETICAL CICNE 18 PROTEIN	ICTALUMU TENTRA VIANA I	200.000		T					
MOI SAIR	CASE PROTEIN	SPROPLAND STVINAS D		017101	T			<u> </u> -	-	İ
PVGI SPV4	CAPSID PROTEIN	SPRUPLANA VIRUS 4	T	T	300. 877	76.0 776		-		
PVG11 HSWI	HYPOTHETICAL GENE 22 PROTEIN	ICTALURED REMERSIVENCES I	,	770	†			1		
PVQ24 HSVII	HYPOTHETICAL GENE 24 PROTEIN	ICTALIAND PERTURNS I	V0. 13.	407.030	1	1	+	1		
PVG28 MSW!	HYPOTHETICAL GENE 28 PROTEIN	ICTALUAD REACES TRACES I	Т			T	-			
PVGIR ALEIV	HYPOTHETICAL GZK PRUTEIM	ARIANIA MONGO GALOMOTO ATINOS	ž		Ī	t	-			
PVG3 SPVIR	GENE 2 PROTEIN	STRUTABLE VIEWS STYING B	Т					 		Ì
PVC2 SPV4	GENE 2 PROTEIN	SPIROPLASMA VIRUS 4	J	62.62	01(-70)	1	1			
PVC34 HSV31	HYPOTHETICAL GENE M PROTEIN	ICTALURUD HERPESVIRUS I	27.73				1			
PVG37 HSVII	HYPOTHETICAL GENE 37 PROTEIN	ICTALUND HERPESVIKUS I	442-460					4		
PVG19 HSVII	HYPOTHETICAL GENE 39 PROTEIN	ICTALURUD HEAPESVIRUS I	829-159	1088-1115						
VOTAL ANTENA	HAPOTHETICAL GIL PROTEIN	AMSACTA MODREI ENTOMOPOXVIRUS	13-29							
BINES IDA	CENT 1 PROTEIN	SPIROPLASMA VIRUS SPVI-RIAZ B	15-49							
7/60 10/4	CSNR 1 PROTEIN	SPIROPLASMA VINUS 4	18-52	87.148						
Trace of the control	INVANTURED AT ABOUT AT BEATERN	WERPECVIALIS SAIMINITATION !!	138-165							
	ATTOCKED TO A WAR AT VACABLETIN	ICTAL INDIA AFRIDECVIRUS	Ū	346-373	101.034	913-1007				
PUPLIS DRIVES	HYPOTHETICAL GENE 42 PROTEIN	HEADESVIAUS SALIABLI (STRAIN !!)	366.384							
VOTE ALCOVA	CAR PROTEIN	AMSACTA MODREI ENTOMOPOXVIRUS	153							
1000 PM	GENOR & PROTEIN	SPIROPLASMA VIRUS SPVI-41A2 B	116-146					Н		
PVOST MEVIT	HYPOTH GENE SI MEMORANE PROTEIN	ICTALUAD HEAPESWAUS I	34-61	17.114						
PVG33 HSVSA	HYPOTHETICAL GENE 32 PROTECN	HEAPESVRUS SADATU (STRAIN II)	47-74							
PVGW HIVE	HYPOTHETICAL GENE S6 PROTEIN	ICTALUND HELPESVIAUS I	382-609							
PVOS SPVIR	OENES PROTEIN	SPIRIOPLASMA VIRUS SPVI-RIAZ B	65-92							
PVQ SVV	CLENES PROTEIN	SPRIOPLASMA VIXUS 4	56-83							
PVOLD HSVII	HYPOTHETICAL GENE 63 PROTEIN	ICTALURED HEXPESIVENUS I	550-584							
PVC# HSVII	HYPOTHETICAL CENE 64 PROTEIN	KCTALURD HERPESYDRUS I	477.504				-			
PVG63 HSVII	HYPOTHETICAL GENE 45 PAOTEDI	KTALIAID HEXPESVRUS I	1213-1254							
PVC44 HSVII	HYPOTHETICAL CASHE 64 PROTEIN	ICTALUNID HEILPESVINUS I	362-406							
PVC67 HSVII	HYPOTHETICAL CENE 67 PROTEDY	ICTALURID HELPESVIRUS I	1342-1369							
PVG64 HSVI)	INYPOTIETICAL GENERA PROTEIN	ICTALUAD HEAPESYIAUS I	261-288							
PVG72 HSV11	HYPOTHETICAL GENE 72 PROTEIN	KCTALURID HEAPESYIRUS I	447-481							
PVG75 HSVII	HYPOTHETICAL GENE 75 PROTEIN	ICTALUND PEAPESVAUS I	388-422							
PVO76 HSVII	HYPOTHETICAL GENE 76 PROTEIN	ICTALURD HENVESVOLUS I	200-227						\downarrow	
PVQ7 \$PV4	GENE 1 PROTED	SPIROPLASMA VIRUS 4	14-44							
PVGF! DVB	FI PROTEIN	AVIAN DEECTIOUS BRONCHITIS VIRUS	1230-1260	2406-2435						
TYGE CYBE	E2 GLYCOPAGTEN PRECURSOR	BOVIDGE CORONAVIBLIS (STRAIN F15)	398-426	642-676		1278-1305				
PWG2 CVM4	E2 GLYCOPROTED PRECUASOR	BOVING CORORAVIRUS (STILATA L9)	399-426		1033-1084	1378-1305				
PWGL2 CVILY	E2 GLYCOPROTEDI PRECURSOR	BOYDRE CORORAVILUS (STILAIM LY-1)3)	399-436	642-676	1022-1064 1278-1309	1378-1305				
PVGL2 CVBM	E2 GLYCOPROTEIN PRECURSOR	BOVING CONOMAYINUS (STRAIN MEBUS)	399-426	613-676 613-676	1022-1084	1278-1305			_	
PVGL2 CVBO	E2 GLYCOPROTEIN PRECURSOR	BOVING CORONAVINUS (STILAIN QUEBEC)	399-426	642-676	1022-1064 1278-1305	1378-1305				
PVG13 CVBV	E2 GLYCOPROTEIN PRECURSOR	BOVING CORONAVIRUS (STRAIN VACCINE)	399-426	412-476		1378-1305				
PVGL CVRD	EZ GLYCOPROTEIN PRECUISOR	HUMAN CORONA VIXUS (STRAIN 229E)	110-767	\$69-606	1056-1112					
PVGL2 CVM	E3 OLYCOPROTED PRECURSOR	MUNITURE CORONAVIAUS MAYV (STRAIN WILD TYPE 4)	¥ (3	1030-1093						
PVCL2 CYMAS	E2 OLYCOPROTEDN PRECURSOR	MURENE CORONAVERUS NOVY (STRAIN AS9)	36.5	591-632	92-10		+			
PVGE3 CVAUC	E2 CLYCOPROTEIN PRECURSOR	MARING CORONAVIRUS MAY (STILAIN INDAY / VARIANT CL.2)	3	1030-1092	T	1	+	+		
PVGL2 CVAUN	E2 GLYCOPROTEIN PRECURSOR	MURLINE CORONAVIRUS MAY (STRAIN 1704)	X :X	156-621	1	1		-		

PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS PYGLI CYPIS		VIRUS									
		A STATE OF A LAST MARINE IN CARCHEOPINI SECURITION OF THE PARTY OF THE	٦	1							
	PROTEIN PLECURSOR	PORCINE TRANSMISSIEUR CASTROENTERITIS CORONAVIRUS (STRAIN MILL 60	٦	╗	00-110	1331-1367					
		PARCINE TEANSMISSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN PURA 73-10)		11.000	067-1141 1131-138	(1)					
	ES CE YCOPEOTERN PRECUASON	PORCINE TRANSMISSINGE GASTAGENTFAITIS CORONAVIRUS (STRAIN FURI) 69-107	Ī.	T	139-1165						٤
T		PORCINE RESPIRATORY CORONAVIRUS (STRAIN BOLLYNOW / BALLLISH LICENTING	Ι.	T	1129-1165						•
T			Τ	Г	1067-1143	133-1307				1	1
	A STATE OF THE PRECURSOR	POLCING TLANSPOSSIBLE CASTROLATION CONCINCION (81-102	2								1
T	MONABLE MEMBRANE OLYCOPROTEIN	EPSTEDLEADER VINUS (STRAIN 893-4)		18793	_	1073-1148	=======================================	_			
T	ES OL YCOPROTEIN PRECURSOR	FELING DOECTIONS PENTONITIS VINUS (STRANGARY)	ī	=	1023-1071						1
	S GL YCOPROTEIN PRECURSOR		Т	175.902	1056-1090					1	\downarrow
	S OF VOOPROTEIN PRECURSOR	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	Т	г	1001-1001						1
T.	ES CE VICAMOTEDA PRECUNSOR		Т	175-902	0801-950					1	1
T	ES CE VOCABOTEDA PRECURSOR		Т	۴	056-1090					4	1
	ES CA VOORBOTEDA PRECUMSOR	RUS (STRAIN MAI)	Т	t	Τ-						1
T	CI VCOMPATERNICES TO PRECURSOR		Т	L	440-467	181-170					4
	CICCIONICIONICIONICOS	AIN AD169)	Ţ	Т	Т	832.179		L			
1	A VOTAL I PACAGEOR	.)	1	Т	Т				L		
	CLYCOPILOTEIN B PRELUXUA		× 2.7.2	1					-	_	
PVCLE HEVBI	OLYCOPROTEIN I PRECURSOR		7						ļ		L
Г	GLYCOPKOTEIN B-1 PRECURSOR	(SA)	441-470	934-961						-	-
1	A YCOMOTED B PRECUSOR		426-513 6	616-643					1	-	+
L	A YCOPROTEIN B PRECURSOR		6 017-(17	196-96					-	1	+
1	CH YCOPROYEIN B PRECURSOR		443-470 9	934-961					$\frac{1}{4}$	-	1
T	C. V. COSECTEIN B PRECURSOR		Т	613.960		L				$\frac{1}{4}$	+
Was rove	STATE OF THE PRESENTATION	(0)	Т	20.17		ľ	L				-
Т	CALTCOPROPER BARECIES CO.		Τ.				_	L			-
٦	OT YCUTCHEN B PACKAGO		1						-		
PVCLB MON'S	OLYCOPROTEIN B PRELUXUA		409-510				-		-	L	L
	CLYCOPIOTEIN C PRELUASOR	6	469-510				\downarrow	1	L	L	L
PVCLC HSVIK	GLYCOPROTEDI C PRECURSOR		134-151				1	1	-	L	-
	CLYCOPROTEDIC PRECURSOR		295-122				1	ļ	-		-
	CLYCOPIOIEM OF		200-002	T			-		L	_	L
	GLYCOPROTEDS GPV							1	ļ	-	ŀ
	CLYCOPIOTEDI E PRECURSOR	L VIRUS (STRAIN AS1908)	1	70				1	-		-
	FUSION OF YCOPROTEIN PIECUASOR	(AGEN)	٦	٦	7.0			-	-	-	-
Γ	FUSION OF YCOPROTEIN PRECURSOR			٦	200				+	+	+
	FUSION OLYCOPROTEIN PRECURSOR		132-293	340-367			4		+	1	+
WELF COVO	FUSION CLYCOPROTEIN PRECURSOR	B / STICAIN 18937)	38-65	154-203	42.73	2	1		+	+	+
	FUSION OF YOSPROTEDN PRECURSOR			_ [2 2	2	7	\downarrow	1	+	+
	FLISTON OF YCOPLOTEIN PRECUISOR.	A / STRAIN LONG)	38-65		200	3	200		+	-	+
١.	FUSION OF YCOPROTEDY PRECURSOR	RUDAN RESTRACTOR STATE VALUE (STRAIN RSS-2)	38-65	154-202	213-243	£2.	5		4	+	+
	FUSION OF YOOMOTED! PAECURSOR	HUNDAN RESPUENT ON 1 STIME TO STAND AND HALLE)	226-262					1	-	+	+
PVOLY MEASE	FUSION OLYCOPROTEIN PRECUISOR	MANAGE CONTRACTOR OF THE PARTY	592-102				4		+	\downarrow	+
PVCLF MOLASI	FUSION GLYCOPROTEIN PRECURSOR	WEASLES VIRUS (STRAIN 127-27)	228-262		L				4	+	\dagger
WOLD LORASY	FUSION CLYCOPROTEIN PRECURSOR	MEASURE VICTOR I AMONTON	X of	447.486					-	+	+
WOL LAND!	FUSION GLYCOPROTEIN PRECURSOR	MONOS VILLOS (STRAIN SEL-1)	X A	417486					-	-	+
100 100 1000	FINISH OF YOOPBOTED PRECURSOR	MORES VOLUS (STRAIN BUT ANALA VACCUTE)	Γ	447-486		L				-	+
	STREETS OF VONFROTEIN PRECURSOR	MUDGES VIRUS (STRAIN RW)	Ţ	426.511		L	L			4	4
1000	EL MICH CLYCOPROTEIN PRECURSOR	MUMO'S VITUS (STRAIN SBL.)	151-178	426-512	L	L	L			-	\dashv
TANK I W	FINITION OF YCOPROTEDN PRECURSOR	NEWCASTLE DISEASE VILUS (STRAIN AUSTRALIA VILLE)	11:131	426-512	L		_			-	-
TACK I FOR	FUSION OLYCOPROTED\ PRECURSOR	NEWCASTLE DESEASE VIEWS (STRAIN BEAUDE 115 CV.)	151-178	426-512			_			-	+
CE W NOVOR	FUSION OF YCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN NEWS)	131-178	426-512	L					$\frac{1}{1}$	+
ACA B NOVIA	FUSION OF YCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VICES (STIMMED BY THE COLUMN STATE OF THE CAST THE COLUMN STATE OF THE CAST THE COLUMN STATE OF THE CAST THE CA	151-178	426-512	L				4	1	+
MOL LOW	FUSION OF YCOPROTEIN PRECURSOR	NEWCASTLE LABORAGE VIXOS (STRAIN) A CAGA	151-178	192-219	426-512			-	1	+	+
WOLL NOW.	FUSION CLYCOPIOTEDI PRECURSOR	THE WORLD CHICKAGE VINITE (STRAD) INTRODUCED (STRAD)	151-178	215-200			-	-	\downarrow	+	+
VOL. YOW	FUSION OF YCOPROTEIN PRECURSOR	NEW CASILLA MAGAZA WALIS (TRAIN OLIEBASI AND MA)	151-170	\$15-CC+			4	-	+	+	\dagger
VCL NOVO	FUSION OF YCOPROTEIN PRECUISOR	CHANCACHT B DICEACH VIRIS (STEAD) TEXAS)	181-176	426-512		4	4	+	+	$\frac{1}{1}$	\downarrow
VOLU NOVI	FUSION OF YCOPROTEIN PRECUISOR	CHARLES AND A COUNTY (STATIN TEXAS OB 148)	181-178	436-512		4	4	4	$\frac{1}{2}$	$\left\{ \right.$	$\left\{ \right.$

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TRIGING ACCORDING PROCESSAY MANUAL PRINCE VARIA GENOME LEGISLAND 1917 191	MCCENE		(callendar to the calle	1 7487	ABFA?	APFA 3	ARFAI	<u> </u>	5			
Trained Composition High Control Con	THERAME	PROTEIN		Г	Т	T						
THOSE OF CONTROLS HEALTHOOM HEALTH ALABOLITECAL TIMES (FRANCES)	PVGL NOVO	FUSION OLYCOPROTEIN PRECURSOR		П		109.336				1	•	
THE OWN COMMENTED FRECTIONS HOLDEN PALLING STELLORE STELLOR STELLORE ST	Was Hind	T		Ţ	П						Ī	ŀ
INTEGRIC SECRETORISM PRECURSOR HAMAN PALAMETERS A 7 VIRIS (TRANS 10581A) 10-157 3 18-246 INTEGRIC SECRETORISM PRECURSOR HAMAN PALAMETERS A 7 VIRIS (TRANS 10581A) 10-157 3 18-246 INTEGRIC SECRETORISM PRECURSOR HAMAN PALAMETERS A 7 VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HAMAN PALAMETERS A 7 VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HAMAN PALAMETERS A 7 VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HAMAN PALAMETERS A 7 VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRANS 10581A) 11-151 3 18-246 INTEGRIC SECRETORISM PRECURSOR HEAD A VIRIS (TRAN	MOL POH	T				138-166	63.53					+
NERRON GLYCOPHOTERN RECURSOR NERRON GLYCOPHOTERN RECURSOR	PVCLF PIZHO			1	7	99.	20.5				1	4
FURNOR OLYCOPHOTEN PRECUESOR READAN PALASON FUNDS (FTANT NIT)	THOUS PERH		(STRAIN TOSHIBA)	٦,	Т	907-161						•
PRISON OF COMPOTER PRECINCIAN PROCESSIVE CONTROL OF	PVQLE PILE	T	BOVING PARAINGLUENCA JAIRUS	Т	Т	13.49)						
PRISON OF COPPOSITE PRECINGEN SECON VALIS (FILLAN FOLLOWS) 15.10	PVGC PUR	T	HUMAN PACAIN COURTS 3 VINCE (STACIN MILL STACE)	Т	Т							
115-05 115-05	War Line	1		Т	\$6.50							
FIGENIA GLYCONOTION PRECESSIST SEGOLA VILLA (FILLAND PRESENT) 121-149 (11-24) (10-24) 11-244 (11-24) (11	Will a street	T		Т	Т	180-503						
THENG GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) THESP GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) THESP GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) THESP GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) THESP GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) THESP GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) THESP GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) THESP GLYCOMPTER PRECURSOR SEGON VILLS (TRANSPO) SEGON VILLS	AVE STATE	T	SENDAL VILLS (STRAIN FUSHDA)	Т	Т	180-507						
INTERIOR OF TYPOTOTES PRECINGUE	Mary Same		SENDAL VIBLIS (STEADY HARUS)	Т	Т	180-507						
155000 GUYODROTEN PECURSON 155000 VILLES (TELAN VILLE) 151-244 151-2	Was tomi		SENDAL VIRUS (STRAIN HV))	122-149	Г	180-507						
15.00 CH 10.00 CH	PVGLF SENDY	FUSION OLYCOPROTEIN PRECURSOR	SENDAJ VIRUS (STRAIN Z)			480-507						
THEORY OF YORDSTORN PRECURSOR STRAIN OF THE STRAIN OF	PVC2 5 SV4	FUSION OLYCOPROTEIN PRECURSOR				459.496						
FIREGIA CYCOPROTERS PRECINGED FULL NOW HERECALSON THACK THAN WILLS THAN	PVGLF SVS	FUSION GLYCOPROTEIN PRECURSOR		П	П							
STATE OF COPENIES OF COPENIE	PVGL TRIV	FUSION OLYCOPROTEIN PRECURSOR		124-161	╗	457-414						
	PVGLO BEFV	SPIKE GLYCOPROTEIN PRECURSOR		523-557								
MAJON RIPACK GLYCOPROTEIN O MICHAN RESIDATION STRICTLY VINUS (STRAIN REGISS) 65-157	PYCELD BREVC	MAJOR SURFACE CLYCOPROTEIN G	T	20.5								
MADOR SUBFACE GLYCOPROTEIN OF HUMAN REPRINTED STRAIN SUBJECT STR	PVCLO SOLVI	MAJOR SURFACE CLYCOPROTEIN O	Т	101.77								
ALVORAGIEN PRECINGE 1904.00 19	PVGLO IOUSVA	1		20.273					L			
CATCOMOTERN OF PLECTUSON EQUING FELD-EXVBLB FTPE	PAGE DINAS	T	RAIN BASO)	66-93								
CLYCOPROTEIN OFFECUSOR EQUIDE HEDPESVBLIS TYRE (STRAIN ABAP) 191-10 SPREE GLYCOROPIEM PRECUISOR ALGINE HEDPESVBLIS STREET 191-10 SPREE GLYCOROPIEM PRECUISOR ALGISTAL AL STRAIN STRAIN STRAIN GLASCONI) 173-49 191-13 GLYCOROPIEM PRECUISOR MINAJO PRECUISOR 191-13 191-13 GLYCOROPIEM PRECUISOR MINAJO CYTOREGALOVRUS (STRAIN AD169) 105-13 100-13 GLYCOROPIEM PRECUISOR MINAJO CYTOREGALOVRUS (STRAIN AD169) 111-11 GLYCOROPIEM PRECUISOR MINAJO CYTOREGALOVRUS (STRAIN AD169) 111-11 GLYCOROPIEM PRECUISOR MINAJO CYTOREGALOVRUS (STRAIN AD169) 111-11 GLYCOROPIEM PRECUISOR MINAJO CYTOREGALOVRUS (STRAIN AD169) 111-11 JA POLYPROTEIN PRECUISOR MINAJO CYTOREGALOVRUS (STRAIN ED17) 111-11 JA POLYPROTEIN PRECUISOR MINAJO CANA YOUR (STRAIN ED17) 111-10 JA POLYPROTEIN PRECUISOR MANTAAN YOUR (STRAIN ED19) 111-10 JA POLYPROTEIN PRECUISOR MANTAAN YOUR (STRAIN ED19) 111-10 JA POLYPROTEIN PRECUISOR MANTAAN YOUR (STRAIN ED19) 111-10 JA POLYPROTEIN PRECUISOR MANTAAN YOUR (STRAIN ED19) 111-10	ACCES OF THE VIEW	CHANGE OF THE CAR COM	EDAMME PURPES VIRUS TYPE 4	271-298				L				
SPEEG CLYCOPROFER PRECUSOR AMBIES VIRIS (STALM STREET) SPEEG CLYCOPROFER PRECUSOR VASCALAL STRAMS (SEROTYPE PROIANA / STALIN GLASCOW) 172-49 SPEEG CLYCOPROFER PRECUSOR VASCALAL STRAMS (SEROTYPE PROIANA / STALIN GLASCOW) 172-49 SPEEG CLYCOPROFER PRECUSOR MAJANI CYTOMEGGLALOVRUS (STRAIN TOWNE) 160-135 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 161-135 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR REPRESIDUES (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR RANTAAN VIRUS (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR RANTAAN VIRUS (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR RANTAAN VIRUS (STRAIN TOWNE) 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER PRECUSOR ROSPECT FILL VIRUS 171-111 GLYCOPROFER POLYTROFER PRECUSOR 171-111 GLYCOPROFER POLYTROFER PRECUSOR 171-111	NAME OF STREET	CI VOOPEOTEN O PRECUESOR	EDUTINE HERDPESVIKUS TYPE I (STRAIN ABAP)	383-410								
SPECE GLYCOPROTED PRECINSOR VERECULAL STOANTINS VIRIS (EROTYDE FOUNAN / STAND CLASGON) 147-149	TVILLE ENEVT	SPIKE CLYCOPROTEDY PRECURSOR		489-519								
CALTOPROPED RECURSOR ENFERTMAN PRIASE (19-13) 100-135 CALTOPROPER PRECURSOR MICHAN CYTOGGOLOWIUS (STRAIN GS) (19-13) 100-135 100-135 CALTOPROPER PRECURSOR MICHAN CYTOGGOLOWIUS (STRAIN GS) (19-13) 100-135 100-135 CALTOPROPER PRECURSOR HOLAGA CYTOGGOLOWIUS (STRAIN GS) (19-13) 100-135 100-135 CALTOPROPER PRECURSOR HOLAGA CYTOGGOLOWIUS (STRAIN GS) (111-135) 100-135 100-135 ME CATTORIO SEN PRECURSOR HOLAGA CYTOGROLOWIUS (STRAIN GS) 100-130 100-135 100-135 ME CATTORIO SEN PRECURSOR HOLAGA CATTORIO SERVICE STRAIN GS 100-130 100-130 100-130 ME CATTORIO SEN PRECURSOR HOLAGA CATTORIO SERVICE STRAIN GS 100-130 100-130 100-130 ME CATTORIO SEN PRECURSOR HOLAGA CATTORIO SERVICE STRAIN GS 100-130 100-130 100-130 ME CATTORIO SEN PRECURSOR HOLAGA CATTORIO SERVICE STRAIN GS 100-130 100-130 100-130 ME CATTORIO SEN PRECURSOR HOLAGA CATTORIO SERVICE STRAIN GS 100-130 100-130 100-130 ME CATTORIO SEN PRECU	PWALD VSVIO		VESICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN GLASGOW)	П								
CGLYCOMOTERN PRECURSOR HOLANA CYTOMEGALO/DVBUS (STRAIN SOLID) 105-134 20-277 CGLYCOMOTERN PRECURSOR HERFES SEMPLEX VRUS (STRAIN GS) 62-89 150-401 CGLYCOMOTERN PRECURSOR HERFES SEMPLEX VRUS (STRAIN AD169) 47-111 GLYCOMOTERN PRECURSOR HERFES SEMPLEX VRUS (STRAIN AD169) 47-111 JE CALVORMOTERN PRECURSOR HUNYANDUS GERAGISTON 113-130 JE CALVORAGIERN PRECURSOR BUNYANDUS GERAGISTON 113-130 JE CALVORAGIERN PRECURSOR BUNYANDUS GERAGISTON 113-130 JE CALVORAGIERN PRECURSOR BUNYANDUS GERAGISTON 113-130 JE CALVORAGIERN PRECURSOR BUNYANDUS GERAGISTON 113-130 JE CALVORAGIERN PRECURSOR HANTANA VRUS (STRAIN ED.) 15-102 JE CALVORAGIERN PRECURSOR HANTANA VRUS (STRAIN ED.) 15-102 JE CALVORAGIERN PRECURSOR HANTANA VRUS (STRAIN ED.) 15-102 JE CALVORAGIERN PRECURSOR HANTANA VRUS (STRAIN ED.) 15-102 JE CALVORAGIERN PRECURSOR HANTANA VRUS (STRAIN ED.) 15-102 JE CALLAGIERN PRECURSOR HANTANA VRUS (STRAIN ED.) 15-102 JE CALLAGIERN PRECURSOR	FVCCH EBV		EPSTEIN BARK VIRUS (STRAIN 805-8)	Т	19-648							
CLYCOPROTEIN HECURSON HEAPES SIGNEY VALUE (STRAIN GS) 131-19	PVCEN HOLVA		MUMAN CYTOMEGALOVINUS (STRAIN AD169)	07.136	170-207						Ī	
CLYCOPROTEIN PRECURSOR REAPERSTRUCK ACTION (STRAIN AD169) 318-415 31	WOH HOW		HUMAN CTICMEDALUVIRUS (SINAIN TOWNE)	Ţ	107 091							
GLYCOPROTEIN PRECURSOR HUMANY CYTOREALDVING STRAIN AD169) 47:111	PVGLH HSV60	CL YCOPROTEDN H PRECURSOR	MEMPES SUMPLEX VIXUS (1175 of STAKIN US)	1								
MOCYPROTEIN PECUNSOR BUNYAVRUS GEALISTON 113-1515	WOLK HOWA	CLTCOTROILLY H FRELUXOR	INDIANA PYTOLIFCAL OVER 15 (STRAIN AD 169)	111.49	Ī							Ĺ
W POLYPROTED PRECINSOR BUNYANDRIA VRIUS 11,199 11	AND HOW	LI POLYMONTEN PRECIENCE	hiby Ayrus GEARSTON	\$12.546	14.94	1128-1255	L					
W WPQLYPROTEIN WECURSON BUNYAANVELA VRUIS 194-174 194-174 194-174 194-174	L PAIR TOA	M POLYPROTEDY PRECUASOR	BUNYAVRUS LA CROSSE (ISOLATE L'14)	913.950	П							
W MOGYPROTED PRECIDES DUCABLY VALUE (STRAIN B-1) 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100 619-730 17-100	PVGLM BUNNY	M POLYPROTEIN PRECURSOR	BUNY AKWERA VIRUS	340-374	П	682-709						
M POL VPROTEEN PRECINSOR MAYTAAN VOUS (STALIN HOLD) 75-102	PVCLM DUGBV	M POLYPROTEDN PRECURSOR	DUCAE VIRUS	248-972								
M POG TYROTEN PRECURSOR MAYTAAN YOUS (STRAIN LED) 15-102 15-102 15-102 16-102 1	PVCLM HANTE	M POLYPROTEIN PRECURSOR	HANTAAN VIRUS (STRAIN B-1)	82.7	827.780							
MOCYPROTERN PRECURSOR MAYTAN VIRUS (STAUN *LLE) 75-104 75-	PYGLM HANTH	M POLYPROTEIN PRECURSOR	HANTAAN VELUS (STEALM HOJO)	70.4								
MOC TROTTEN PLECUASOR PROSPECT HOLL VRUS MOC TROTTEN PLECUASOR PROSPECT HOLL VRUS MOC TROTTEN PLECUASOR PROSPECT HOLL VRUS PROSPECT HOLD VRUS PROSPECT HOLD VRUS	Walk Harm	M FOLTFROILE PRELUESOR	HAMILAND VINUE (470 AND 74.110)					_				
M. MC TRADER PRECUISOR PLOBALA VILUS MOST PROTECT HILL VILUS M	WGW HWIN	M POLYFROIGH PRELUKSON	INCOLUMN MECHANIC CONT.	114164	1069-1107							
H. HOLYMOTERN PRECUESOR PUBMALA VIRUS (STRAN HALLINAS BI) 72-110	PVGLM DASV	IN THE THROTEIN PRECUESOR	PARAMETERS REMOVED TO THE PARAMETERS OF THE PARA	8.99								
W POLYMOTED FECURSOR PUDALLA VRUS (STRAN) SOTRANO 73-110	SUCE IN WHALE	M POLITON PER PRECIESOR	PUBLIALA VILUS (STRAIN HALLINAS BI)	72.110			L	L				
M POLYPROTEIN PLECUAGOR SECOL VILLIS (STALIN BA-19) 111-540 691-720	PVC N PUBLIS	M POLYPROTEIN PRECURSOR	PUDMALA VIRUS (STRAIN SOTKANO)	72-110								
M POL VPROTEIN PLECUAGR SECUL VILLS (STRAIN R.2.) 73-100 513-540 504-721	PVCLM CROUP	M POLYPROTEIN PRECURSOR	SECUL VIRUS (STRAIN ED-19)	513.540								
M PGLYPROTEIN PRECURSOR SECOL VELUS (STAALN SR.11) 71.100 311.140 904.211 NONSTRUCT CHLYCOPRO GAS PRECURSOR BENNE WALE FEVER VIRUS 131.544 144.17	WILM SEOUR	M POLYPROTEIN PRECURSOR	SECUL VIRUS (STRAIN R22)	73-100	ГΙ	121-169						
MONSTRUCT GLYCOPRO GNS PRECURSOR BOYDE EPREMEALAL FEVER VIRUS PERCORES GLYCOPRO GNS PRECURSOR BOYDE EPREMEALAL FEVER VIRUS GLYCOPROTEIN PRECURS GLOWN ALENANDER CANAGE CANAGE CANAGE CANAGE PRECURS GLOWN ALENANDER CANAGE CANAGE CANAGE CANAGE PRECURS GLOWN ALENANDER CANAGE CANAG	PVGLM SEOUS			33.100	1	694-721						
PERÍODER GLYCOPROTER PREUMAOR BEANE VALUS GAYCOPROTER PREUMAOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPROTER POLYMOTER PRECUNSOR GAYCOPR	PVGLN BEFV			23.55								
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GLYCOPROTEIN POLYNOTEIN PRECURS (AND KAND) GLYCOPROTEIN POLYNOTEIN PRECURS (AND KANDA) GLYCOPROTEIN POLYNOTEIN PRECURS (AND KANDA) GLYCOPROTEIN POLYNOTEIN PRECURS (AND KANDA) GLYCOPROTEIN POLYNOTEIN PRECURS (AND KANDA) GLYCOPROTEIN POLYNOTEIN PRECURS (TACARDE VOUS)	PVCLY JUNDY	GLYCOPROTEIN FOLYPROTEIN PRECURS.	JUNE ALERAVEUS	7								
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GLYCOPACIEM POLYPROTEIN PRECURS FICHINGS AREAN VALUE GLYCOPACIEM POLYPROTEIN PRECURS FACULATION (199-116	PVGLY MOPE	GLYCOPROTEIN POLYPROTEIN PRECURS.	DMOPELA VIRUS		316-346							
GLYCOPKOTELN POLITYKOTELN PRECONSALTALSOME VINOS	PVG.Y PIARV	CLYCOPROTEIN POLYPROTEIN PRECURS	PICHINGS ALENA VICES	100.100	91,				\downarrow			
	PVGLY TACV	GLYCOPROTEDY POLYPROTEIN PRECURSO	TACALIBE VIRUS		105-230							

	THE STATE OF THE S	ESTALIN DG) BRS-4) OKE) PHIAGEN ENHAGEN ENHAGEN	107-317 107-318 107-318 106-149 136-319 136-319 137-166 113-166 113-166 113-166 113-166 113-166	+++					
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	NA PEDCASE II NA PEDCASE II NA PEDCASE II ERALY PROFEM!	VACCINIA VIKUS (STRAIN COPENHADEN)	146.180						$\frac{1}{1}$
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Ī	NA WELCASE B NA WELCASE B NA WELCASE B EACALY MOTED!	WALLAND TO THE STATE OF THE STA	290-317	X1-575 S	593-633	-			+
		VACCINIA VICUS (STIVALM CUPERTANCEM)	Ī	542.575	593-632				1
Ī		VACCINIA VIDUS (STRAIN WR)	T	T	CO1 A13				_
Ì		U. A. 170 X	٦	7					
		CONTRACTOR OF STREET	261-288						-
Γ		MULINE CT I CHECKEN THE CONTROL OF T	155-315						1
1000		ONOYIA PERIOTSUCATA MILITICATSID POLITICATSUS VINCES	Т	007-171					
1		AITTOCHAMIA CALIFORNICA MUCLEAR POLYHEDROSIS VIKUS	Т		\dagger	-	-		
VIEW NOVAC IE-NEE		THE TANK AND REPORTED THE PROPERTY OF THE PROP	62-23		1				-
WINTER VIEW		ALL ALL DA MANAGE WITH WASHINGTON ATE AGM / CLONE GRU-1)	2-36		1	1			
		SUCIAN DEMINISTRATION OF THE ABOUT THE ABOUT	147.174						\dagger
		EQUINE HELDES VILLUS I YPS I (3 FALIN ABAY)	103						+
	PATECRAL MEMBRANE PROTEIN	HERPESVIKUS SAINGIN (STIKADY 11)	8					_	-
	Γ	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI				-	L		_
MINISTER SALES		VACCIDITA VILLE (STILAIN COPENGIAGEN)	*	T	\dagger				
1		VACCINGA VIBUS (STRAIN WR)	2		1				-
		VARIAN A VIRUS	2		1	+			ŀ
VAL VALV		CATHACTAR BARBIT (SUCPE) PAPILL CALAVIRUS (STRATN KANSAS)	111-113		1		1		-
			38-45						+
VI I FPVI. PROBL	PROBABLE LI PROTEIN	AVIAM PARLUMA TINUS TO THE	154-392						+
	PECTE ALL PROTEIN	HUMAN PAPELLOMA VIRUS 1 TPE 6	310			L			
	MILLIA I I DECITION	HUMAN PAPELOMA VIRUS TYPE II			+		-		
	Thursday of the Original	HUMAN PAPELOMAVIBUS TYPE 33	2						ŀ
	Male Li rivorcio	INDIAN PAPELOMANDUS TYPE 41	345-377			1			-
	PROBABLE LI PROTESS	THE LAND BABILITADA VIRIES TYPE SI	19.46				1	-	
VLI HPVS1 PROB	ABLE LI PROTEIN	THE AND THE CALL CORES TARES AT	45.72						\mid
Ī	PLOBABLE LI PROTEIN	INCHANGE OF A STATE OF THE STAT	407.445						+
VI 1 HOVIA PROB	PROBABLE L2 PROTEDM	HUMAN PACIFICATION CANADA CONTRACTOR	415.442						
	PROBABLE 1.2 PROTEIN	HUKAN PAPILLUNAVIDUS 1 TE 41	136.357					-	1
١	ACTION CORE PROTEIN LANGEDA 3	REOVERUS (TYPE 37 STRAIN DEALING)	110,157						
T	Amine Cour PROTEIN LAMBOA 3	REOVERLIS (TYPE 1 / STEALN LANG)		(37.363					
	7.00	TOUR DIDESCENT VINUS	301		1	-			ŀ
	THE PROPERTY OF THE PARTY OF TH		250-317						
_	ACNOR VIDION STRUCTURAL PROJECT		625-662					1	t
e	MAJOR VIRLON STRUC PROTEIN MU-17MU	HCOVENS TITLE STATE TO SERVICE	624-661						
Γ	ON VIBION STRUC PROTEIN MICHARD	L. REDVIKUS (TTPE 37 81 FAUN DEADAND)	177 767						4
J	LANGE WRITIN STRIPE PROTEIN MULIANUM	HREOVIRUS (TYPE 2 / STRAIN DS/ONES)		20,000	107.757	997109	-		
T	N-DY NATIONAL IN THE PARTY NO.		2	2	Т			-	-
٦	MAKA MASARAMAN		75-127						1
٦	TILL GCTCUPPLIED MA	LY INJANA RESERVATION SYNCYTIAL VIRUS (STRAIN A2)	124-151						t
	MATRIX GLYCOPROTEIN MA	SOUTH SECOND A YOR Y SYNCYTIAL VIRUS (STRAIN AS 1904)	219-246			-			t
	MATRIX PROTEIN	BUTING MATCHES AND A CONTOUR VIBILE (STRAIN A2)	219-246						1
	MATRIX PROTEIN	HUMAN KESUA I OM I STACT I DE CONTROL OM I DE	151-185						
Γ	MATRIX (A) PROTEDY	DOLUMACA C VICOS (SI INAM CIRCO)	247.274			-			
Ī	LATEUX PROTEIN	NEWCASTLE DISEASE VIXUS (STRAIN AUSTRALIA: VICTORANIA)	121			-			
T	THIN PROTEIN	HUNCH PARAMETURIZA 3 VIRUS (STRAIM TOSHIBA)							

ومن دود	1.67-17804	All Viraces (as bacteriophages)	П	П	\Box			1 2 4 4 6 7		
FILL NAME	PROTEIN	YIRUS	J	1	7	1	_			
PVACAT PUB	MATRIX PROTEIN	BOVING PARAINGLUENZA I VIRUS	101-23		1		†			
PVMAT PUM	MATRIX PROTEIN	HUMAN PARADITUENZA I VIRUS (STRAIN NIII 4788S)	167-102		1		╁		1	
PWAAT SVAI	MATRIX PROTEIN	SDALAN VIRUS 41	200				1	1		
MAY! CYBIN	Es di Voorgotein	BOVING CORONAVIRUS (STRAIN MEBUS)	80C				t	1		Ţ
PWG! CVTKE	EI GLYCOPROTEIN	TURKEY ENTERIC COROMAVIRUS	175.209		Ì		+	1		1
l	EI GLYCOPROTEIN	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN 642)	1	-		+	†			ŀ
	EI GLYCOPROTEIN	AVIAN DOECTIOUS BRONCHITIS VIRUS (STRAIN MEAUNETIE)	T		1	†		-		1
L	EI CLYCOPIOTEIN	AVIAN DEECTIOUS BRONCHTIS VIRUS (STRAIN BEALTHEITE NAT)			1		T	-		
l	EI CLYCOPROTEIN	AVIAN BRECHOUS BRONCHTIS VIRUS (STRAIN KRISS))	T			1	1		1	
PWO CAME	MOVEMENT PROTEIN	CALL IFLOWER MOSAIC VIRUS (STRAIN CALIBAI)	Į.	;		:	<u>:</u> :			-
PVALP CAMPO	MOVEMENT PROTEIN	CAULD'EDWER MOSAIC VIRUS (STRAIN DAI)	٦	20.2	2		i	-		
PAG CLAME	MOVEMENT PROTEIN	CALL IFLOWER MOSAIC VIRUS (STRAIN BBC)	Т	27.17			1		1	:
TWO CLIM	MOVEMENT PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN NYBIS)	2	*			1	+		i
PWD CUWS	MOVELERY PROTEIN	CAILIFLOWER MOSALC VIRUS (STRAIN STRASDOURG)	20.25	277.734		1		1	-	
PYNO CUM	MOVEMENT PROTEIN	CALLIFICATE MOSARC VIRUS (STRAIN W260)	× 2.0	2		<u> </u> 	<u>:</u>		:	
PWG CEAV	MOVEMENT PROTEIN	CALMATION ETCHED RING VIRUS	3	2	T	i		<u> </u>	-	:
PARP SOCIA	MOVELENT PROTEIN	SOYBEAN CALOROTIC MOTTLE VIRUS	-			+	†	1		
PVASA HEBIE	ALAJOR SURFACE ANTIGEN PRECURSOR	HEACH HEPATITIS B VIRUS			-	+	<u>;</u>		:	:
PVATI DHVII	MATRIX PROTEIN I	DHORU VIRUS (STRAIM INDIANULLIAM)	Т	277.76		1	+			
PVACTE MYXVI.	M-18 PROTEIN	MYXONA VIRUS (STRAIN LAUSANNE)	8			1	1			Ī
PUNCTS MATERIAL	MT-9 PROTEIN	MYXOMA VIRUS (STRAIN LAUSANNE)	407-407				+	<u> </u>		:
PANSA BOTTIC	NONSTRUCTURAL PROTEIN NS34	PORCINE ROTAVIRUS (GROUP C / STRAIN COWDEN)	<u> </u>				1	+	\ 	
PWACH PAVISO	PROBABLE MONCAPSID PROTEIN NPI	BOVING PARVOVIRUS	49-136				1	1		
PWC ABVO	MONCAPSID PROTEIN NS-1	ALEUTIAN KINCK DISEASE PARVOVIRUS (STRAIN G)	86-148		Т	Т	Т			
PVNCS AEDEV	MONCAPSID PROTEIN NS-1	AEDES DENSONUCLEOSIS VIRUS (STRAIN GKV 002 002)	7	279-319		219-612	760-817	871.72		
TANCS MARKEN	NONCAPSID PROTEIN NS-1	MUNINE MINUTE VIRUS (STRAIN MYA!!)	3	26.2.289			1			
PYNCS MUMON	HONCAPSED PROTEIN NS-1	MUNIOR MANUTE VIAUS	3.62	262-289			1			
PYNCS PAYIG	NONCAPSED PROTEIN NS-1	HUBLAN FARVOVIRUS B19	2				\dagger	1		Ī
PANCS PAVIET	NONCAPSID PROTEIN NS-1	HAMSTER PARVOVINIS HI	7	70, 07,	***	\dagger	1			
PVMCS PAVPN	NONCAPSID PROTEIN MS-1	POSCINE PAR VOVIRUS (STRAIN MADI-2)		2	2		\dagger		-	
WASI DOW	MONSTRUCTURAL PROTEIN NS	ENZOOTIC REMUMERATALIA (MAEANE VIRUS (SERVI) TTE 27 STRAIN ALTERATOR					 		-	
PASI LALA	NOMSTRUCTURAL PROTEIN MSI	DATE LIESTA A VINCE (STRUM AND AND AND MAKE)	171-198		T		t			
MASI WARM	MONSTRUCTURAL PROTEIN PS	INCLUSION A VIDER (STRAIN ACHII \$1/4))	171-196							
PWS! IACH	NONSTRUCTURAL PROTEIN NO	INTERIOR A VIETE PETAIN ACTION FROM ANY NAVIO	171-198		Ī			-	_	
WASI MOXO	NONSTRUCTURAL PROTEIN NS	INTEREST A VALIS (STAD) ACHICLEMIA AND ()	166-195							
PUNCT IN DAY	MONETH INTEREST PROTEON NS.	INTLIENZA A VIDUS (STRAIN ADUCKVALBERT ANSOTIS)	171-198							
PVNSI IABOM	NONSTRUCTURAL PROTEIN NS!	INFLUENZA A VILUS (STRAIN AFORT MONMOUTIVIM?)	171-191						-	
PANS) IAFOW	NONSTRUCTURAL PROTEIN MS!	INTLUENZA A VIEUS (STRAIN AFORT WARREWIYS)	171-198				1			
PWSI MEI	NONSTRUCTURAL PROTEIN NSI	DATLUENZA A VIRUS (STIAIN A/LENINGRAD/134/3)	171-191				1			
PVHSI_LALAA	MONSTRUCTURAL PROTEDN NS:	DIGITIES A VIDUS (STRADY AMALLARDYALBERT ANS/16)	171-198				\dagger		+	
PVKSI LAPII	NONSTRUCTURAL PROTECN INSI	DOLUENZA A VIKUS (STIVAN APINTALUALBERTA/121/79)	171-198				1			
PVNSI_LAND	NOWSTRUCTURAL PROTEIN NSI	INCLUENCA A VIRUS (STRAIN AFFINI ALLALBERTAN)	K				1			
PWSI IATED	MONSTRIPCTURAL PROTEDNINS	INCLUENCE A VICTOR (STRAIN A TOWNER THE INCLUENCE OF THE PROPERTY OF THE PROPE	111.104				T		-	I
PWSI INTIC	NONSTRUCTURAL PROTEIN NS	INCLUENCE A VICES (STEAM ATTENDED INCLUENCE)	191.198				 		_	
AND MIKE	ACCRETE THE AT BROTTER MS	DEFI (FRIZA A VIBLIS (STRAIN AUDORNIO)772)	171.198							
PANEL MANEE	MONSTRICTION PROTEIN NS	DRELUENZA A VIRUS (STRAIN AAUSSIK9077)	171-198			-				
PANCE BOND	MONSTREATTURAL PROTEIN NSI	DOLUENZA B VIRUS (STRAIN BAPAN9)	171-196							
PWG ATCA	NONSTRUCTURAL PROTEDI MS2	INTLUENZA A VIRUS (STRAIN A/TURKEY/OREGON/11)	87-114						·	
PANESS DOLLE	HONSTRUCTURAL PROTEIN NS2	DYFLUENZA B VIXUS (STÅKAIN BALEE/40)	81-18							
PVNC DOYA	NONSTRUCTURAL PROTEIN NS2	INTELENCA B VIRUS (STRAIN BY AMAGATAIM)	21.73						 	
PVNS1 Becli	NONSTRUCTURAL PROTEIN NS2	INSTLIENCA C VIRUS (STRAIN CILVO)	21.9							
PVAKS CVPFS	NONSTRUCTURAL PROTEIN 3-1	PORCONS TRANSLOSSIBLE GASTROENTERITIS CORONAVIRUS (STRAIN FS772					†	1	-	
PWSA CWD3	NONSTRUCTURAL PROTEIN A	HUMAN CONORAVINOS (STRAIN 229E)	2 3				\dagger		+	
PAGA ILEV	MONSTRUCTURAL PROTEIN 784	CANNO BATERIO CORONAVIRIIS (STRAIN X 178)	7				T	-	+	
PWS) CVCA	NONSTRUCTURAL PROTEET !	LANGE ENTENE SONO TOTAL CONTRACT								

PCCENE	107217014	All Viruns (so bacteriophages)	LENA LENA	AND LAND	ANIA - ANIA	N. STATE	OHEAT AN	रुप्तर रुप्तर
¥	ROTTIN	VIKUS	7	1				
Γ	MONSTRUCTURAL PROTEIN 7	PELINE ENTENCE CONTRACTOR OF STROET STATES CORONAVIRUS (STRAIN FS773	34-61			-	:	_
PVNS) CVPFS	NONSTRUCTURAL PROTEON?	THE THE TAKE WESTER OF THE WITH THE CONDINAVIRUS (STRAIN PURI)	146		;			
Г	NONSTRUCTURAL PROTEIN ?	TORCING INAMESTICAL CONCONNICIONAL	1991		1	:	<u>!</u>	
	NONSTRUCTURAL PROTEIN 7	TOALINE MICE TO SEE TONITIS VIRUS (STRAIN 79-1146)	Ĩ					-
	HONSTRUCTURAL PROTEIN 7	PELINB MY CUITOR CONTRACTOR (STRAIN CI. 1483)	41.35	1				
	NONSTRUCTURAL PROTEIN C	HORAN TAXABLE COLORS (STRAIN NIM 17815)	56.99					-
PUNC MIN	NOWSTRUCTURAL PROTEIN C	HUMBAN CANADA COLOR CANADA CAN	162-296		1			-
PANEL DEV	NONSTRUCTURAL PROTEIN NS-M	DAPATIENS PELROIR, SPOT VINOS	57-84	-	<u> </u> -	: 1		: - !
SAME AIRST	NONSTRUCTURAL PROTEIN NS-S	BUNYAVRUS LA CRUSSE	146-180	_				
1000	MONSTRUCTURAL PROTEIN NS-5	TOSCANA VITUS	111.164					1
3	701100000000000000000000000000000000000	ENOLA VIRUS	100		-			
PYNCE EDOV	MULEUTROIEIN	INFI LIENZA A VIRUS (STRAIN AVANAS ACUTAPRIMORUE/695/76)	200-07					
PVMUC IMANA	MICLEOFICIEIN	PACE TENZA A VIRTIS (STRAIN AANN ARBORUSES)	378-403					
PVAIL IAAM	MACLEOPROTEIN	AMELIENZA A VIBITS (STRAIN A/BRAZIL/11/78)	378-403			-		
PUNC IABIA	NUCLEOPROTEIN	THE COLUMN AND THE PARTY AND AND THE PROPERTY OF THE PART	378-405			+		
PWATE WALLS	MUCL EOPROTEIN	INTURE A TANGET OF THE AIR A IN TAILED TO A INTURE AIR A	378-405					:
BUNKIN IAPAI	MUCLEOPROTEIN	INCLUENCA A VIACO (STANIS CONTRACTOR AND	378-405					
The state of	MINISTEDA	INFLUENZA A VIRUS (STRAIM ACTITUDE CONTROLL OF ALL ALIAN)	378-405					1
TANK MAN	MONTH FORMOTEDA	INFLUENZA A VIRUS (STRAIN ACTUCKENTERNS IL VANDO	178.405					1
ACC. MC.	NA CALE COMPANY	INFLIENZA A VIRUS (STRAIN ADUCECAUSITALIA 1978)	118.405					1
PWGC IADAU	AUCTEURALEM.	INTLUENZA A VIRUS (STRAIN AMOUCIC/BEIJING/I/TI)	330 406		_			
PYRIC INDRE	KUCLEUTKUICA	INSTITUTION A VIRUS (STRAIN ADUCKICZECHOSLOVAKIA))	2000	+				_
PWACE LADOR	NUCLEOPROTEIN	CHEST WAS A COST OF THE AND AND CHENCLANDY!	376-405	1	1	 -		
PVALIC IADE	MUCI EOPROTEIN	MALLOS AND	331-405		1			
TOTAL LANGS	MINIST FORBOTEIN	INTLUENZA A VIKUS (SI PALIT MUNICIPALITY MONTHS)	378-405	_				1
THE PARTY OF THE P	Manual Ma	INSCUENZA A VIRUS (STIALIN ANDU-ANDUM NOTO TO TO	128.401					1
	The Part Age Age for	INGLUENZA A VIRUS (STIVAIN ADUCKMENTHISMAN)	347					
PARIC IADA	NUCLEUR CENT	THEIR LENGTA A VIRUS (STRAIN ADUCKAIANITOBALIA))						
PWILC LADALA	MUCI EOPTOTEIN	MACHINERY A VININ STRAIN ADUCKNEW ZEALANDY) (76)	378-403			-		
PYRIC LIDIX	MUCLEOPROTEIN	PART THEN A LIBITE STRAIN ADUCKARRANE 200)	378-405			+		-
PUMIC IADUS	NUCLEOPROTEIN	INCLUSION CONTRACTOR AND APPLICATA AND APPLICATA AND APPLICATA AND APPLICATION APPLICATION APPLICA	378-405			+		-
PANTE INDICE	INDC EOPROTEDI	CAPLUEZCA A VECUS (STANCE) CONTRACTOR (CAPACITALIZATION)	371-405					-
AAA TENAN	NAICH EGREDIEDA	DATUESCA A VECUS (STEAM) A PERSON LA SECTION	378-405	-				1
THE PARTY OF	LANT POPEOTEIN	INTLUENCA A VIRUS (STRAIN APORT A ACTOR CONTRICTOR)	378-405	_				
AND MAC	THE PARTY OF THE P	INFLUENCE A VIRUS (STRAIN AFONL PLAGUE VIRUS/DOBSON DOLLARS	+	-				
PWC MP	MULEUM	INFILIENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSTICS TOURS)	7	+				
PVNUC LATTE	MUCI EDPROTEIN	MET TENZA A VIRUS (STRAIN AGREY TEAL/AUSTRALIA2/79)	272-603	+				L
PVACE LAGRE	NUCL EOPROTEIN	THE STATE OF THE PARTY AND	178.405	1				-
PVNRK IAGUI	MUCLEOMOTEIN	INCLUSIVE A CARLO CAPE AND ARCHA LAKENTANDOUTT	378-405					-
WATER TARIES	NUCL EOPROTEIN	INCLUENCE A VALUE (STEWN) PROCESS AND STANDARD (CR.)	378-405					
NAME INCHIN	NUCLEOPROTEDA	DOLUMENTA A DULA (SI DOLUMENTA AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL AND AL	378-40\$			$\frac{1}{1}$		
MANAL MANA	MINICI EDPROTEDI	INTLUENCA A VICUS (3) INCLUENCE IN EVEN A VICA MONTHAL	378-405					
	NAME OF POST OF PARTY	DISTUBLEA A VINUS (STRAIN AGOLL AS INCOMES IN THE	307811					
A TOWN	TO STORY BY BUT BY	DIFLUENCE A VIRUS (STRAIN AGULLMASSACHUSE I SASSIO)	70, 81		-			-
PVAC MOUN	NO. LEWIS CO.	INFLUENZA A VIRUS (STRAIN A/GULLA/INNESOTA/945/40)	100	+				
PARTIC INCIDE	MOCLEGAM	INSTITUTED A VIRUS (STEASIN APLICKOX/40)	378-03	+				-
PWAIC WAD	MOLEUM	INTELLIBRICA A VIRUS (STRAIN A/EQUINE/ILLIBVING)	378-403	+				-
PWRIC WHI	MICHERAN	PARTITION A VIRIES (STRAIN AEQUINEAD/BODIN(416/7))	378-403	†			-	
PARK MED	NUCLEOPROTEDI	ANTI- 1 POLITICAL A STREET (THE ATM AND UNE MILAMIN 1/63)	378-405					-
PYRIC IMPO	NUCL EDPROTEIN	CHARLES A CHIR (CIRAIN ANIONO KONGINA)	378-405			+		
DAY IC IANO	NUCLEOPIOTEIN	INTERCEPT A CANONICATION AND INCOME OF THE CANONICATION AND IN	378-405					+
Will Market	NI CLEOPROTEDI	DOLUBIZA A VIKUS (SIRVAN ANDING KONTO)	178-405	F				1
300	AND ECHANTED	DOLUDICA A VOLIS (STIVAN ARQUINETRACOS 1730)	178.461	-	-			-
AND THE PERSON NAMED IN	TO A SOME OFFICE	DALLIENZA A VIRUS (STIAIN ARQUINE) LENNESSEE JANO)	307 00.1					
PVNOC IANIE	NOTICE WATER	INFLUENZA A VIRUS (STRAIN AKIEVISOTO)	2000	+		-		_
PWRUC IAKE	NUCLEURAN EN	INFLUENZA A VIRUS (STRAIN ALENINGRADISALI)	378-403	+		-		
WAC LED		PART TENDER A VIRUS (STRAIN APART LAIDVASTRAKHAND44/82)	378-403	1	1			
PVNUC JAMAA		THE THEAT A VIBILE (STRAIN AMALLANDINEW YORK)	178-405	1				
PVNUC LAMAN	Г	THE LUCKEY A VINITE OFTER AN AMERICANTED ENVIRONMENT	378-405			+		
PANEL LANDA	Г	ENCLOSIVA NAME (STORM PROGRAMS)	178-409					
LENAL TANKE	NUCL EDPROTEIN	DEPLOEMENT A TONG COLORS OF A PRINCES	378-405			-		
ALVAN TANTA	Т	DOT UENZA A VINUS (STRAIN ANT INCHAS)	378-405	-				
PVALLE LANGE	T	INFLUENZA A VIRUS (STRAIN ACHIOMAS)						
PVNUC IAUR	٦							

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	10/11/02/		X	AREA 2 AR	AREALIAR	ARIAI	2 6 2 6		1		
П	TROTTE	VIRUS	Г	Т	П	Г					١
Γ	NUCLEOPEDIEIN		378-405	-	-	-					
Γ	NUCLEOPROTEIN	T	178-404		\mid	-	-				
	NUCLEOPTOTED	2000	172.401			-	-	-		-	
	NUCLEOPROTEIN	DELUENZA A VELOS (SI RAIN ADEACMADOACHIOSCHI SI MA)	178.405	$ar{}$	-	-					
	NUCLEOPROTEIN		174.405			_					
	NUCLEOPROTEIN	INFLUENCE A VIRUS (3) PAIN ASSIMUATORE (127)	178.405	l	-	-		-			•
Ī	NUCLEOPROTEIN	INTUREZA A VIACIO (SIGARIA A INVINITARIA MARIANTENTA ILIANIA)	171.40	l	-	-	-				
PVNUC LATKN	NUCL EOPROTED		378-405		-	-					ļ
	RUCI EOFROTEIN		138-404		-				 		İ
	NUCLEOPROTEIN	INFLIENZA A VIRUS (STRAIM ATTERMOUTH AFRICANT)		<u>:</u>	:	:	,	<u>. </u>	•		
NUC LATRIT	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ATHENTURKANI-MAZINZ)	1	1		+			├	l	
PVALIE LATX!	NUCLEOPROTEIN	INFLUENCE A VIRUS (STRAIN ATEXAS/I/T)	2	$\frac{1}{1}$	\dagger	\dagger	\dagger	\dagger	l	t	
ALP TAIRO	NEXT EOPROTED	BALLENZA A VINUS (STRAIN AADDRANDITT)	378-63	+	1	\dagger	+	\dagger	$\frac{1}{1}$	t	1
715 Tallet	With Englishment	INFLUENCE A VIRUIS (STRAIN AAUSSRAWNT)	178-405			1	+		1	t	
TVNUC MOSS	Modern Forestrend	INCHITENZA A VIRUS (STRAIN AMICTORIAMAS)	378-405						-	:	:
NOT TAKE	MUCH POPPORTING	INSTITUTED A VIRUE (STRAIN AMILA) EMAINE() 1884)	378-405					+		1	ł
LANGE IMARIA	TOTAL PORT OF THE PARTY OF THE	INTELLIFICA A VIRUS (STRAIN ANVIOLEPACIFIC OCEANISMS)	378-405			1	+	+	1	1	
AUC IAWH	MUCLEUP RIN	TAKE LIEWYA A VIBIR (STRAFN ANVILSON SMITHS))	378-405						1	1	
PVMUC IAWIL	MUCLEUMOJEIM	INSTITUTE A VIRIA STRAIN ANISCONSOVISSIND	378-405	H				1	1	1	
PVNUC LAWIS	MOCLEOWNOI EIN	PART TENDA A VIRING (STRAIN A/SWINE/2017)	378-405				1	+	+		
MC IAZO	MULTEURIN	INCLUSION A VIBIR CONTRACTOR AND INCREMENTAL (40)	378-405		-		i	-	_	-	•
PWRUC IAZAI	NUCLEURIO EST	INCLUENZA A VIRIK (CTRAIN ASWINGACAMBRIDGAS)	378-405					- 1	-	1	1
WILE INZEA	MUCLEUM EIN	INC. IEDZA A VIRIS (STRAIN A/SWINE/DANDONG/9/3))	378-405			Н		-	1	1	
MUC IAZDA	MULEURUIEIN	INCLUENZA A VIBIR (CTRAIN A/SWINE/CERMANY/A/SI)	378-405			-					
PYNUC IAZGE	MUCLEUM	INTELLEMENT A VIRILE (STRAIN A/SWINE/KONG KONG/6/16)	378-405			H				1	
ACC INCHIL	TOTAL PARK AND DAY	INFI ITENZA A VIRLIS (STRAIN ASWINEMONG KONG/126/12)	378-405					+		1	
PVINCE MAN	AUCTOO BAN	INTELLENZA A VIELIS (STRAIN ASWINEARONG KONG/121/112)	\$00-846						1		ļ
VANDE BASIN	MINI ROBBOTHING	INFLUENCE A VIRUS (STRAIN ASWINGROWALISTO)	378-405		+	1	1	+	+	1	
WALL LAND	ANCI POPROTEIN	INFLUENCA A VIRLIS (STRAIN ASWINEROWA/1996/1)	200	1	+	1	†	+	+	†	1
WALL LAZES	NUCLEOPROTEIN	INTLUENZA A VIRUS (STRAIN ASWINEADWAM)	S I		\dagger	+	+	\dagger		T	
WAUC IAZII	MUCLEOPROTED	INFLUENCA A VIRUS (STRADA A/SWINE/ITAL Y/43776)		1		†	†		\dagger	T	
WRIE IAZZ	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/SWING/ITALY/1/17)	378-405		1	†	1	\dagger	\dagger	t	
WALC IAZIS	NUCLEOPROTED	DIFLUENZA A VIRUS (STRAIN ASWINEATAL Y/14/A1)	0	1		1	1	\dagger		T	
WRIC IAZIA	NUCLEOPROTEDM	INFLUENZA A VIRUS (STRAIN ASWINE/ITAL YA1949)	0	1	\dagger	\dagger	\dagger	+	Ì	T	
WALL LAZIA	NUCL EOPROTEIN	INTLIENZA A VIRUS (STRAIN ASWINE)/AUGSBURG(42)	207			+	T	\dagger		T	
PVNUC IAZMA	NUCL ECHNOTED	INTLIENZA A VIRUS (STRAIM ASWINEPRATOR)	107 101	$\frac{1}{1}$	l	T	T		\mid		l
WHUC LAZNE	NUCL EOPROTEIN	INFLUENZA A VIKUS (SIIKAIN ADMINENEI NEALANDSI (213)	200		l	T	T	l	-		
PVNUC IAZOH	NÚCI EDPROTEIN	DPLUEZA A VICUS (STRAIN ACS WINE CONDUCTORS)		\dagger	\dagger	t	T		-		
WHUC IAZON	NUCLEOPROTEIN	INFLUENCE A VIRUS (STIMIN ADMINISTRACESEED)	1		\dagger	t	T	t			
PANUC IAZTE	NUCLEOFROTEIN	DOLUMEZA A VIKUS (SI KALA ASWIRIZ) ERAKESEEZA (1)	12.0		l	T	T			T	
WALL INTWI	MUCLEOPROTED	DATIONAL A VIDER (CTRAIN AND INTERPRECIONS IN (MILE)	378-405	İ			T				
PVNUC IAZWZ	MUCLEOTROTEIN	INCHIENZA C'VIRIS (STRAIN CYCALIFORNIA/II)	T	416-443 45	451-478						
PWNUC DRCA	MULEUTRO EUR	MARRIED VINUS ISTRAIN MUSOKE)	366-407								ļ
VALUE MAGNET	MAICHEOGRAFIA	MARBURG VIRUS (STRAIN POPP)	166-407						1	1	-
אינטון אינטנו	PROTECTION	VACCINIA VIRUS (STRAIN COPENHAGEN)	76.7	Г	809-185					1	
VAN VAN	PROTEINO	VALIDLA VIRUS	13.	8 13	8				+	1	
NO. I FOW	152 KD PROTEON	FOXTALL MOSAUC VIRUS	1023-1050	1	1	1	1	+	Ì		1
ANDRI MACA	184 KD PROTEDY	NARCISSUS MOSAIC VIRUS	98-103	1327.1361				1	†	1	
PVOR1 PACY	176 KD PROTEIN	PAPAYA MOSAIC POTEXVIRUS	948.978	1401.1532	1	1	1	+	†	Ť	
PVINE PVINE	22) KD PROTEDY	POTATO VIRUS M (STRAIN RUSSIAN)	207-627				1	1		1	
PVOR PVX	165 KD PROTEIN	POTATO VIRUS X	2	1017.104	1	1	1	1	\dagger	T	
WORL PYXXX	165 KD PROTED	POTATO VIXUS X (STRAIN X3)		16.	t	1	T	1	T		
PVORI SAMEA	190 KD PROTEIN	STRAMBERT MILD TELLOW ELVE-ASSOCIATED VINOS				Ì			1	İ	-
PVP10 NPVAC	PIG PROTEIN	CHANGE BEFORE THE AND THE APPLICATION OF THE DROSES VIRES	17.	I		T	Ī			Ī	

П				AREAL	1	3	4				
T			Г								
		RICE GALL DWANS VIRUS	L	227.254							
200			23.60								
Ī			101-10								1
T			11.108								1
2			71.100								ŀ
T			31.100								
PVP19 AMELY	Ī	I CHERRY)									
TOSVC			2					-			
VP33 HSVSA	TELK VEZO	AIN ABAP)	ş				1				
VP26 HSVEB			7				\downarrow				
VP26 HSVSA		CEROTYPE 4 / STRAIN VACCINE)		410-437	30.5	8003					ļ
WP2 AMSW4			813-846								1
Was Brills			191-925								
			19:14								_
VIVE BIVIA		: :	·	197 947				_			_
VEZ BIVIS			Ī				 -	! !	_		
PVP2 ENDVI			٦					-			L
VP2 KOTER				574-554							
PVP1 ROTBU		CIBAIN WAL	101-05	55-567			-				L
WILDING		5	8.5	138-156	\$11.45	20.746	<u>:</u>	1	-	:	_
SVA BOTH		The state of the s	36.36		<u> </u>		_				
The state of	BNA. ROMONG PROTEIN VP3		10.75	:							
VP 10 ASSET		7.)	2			1	1			L	
VINIS ASSET	Т		٦				-		-	-	L
PVP33_EBOV	Т	IN (STEAD) MUSOKE)	Į	20.5		1	1	-	1		L
S MABUM	POLYNORASE CONOLLEX PROTEIN VEZI		101-01						1	-	Ļ
WATS MADY	٦	CONTINUE AND MIFOROSIS VIRUS	270-297					1			ļ
VALLE NOVAL	П	AUTOGIAPHA CALIFORNIA POCECE VIBILE	101-99							-	4
TOWARD S		BOARYX MOIL PROLESA PULTIESMOSIS VINOS	178.205		L			_	_		1
200		VACCINGA VIRUS (STRAIN WR)	114.141	264.201		L					4
		AUTOCAANIA CALIBORNICA MUCLEAR PULTIEDROSIS VINOS	100			L	-		_		
1	CALCAS PARTIES	ORGYIA PSEUDOTSUGATA MALTICAPSID POLYTIEDROSIS VIRUS						_	_		
1		AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4/STRAIN VALLINE)				-	-	L	L	L	
		BE EFFORCED VIDUS (SEACTYPE 10/15OLATE USA)	767-017			-	-			-	L
Wes BTV10	VP) COLL PIUI EUR	BI ITE TOWARD IN VIRIAS (SEROTYPE 17/1SOLATE USA)	214-232			1	1	-	-	-	L
Wy DIVIT	VP) CORE PROTEIN	al he fractiff Vibils (SEROTYPE I / ISOLATE AUSTRALIA)				\downarrow				-	-
PVP) BTVIA	VP) CORE PROTEIN	TENDENCY LELPARMACIC DISEASE VIRUS (SEROTYPE 1)	204-243	2		4	1	1		-	1
WHI ENDVI	VPJ CORE PROTEIN	EPICOLIC MEMORIAGIC DISEASE VIRUS (SENOTYPE 2 / STRAIN AUSTRAL	798-132				_	1	1	1	1
PVP1 EXEVA	VP3 CORR PROTEIN	EPICOTA REMOVEMENT OF THE STATE	38-13		L			4	4	-	1
April (BILV	P) PLOTEIN	GRATE PARLEY VIACE	38	329.384					4	4	1
THE PARTY	INDEA CORE PROTEIN VP)	PORCINE ROTAVILUS (GROUP L'ASTRAIR COMPLIA)	198	156.33	451-497	619-692	L				-
	PANCE CHER PROTEIN VP.3	SUMBAN II ROTAVIRUS (STRAIN SATI)	90.00			Г		L			
	A SECTION PAGE	EPSTEIN-LAND VIDLIS (STRAIN 899-4)						-			_
À11		HERPESVIRUS SADADU (STRAIN 11)	2			-		-			L
PVP-0 HSVSA	CANDING	PASS CHOUS LARYNCOTRACKEITIS VIRUS (STRAIN THORNE VIII)	£			1	-	+	\mid	-	ŀ
C LTVI	CASUTACIONE	VARY PILA 20STER VIRUS (STRAIN DUNIAS)	174-208	77.		-	+	-			L
QAZA OHA	CAPSID PROTEIN PRO	SPACE II BOTAVBUS (STRAIN SAII)	1.35	2 2 2 2 3		-			+		ļ
PVP41 BOTS1	DUTER CAPSID PROTEIN VIV	Endal to borravity (CTRAD) SA!!)	£3	584-622		4	$\frac{1}{1}$	1	+	1	\downarrow
PVP42 ROTS!	OUTER CAPSID PROTEIN VP	SUMMAN CONTRACTOR AND COMPANIES	48.75					-		-	+
AA VACCE	MAJOR CORE PROTEDY MA PRECURSOR	VACLINA VINO (SINAIN CONTRACTOR)	48-75	L	L	L				-	4
A VACA	MAJOR CORE PROTEIN MA PRECURSOR	VACCINIA VIXUS (3) BANIN WIN)	48.75	L		L	L				4
70.00	MANOR CORE PROTEIN PAA PRECURSOR	WAROLA VICES	97.70		L	_	L	L			4
200	NA YOR O'RER PROTEIN PAB PRECURSOR	FOWLAOX VEXUS				ļ		-	L	<u>.</u>	
	11 TO COME DECITED PAR PRECIDEOR	VACCINIA VIRUS (STRAIN COPENHAGEN)				+	+	ľ		-	L
WAS VALLE	A A LAB COME DECITED PAR PRECURSOR	VACCIMIA VIBLUS (STRAIN WR)			\downarrow	+	-			L	L
ANA EVA	SOUTH TOTAL MOTERN BAR PRECITE SOR	VANOLAVBUS			-	1	+	+			L
PVP48 VARV	MADA CORE PROTEIN	RI LIETONGUE VIRUS (SEROTYPE 10/ISOLATE USA)	2	3	1	\downarrow	+	1	-	-	ŀ
PVP4 BTV10	VP4 COUR PROTEIN	RELIESTONGUE VIRUS (SEROTYPE 1) / ISOLATE USA)	*	200	1	-	+	1	+	-	-
WP4 BTVII	VIN CORE PROTEIN	BY THE TOWARD IN VIRIAS (SEROTYPE 2/ ISOLATE USA)	200	200		+	1	-	+	-	+
VIN BTVI	VIN CORE PROTEDI	NEBRAGA CALE THABANDA VIRUS (STRAIN MCDV-LINCOLN)	353-613			4	1	1	+	+	+
BURG BITUTA											

PCGENE	1103213014	Att Viruses (an hacteriophages)					_	Н	
FILENAME		YIRUS	AREAL	AREA!	AREA AREA	AREAS	AREA AREA	Z OREA	1
PVP4 ROTIM	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVILUS (STILAIN CARS)	9	770-00	-			-	
PVP4 ROTBC	OUTER CAPSID PROTEIN VP4	BOVING ROTAVIRUS (STRAIN UK.)	Т	116 360	417.430				
PVP4 ROTBU	OUTER CAPSID PROTEIN VP4	EQUINE KOTAVIKUS (31 KAIM H-1)	Т	Т					
IVIN ROTEH	OUTER CAPSID PROTEIN VP4	ROTAVILUS (GROUP B / STRAIN IDIR)	T	967 663			-	 	Ţ
PVN ROTGE	OUTEA CAPSID PROTEIN VP4	HUMAN KOTAVIRUS (SEKOLTTE 1/2) IKAIN 10/6)	I	T	141.431				
PVP4 KOTH)	OUTER CAPSID PROTEIN VP4	HUMAN KOTAVIRUS (SEKO) TPE (1 STRAIN AV.)		Т	007.00			-	
PVP4 ROTHS	OUTER CAPSID PROTEIN VPA	HUMAN RULAVINOS (SERVICES) STRAIN STRAIN		T	\$65-621			-	
	OUTER CAPSID PROTEIN VP4	NUMBER BOLD CHANGE SET IT STRAIN COM		1	5	<u>:</u>	_		
_	OUTER CAPSID PROTEIN VP4	HUMAN KOTAVIKUS (SEKULTYT: ZZBIKAININI)	i	Ţ	-	:	_		
1	OUTER CAPSID PROTEIN VP4	HUMAN KOTAVIKUS (SIRKIP K.)	T	Ť	107 100 100				I
1	OUTER CAPSID PROTEIN VP4	HUMAN KOTAVKIUS (STIKALIN KU)	T	1	Т				
PVN ROTHE	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN L36)		7	170 6		1	1	
	OUTER CAPSID PROTEIN VP4	HIDAAN ROTAVIRUS (SEKOTYPE I / STRAIN M37)	T	010-7/5				1	
PVP4 ROTION	OUTER CAPSID PROTEIN VP4	HIMAN ROTAVIRUS (SEXOTYPE 3 / STRAIN MCN1)		573-628					1
PVM ROTIO	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE) / STRAIN P)		П					
PVP4 ROTHU	OUTER CAPSID PROTEIN VP4	HUMAÄN KOTAVIKUS (SEKOTYPE 3 / STRAIN RRV)	1-38		235-262				
PVP4 ROTHIT	OUTER CAPSID PROTEDY VP4	HIDGAN ROTAVIRUS (SEKOTYPE 4 / STRAIN ST. THOMAS 3)	56-1						
PVP4 ROTHY	OUTER CAPED PROTEIN VP4	HIMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VAN)	1-35	S 901-647	119-065				
What Bothw	CALTER CAPKIN PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1/STRAIN WA)	8:35	119-115					
PATOR MOVE	CHITER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (SEROTYPE 5 / STRAIN OSU)	112-146	\$14-625					
ATOM SAVE	CANCEL CARRIED BECTERN VOA	PORCINE ROTAVIRUS (GROUP C./ STRAIN COWDEN)	5.53	115-161 2	293.320			_	
OHO!	CATES CAPED PROTEIN VPA	PORCHAE ROTAVIRUS (STRADA COTTFRED)	8:38	372-628				_	
A LOTA	OTHER CAPED PROTEIN VPA	PORCING ROTAVIRUS (STRAIN YAS)	Γ	Г	\$14-625			L	
Mary Park	CATEGORA PROCESSA VAL	EMPCIN BOTAVIRIS	12.5	584-622					
5000	CONTENT PARENT BEOTECN VILL	SINTAN II BOTAVIRIIS (STRAIN SAIL FEAD	Γ	619-685					
2000	WHEN CAREM PROTECT VAL	CINTANT IN BOTAVIRIES (STRAIN SAILSEM)	5	Т	564-622				
	NOVEMBER AT SECTION SALES	WORLD TIMEN VALUE	28-62	Т					
2000	CATTER PARCET BEOTER UPC	AFRICAN MORSE SICKNESS VIRUS (SEROTYPE 4 / STRAIN VACCINE)	13:183	191-216					
OIAL PARE	Octres CAPter PROTEIN UP!	RI LETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	53-60	95-126	<u> </u>			_	
PVF STVII	OUTER CAPSED PROTEIN VPS	BLUETOWGUE VIRUS (SEROTYPE 11/15OLATE USA)	\$3.00	921.26			-		
PMPS BTV13	OUTER CAPSID PROTEDY VPS	BUIETOWOUR VIRUS (SEROTYPE 1) / ISOLATE USA)							
PVPS BTVIA	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIXUS (SELOTYPE 1 / ISOLATE AUSTRALIA)							
PVP3 BTV1S	OUTER CAPSID PROTEIN VPS	BLUETOWOUR VIRUS (SEROTYPE 1/ISOLATE SOUTH AFILICA)			148-182				
WHY BIVIA	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	53.80	П				-	
PVPS ENEW!	OUTER CAPSID PROTEIN VPS	EPIZOOTIC HEMOREHAGIC DISEASE VIRUS (SEROTYPE I)	3.60	191:218	199-426			1	
PVP3 WTV	OUTER COAT PROTEIN PS	WOUND TURKOR YOUS	548-675				-	1	
PVP61 BTV10	VP6 PROTEIN	BLUETOWGUE VINUS (SENOTYPE 10/15OLATE USA)	161-193					1	
PVP61 LOUDV	PROS NONSTRUCT 41.0 KD PRO	MAIZE KÖUCH DWANF VOLUS	153-202	1					
PVP61 NOVAC	61 KD PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAU POL THEDRUSIS VIRUS							
PVPG BTV10	VP4 PROTEIN	BLUETOWOUS VIKUS (SEKU) YPE 10/150LATE USA)	13/-189	1				1	
מאלא אינה	MAJOR ENV CE YCOPRO PRECURSOR	CACATA PSEUDOISCANIA MULTICATSIO POLITICAANIS VIAUS			1				
PVP6) NPVAC	MAJOR ENV GLTCUPRO PIELURSON	AUTOMORPH CALL CACACA POLICIAN FOR TRESPOSE FINES	167.180	1				+	
	Va ROLEIN	BLUELONGO VALIA (SEROTVE 11/10) ATÉ LISA	13.	 					I
PUR REVIS	VPS PROTEIN	BLUETONGUE VIXUS (SELOTYPE 17/1SOLATE USA)	157.189	T				-	
PVP6 BTVIS	VP4 PROTEIN	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFALCA)	161.183				-		
PVP6 BTVZA	VP6 PROTEIN	BLUETONGUE VINUS (SENOTYPE 27 ISOLATE USA)	22-172						
MAK NOV	STRUCTURAL PROTEIN PS	BLCS DWALE VIDUS	डि	354-381				L	
PVP74 NPVAC	P14 PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDRÓSIS VIRUS	413-440						
PVP3 HSVSA	PROBABLE MEMBRANE ANTIGEN 19	HELPESVIRUS SADKINJ (STRAIN 11)	#	116-686					
PVP79 NPVAC	79 KD PROTEIN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	44.78	170-197					
PVP) ENDVI	VP7 CORE PROTEIN	EPIZOOTIC HEMORULIAGIC DISEASE VIRUS (SEROTYPE I)	3						
PVP7 WITV	NONSTRUCTURAL PROTEIN PMS?	WOUND TUNIOR VIRUS	458-485						
PVPED NEVAC	CAPSID PROTEIN PRO	AUTOCRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	20:00	240-298			+		
PVP81 NOVOP	CAPSID PROTEIN PAT	OLIGITA PSEUDOI SUCATA MULTICAPSID POLTMEDROSIS VIAUS	20.20	1			1		
PVPE BTV10	NONSTRUCTURAL PROTEIN PI	BLUEIGHOUB VIAUS (SEKULTYB 107 ISULATE USA)	71.51	1	†	T	1	1	I
PVPB FOWPV	STRUCTURAL PROTEIN VESTALLUNGON	IOMETON VINOS		1	-				

				AREA	7	1					
		YIRUS	Г	113-143				1		Ì	١
		WOLDED TURIOR VIRUS	ļ								
WIN WIN	I	TO THE WELK			Ī				Ī		
AGI &	N PRIST		22-49						-		ŀ
		WOCAO TUMOR VIRUS	22-49								ļ
		WOUND TIDAOR VIRUS (STIVLIN NJ)	19-223						1	1	1
2	A SAME AND A LEWIS COST PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POL TREDAGGIS VINGS	١.	211.265						1	ŀ
VANGE NOVAL	Ц	ORGYTA PSEUDOTSUCATA MULTICAPSID POLYHEDRUSIS VIKUS	Т							Ì	-
AND BANG	Т	MOUSE ADENOVIRUS TYPE								_	
PVPRT ADEMI	36	THE LAW HAND MODE FICTENCY VIRUS TYPE I (ARV2/SF2 ISOLATE)	1			1	:		-	_	
PVPU HVIA2		HEALTH HAM BY OF FICTENCY VIRUS TYPE I (HILLO AND LIXID) ISOLATI'S)	7.								
PVPU HVIBI		HUMAN LEMANAGERICAN VIRIS TYPE I (DISS SOLATE)	21-48								
VALUE AND BEE	VPU PROTEIN	HUNDAN DESCRIPTION OF THE CONTRACT OF THE LOSS AND LICED A THE	33-49						Ì		
THE PERSON NAMED IN		ALLAN BOARMODEFICIENCY VINUS 1178 (CANIF. 1504 12)	3								
NA INC		HISTON BARINGOERCIENCY VIRUS TYPE I (BRU ISOLATE)					_				١
PVPU HVIBE		MAZAN MAMPADEFICIENCY VIRUS TYPE I (CDC-451 ISOLATE)									
PVPO_HVICA		TOWARD TO THE PROPERTY VIRIA TYPE I (ELI ISOLATE)	6-33								
PATRICE INVIER	VPU PROTEIN	NUMER BOLDS OF THE STATE OF THE PARTY OF THE	3.41								
47100		KINGAN BOADNOEF KIEW. T VINOS 1176. (1150) 150	8.5			<u>_</u>			1		l
2	Water Indiana	HUMAN BONDNODEFICIENCY VIRUS TYPE I (TH) ISOLATE?	9				L				١
WILL HAVING		HENZAN INDICINODESICIENCY VIRUS TYPE I (PRCSF ISOLATE)									
VPU HVIR		THE BLAND IN A PARTICULAR TO SEE I (MAL ISOLATE)	2								
PVPU HVINA		THE PARTY OF THE PARTY OF THE PROPERTY OF THE PROPERTY OF THE PARTY OF THE PROPERTY OF THE PRO	£33								
ONLY INVE		PULL TELESCOPIED VINE TYPE I (PV)2 ISOLATE)	ī					Ţ	Ī		
74177	VPU PROTEIN	HOMAN DAMANCALE REST. 1 VIACO 1 112 1 12 1 12 1 12 1	\$ 72								I
2	PUSAU BRUTEUN	HORAN DAGORODESICENCY VIKUS 177E J (37102 1900-1-1)				L					
PVPD HVISS		CHIMPANZEE DAKONOGEICENCY VIRUS									
WAL STVCZ	VPU PROTEIN	LACTATH DESIRPROCENASE ELEVATING VIRUS	Š			1					
AGT XAN	VPX PROTEIN	THE PARTY AND AND AND ANY AND AND AND AND AND AND AND AND AND AND	1051-1078				1				
THA BOAT	ALPHA-A PROTEIN	BACLES COMPANY OF A COMPANY CHANGOLD	3								
PAYON BOTTES	VA PROTEDA	BOYING KUIA VIIIA (ANA)	1114-144								
1000	VPA PROTEIN	ROTAVEUS (GROUP BY STRAIN ALMY)	28.55								
	THE PARTY OF THE P	ROTAVILLIS (GROUP B / STRAIN IDIR)					L				
PVXOS KOTO	VERNORM	HOMAN ROTAVILUS									
SOS ROTHC	VP TROIEUR	PORTONIE ROTAVDRUS (CROUP C / STRAIN COWDEN)									
SOU ROTH	VA PROTEIN	ROVINE BOTAVAUS (STRAIN KN-4)				-					
TOT ROTE	GLYCOPROJEM VEV	BOVING BOTAVILLS (STRAIN UK)	8 - 18	2		1	-				L
PVSOT ROTTEU	NONSTRUCTURAL PROTEIN INC. V.	ASSESSMENT AND A VIRIAL (SEROTYPE 5 / STRAIN OSU)	91-146	7.70		-		-			L
PVSOT ROTES	NONSTRUCTURAL PROTEIN INC. V.	TO ALLE SAFA VIEW CTB A DI SA III	91-146	199-236							L
Sof ROTS!	NONSTRUCTURAL PROTEIN NOVE	SUPPLY THE PARTY AND IN THE PARTY IN THE PAR	164-201				1	\downarrow			L
SUCOS BOTTEL	NONSTRUCTURAL PROTEIN MS2/VP9	BOVDO: RUTAVILUS (3) FOUR OR)	164-201	117-251							
	WONSTRINGTURAL PROTEDNINGVP4	SOCIAL II ROTAVILUS (SI KALI SALI)	2		L	L					1
200	C. Schederell Ver	BOVING ROTAVILUS (SEROTYPE 6 / STRAIN BOA!)				-		L			
/SOP ROTE	GLTCornollary VI	ROVING ROTAVIRUS (STIVAIN AS)	2			-					L
PVSO ROTES	GLYCOLEGE VE	ROVINS BOTAVILUS (STRADY UK)	2.2		\downarrow	+	-	-			L
VETON 605V	CLYCOPROTEIN VP!	POTA VIEW (CECAMINE ATTRAIN ADRIV)	210-237								
ACCO ROTGA	GLYCOPROTEIN VP7 PRECURSOR	AUTO CALL MANAGE AND A CTRAIN BULL	1-39			_					ļ
SVEN POTTE	GLYCOPHOTEDI VP7	HUNCA HUINAVAUS (SEAU) STEET STORY IN 1876	62.71	L	L						1
17.10	CH VOOPBOTEDN VP?	HOMAN ROTAVIAUS (SERVI ITE & STEAM (10.2)	5.20		L	L					
100	CH WASH OTHER VP?	HUMAN ROTAVILUS (SEROTYPE G/STRAIN B) //			-	-		L	L		
WWW KULIND	The second secon	HODAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS!)		-	-	-	-			Ŀ	_
VSOS ROTHO	GLYCOMINISM VI	HINAAN ROTAVIAUS (SEROTYPE 1/STRAIN HN126)	2.29			-	+				
PVSOF ROTHON	GLYCOPROTEIN VF/	GALLANDOPAVILLE (SEROTYPE 1 / STRAD) NO 7)	3-79				$\left\{ \right.$	\downarrow			L
PVSOP ROTION	OLYCOPROTEIN VP7	THE ALL BOTTA WHITE (CENTYPE I / STRAIN MO AND STRAIN D)	1-19			4	4				
PVSO9 ROTHO	CLYCOPROTEIN VP7	INCOME TO SECURE A SE	13-29								1
PUCOS BOTTO	GLYCOPROTEIN VP7	HUMAN KOI A TANDS (SEND I TELE A STATE A PARTY)	2.20		L	-					1
SUPPLY BUTTE	CH VCOPROTEDA VP7	HUMAN BOTAVIRUS (SERU) TPE A STRAIN 24)	3.30			-	L				
TABLE TO THE	CA VOCABLOTEDA VP?	HUMAN KOTAVRUS (SEROTYPE I / SI WAIN WA)				-	-	L			
A SOLUTION	CA VOCESCITION VP?	PORCINE ROTAVIRUS (SEROTYPE 1 / STIALIP A 1 / 10)	,	-	-	-	-	-	L		_
VSO TOTAL	Carlo and Carlo	PORCING ROTAVILUS (SEXOTYPE 3 / STRAIN CRW-3)		\downarrow	-	-	-				
VKON ROTT	GLTCorrolled very	SPATAN II ROTAVILUS (STRADY SAII)	3.29	-		1	-				
PVSOF LOTS!	GLYCOPROTELIN VP7	INCOME BOTAVIRIS (GROUP C / STRAIN SHINTOKU)	125-152		_	-					
PVS10 ROTBS	MONOR COTTER CAPALL PROJECT		113-140	_		4	$\frac{1}{1}$				1
PVS10 LOTS!			13-40	114-145		4	-				1
PULL BOTTEU	MENCR OUTER CAPSED PROTEIN	BOVING MOTA WAS CALLED AND WAS IN	97	114-145							1
Vern Borney	MINOR OUTER CAPED PROTEIN	BOVING KOLAVILLE (STREET)	5	-	-	Ļ	_	_	_		
				_						l	I

PCGFNE	10317814	All Viruses (no bacteriophuges)	П	П				V 104 4 4964	e vanv	AUFA
FILENAME					4	-	Т	_	Т	
PVS11 ROTHS		7		5	Ī		T		L	
PVSII ROTID			Ţ			T				
PVS11_ROTHW		N WA)			T	T	İ			
PVS11_ROTEA		(A)				Ì	İ	1	l	_
PVS11_ROTS1		FAVIRUS (STRAIN SAII)	201.1	1			Ì		L	
PVSH MUDON				1		1	T		-	
PVSH MUNDA		(VIV)								L
PVSH MOODS				T		ľ	T		-	
PVSH MULDE	SALAL HYDROPHOBIC PROTEIN					Ī	T			
PVSH MADAD!		(NR)	9			1	-	_	_	
PVSII MIMOR	Ĭ		9-40				1		-	\downarrow
PVCH ANIMA		í.	9-46						$\frac{1}{1}$	
THE PURPLE	CALALL SECTION OF PROTECTION	VACCINE)	13-41							
THE PARTY OF THE P	SALAT WATER BEATTED		Ī							
PASH MUSICE.	SHALL STANDARDED BEOTED	BE VACCINE AM9)	2.5							
LAST MUNIC	SHOULD BE DATE THOUSE FACILITY		26-63	221-12	127-168	652-222				
LVSII MEOVD	SIGMA I PROTEIN PRECUASOR		Ī	110-101		Ī				<u> </u>
PVSII REOVI	SIGMA I PROTEIN PRECURSOR		Τ	25.104	112.160					L
PVSII MEOVE	SIGNA I PROTEIN PRECURSOR		3						_	
PVSIZ REOVD	SIGMA 2 PROTEIN		310.114	Ī						
FVSI3 REOVI	SIGMA 3 PROTEIN		200							ļ
PVSIS REOVO	SIGMA 1-5 PROTEIN	(O)		T					-	
PVSIS REDVIL	SIGMA I-S PROTEIN	(0)		Ī			İ		-	-
PVTJA CAPVI	PROTEIN TJA		7				1		+	
PVTS SPWA	PROTEIN 75	SHOPE PIBROMA VIRUS (STRAIN KASZA)	250-277						1	4
PVTER EBV	PROBABLE DNA PACKAGING PROTEIN		334.390							!
PVTER HOLVA	PROBABLE DNA PACKAGING PROTEIN		13.45	!	:	;	:			
PUTER HEULI	PROBABLE DNA PACKAGING PROTEIN	ANDA-1102)	176-201					-		
PVTER HSVII	PROBABLE DNA PACKAGINO PROTEIN		10.33						-	\downarrow
PVTER VZVD	PROBABLE DWA PACKAGING PROTEIN		25.22				1			_
VIVIT (41V4	VIRAL PROTEIN TPX		8 8							1
IVIT X4IV4	VIRAL PROTEIN TPX		8							
PVV PICHA	V PROTEDY	IN TOSHBA)	3				1			
PY101 SSVI	HYPOTHETICAL 10 I KD PROTEIN		2.64							1
PY108 SSVI	HYPOTHETICAL 16 8 KD PROTEIN		3							
1VS2 911Y9	HYPOTHETICAL 11.9 KD PROTEIN		20.00						1	-
PYIIK TYDVA	HYPOTHETICAL II.2 KD PROTEIN		2					-	1	1
PY13K NOVAC	HYPOTH 13.1 KD IN 39 KD STEGRON	OLYHEDROSIS VIRUS	~ ~							
PY13K \$SVI	HYPOTHETICAL 13.3 KD PROTEIN		39.16							
PVIAK SSVI	HYPOTHETICAL 11.9 KD PROTEIN		Š							
PY16K NOVAC	HYPOTH IN 39 KD PROTEIN STECTON	ALYNEDROSIS VIRUS	6 0 0					1		
PY16K SSVI	HYPOTHETICAL 15.6 KD PROTEIN		=							
PY17K SIVI	HYPOTHETICAL 17.8 KD PROTEIN		28	19-153					 	
PY18K MSVN	HYPOTHETICAL 17.7 KD PROTEIN		2							4
PYICK MSVS	HYPOTHETICAL 17.2 KD PROTEIN	SOLATE)	34.61				1		$\frac{1}{1}$	1
PYZOK SSVI	HYPOTHETICAL 28.4 KD PROTEDN		16-103							1
PYZEK SSVI	INPOTIGITCAL 24.5 KD PROTEDI	SVI	93-164							_
V2 500.6V	HYPOTHETICAL PROTEDY 2	SOYBEAN CHLOROTIC MOTTLE VIRUS	- T- T-					-		
PYSIK SSVI	HYPOTHETICAL 31.5 KD PROTEIN	SULFOLOBUS VIXUS-LINE PARTICLE SSVI	24.97							\downarrow
IVE SEVI	HYPOTHETICAL 31.7 KD PROTEIN	SULFOLOBUS VIRUS-LINE PARTICLE SSVI	233-267							
DVISK NOVAC	HYPOTHETICAL 37,7 KD PROTEDN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	133-184							
VACOR MY	HYPOTHETICAL PROTEIN 3	SOVBEAN CHLOROTIC MOTTLE VIRUS	122-149						+	
200	HYPOTHETICAL PROTECY ?	SOYBEAN CHLOROTIC MOTTLE VIRUS	86-94							
PVICE SEVI	HYPOTHETICAL 15.7 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	11-131	\$46.573	658.700					
VOOR 174	HYPOTHETICAL PROTEIN 8	SOYBEAN CHLONOTIC MOTTLE VIRUS	13-40							
PYRO! FOWPM	HYPOTHETICAL BAMBEORF! PROTEIN	FOWLPOX VIRUS (ISOLATE HP-438[MUNICH])	74.108	152-179	184.23 184.23				1	
PYBOS FOWPM	HYPOTHETICAL BANGGORYS PROTEIN	FOWLPOX VIXUS (ISOLATE HP-438(MUNICH))								1
PYB10 FOWPM	HYPOTHETICAL BANGG-ORF 10 PROTEIN	FOWLPOX VIRUS (ISOLATE HP-433(MUNICHJ)	162-197	25.2			1		$\frac{1}{2}$	

and a second	187217854	All Viruses (no besterdophages)	AREAL	AREAL	ARIAL	AREAs	ABTAS	ত ব্যৱস্থ	AREA 2 ABEA 8	TO SEC.	3
2000	PROTEIN	MRUS	11-38				1	1			Ī
THE MARTIN	INSCRIPTION BANGOOM 12 PROTEDU	FOWL POX VIRUS (ISOLATE RE-23) MIDNIAND	128-167					1	+	1	T
101	DALANCE LA LANGUAR IS PROTEDY	FOWL POX VIRLYS (ISOLATE PO A) SI MONICALI)	17.336							$\frac{1}{1}$	T
	PULL COOLERA	MINIST SPUNKARETROVIRUS	161-188					1	1	+	Ţ
	MONOGET BANK MANAGEMENT	HELLYES VALUS SALMAN (STRAD) 454-77)							-		•
POHI HEVS	HINDIA ALL MUNICIPALITY	LEB PREVILLIS SADORU (SUBGROUP C./ STRAIN 441)								_	1
PYDHI HSVSC	HYPOTH 28.7 KD IN DRUK 3 NEWSON	LES MECURINE SABARL (SUBGROUP C./ STRAIN 488)						-	-		-
PYDE HSVSC	HYPOTH 9:9 KD IN DIGHT THEGON	CALLE DOV LAST ACT AND PARTY.	5							\vdash	
PVF26 KOWP	HAPOTHESTICAL 15.9 KD PROTEIN	PUMILOR TAKES (STREET)	170-204					İ			
TOTAL PARTY	THYNOTHETICAL 26.9 KD PROTEIN	FOWILD'S VICES (31 JOHN 17-1)	33.64	92-136	144-171			1		+	Ī
	HANDEL OF STATE STATE OF THE ST	(VACCINIA VIRUS (STRAIN WR)	11.50	179-206				1		1	Ī
WACEV	HITCH ALL STREET	VARYENIA VIRUS (STRAIN WR.)									
PYRED VACCV	HYPOTH HOST MANUE AV. & BLOCKE	CONTRACTOR VINITE (STRAIN B954)	- R						-		
PYKE EBV	HYPOTHETICAL BKAY'S PROTEIN	CONTRACTOR CARRIED AND MOCKET	19-53								
PYKIA EBV	HYPOTHERICAL BKBF4 PROTEIN	E751ELM-BOOK TIMES (STREET)	47.86					1	-	\mid	Ī
BY IS ADEA!	HYPOTH 12.4 KD IN 33 KD REGION	HOMAN ADERGY WAS 1175 41	27.54							+	Ī
	GOSCOLLETICAL REBET PROTEIN	EPSTEIN BAUR VINUS (STRAIN BYNA)	64.143					1		1	
	THE PROPERTY OF THE PARTY OF TH	CONDUCTOR YELLOW MOTTLE VIRUS								4	
PYOR! COYNY	HYPOTHESINAL DAY PROJECT	COLORGINAL VELLOW MOTTLE VIRUS	•						-		
PYORES COYLAN	HYPOTHETICAL 15 KD PROTEIN	A ANTER AND	2.2							-	Γ
TWO THOSE	Г	WHILE CLOVEN MANNE CHANGE AND	86.89							-	ſ
CAN CONTRACT	Т	WHITE CLOVER MUSAIC VIRUS (3 I POUT C)	92-119							1	Ī
	7	AVIAN ADENOVIRUS GALI (STRAIN PIELL'S)									1
PYON ADED!	MYPOINE INCAL SILS AND SINGLE OF	THER LACE OF EUS TENAX VIRUS I (STRAIN KIAN!)									
PYORA TTVI	HYPOTHETICAL S.I ALL PROTECT	THE PASSED AND IN TOTAL YOURS I (STRAIN KRA!)	77.							ŀ	
PYORT TTVI	HYPOTHETICAL 26.8 KD PROTEIN	THE STATE OF THE PARTY WHITE I STRAIN KIA!	1.1							-	Γ
PYORO TTVI	HYPOTHETICAL 7.3 KD PROTEIN	THE COURSE AND A COURSE OF THE AND READ IN	04-4							1	
A Macha	HAYPOTHETICAL 12.1 KD PROTEIN	THE MOREOTE IN THE VIEW OF THE PARTY OF THE	17.3							\dagger	Ī
	LIVERTHEAL PLY PROTEIN	RICE TUNGRO INCELLIFORM VINUS	14.71							+	T
	LICHOTHER PARTIES	RICE TUNGED BACTLIFORM VIRUS (ISOLATE PRILITERIAL)	101.03	104.157		L	L		-	1	T
PYPIS KIBVE	HINDING TO A SECTION	BUCH TUNCARD BACKEL BOALM VIRUS	21.0	1							
PYT24 RTBV	HYPOING INC. THE PROPERTY	PACE TENCHO BACH LIBORM VIRUS (ISOLATE PHILIPPINES)	31-101								
PYP24 RTBVP	HYPOTHETICAL PARTITION	PARCE HANDED BACH LISORIA VIRUS	156-107	107:76						-	
PYPE RIBY	HYPOTHETICAL P44 PROTEIN	THE PRILIPPINES	\$8-107	197-231					-	l	
PYP46 RTBVP	HYPOTHETICAL PM PROTEIN	THUS TOWNS OF THE WAY FAR POR WIEDROSIS VONUS	14-71							+	
PYPES NOVAC	HYPOTH PRO PLS STEGION	AUTOURATING CALL TOTAL TOTAL POLYMEDICOSIS VIRUS	325-352							1	Ī
CUMAN LYNA	EGION	OKCYTA PSEUDOI BOOM IN MICH. B.A. WIENDORS VIRIUS	116-13	L	L					\dagger	
CANAL MAN	HYPOTH 21 4 KD IN POLYNEDAUN STEGIO	O AUTOGRAPIA CALIPURALA RULLEAN TALLINGO	253		L	L				+	
			5	800	156-183	_	L				
100	THE STREET AT MOTHER IN THE STECTION		100								
YOU AND				300							
PALST HSV80	HIVITAL TANKS	MERPES SIMPLEX VIXUS (TYPE 6 / STRAIN GS)									
PYRU1 HSV60	HYDING ILAL PROJECT IN	HERDER RAZALEX VIDUS (TYPE 6 / STILAIN OS)	201-1-1-1							-	
PYNUT HISVED	KYPOTHELICAL PROJECT IN	HER PER KINDH BX VIBUS (TYPE 6 / STRAIN OS)	7								
PYRF4 HSV60	HYPOTHETICAL PROJECT AND	Acti o minescent VRUS	ğ								
PYRES DAVE		W. CONTA VIRGIN AND COPENSIAGEN	7-34								
PYVAG VACCC		TO SCHOOL WATER CATE AND COPENHAGEN	111-112						$\frac{1}{2}$	t	
PYVAH VACCC	r	WACLIAN VINCE (STICK)	17-17			_				†	
NAME VACOC	Г	VACCINIA VICO (SI MAIN CONTINUE)	46-77	L		_				†	
2010	T	VACCINIA VIDIUS (STRAMA WA)	9			L	-			1	١
ATTIVA BOALL	Ţ	VACCINGA VIBLUS (STRAIN WIR.)			-	L					
TANK AWAY	Т	VACCINIA VIDUS (STRAIN COPENHAGEN)			ļ			-			
PAYCE VACOL	1	PPSTEDLEARR VIRUS (STRAIN 895-4)	27:75								
PYZL3 EBV	HAPOTHETICAL BALFA PROTEIN										

TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

	101011111	All Virgons las bacteriaghages	7	APEAL	AREAL	ABEALIA	ABEA1	ABEAL	AREAL	AREA!	2 6 180
NAME OF TAXABLE						j	j	İ		Ì	
			11.34	<u> </u>				j	<u> </u>	j	
Ī		AKY MARDE LEIMENDA VIKUS	100.00	İ					-		i
212			ī	19:50						•	-
	NO PROTEIN		1		İ	ĺ		<u> </u>			
THE WALL			1		Ì	Ī	İ		-	İ	
PAINC AVEC		2				ĺ	İ	İ		İ	i ,
PLINC AVOK.			=				İ	İ	İ	İ	-
WI TONE			137-72				Ì	İ	İ	İ	Ì
PVGLE HSVBI	•	15 AND 141	20.00							İ	-
PRILL ISSUES	ALBONIC DONOSHI REDUCT SAALL OW		10.00					İ		i	İ
PUCT B MCVB	CLYCOPACTED 6-1 PARCUMSON		1	1977	200-151			:		İ	
			Ī	ī	1	1	Ī	Ī			
VE.VV			i				İ	Ī	İ	Ì	Ì
1			104-11						İ	Ì	i
	DAY FOL YPLOTEIN	DOUBLE LEGISLAND AND LOCAL	2							İ	İ
ı		DOVOG LEIKENDA VIKUS (ANGRICANISCIANIS VANI)	15.72								
ı		DOVINE LEUKENBA VIRUS (AUSTRALIAN ISOCATE)				Ī			İ		
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BEACH BE VI		BOVING LEUREMIA VIXUS (IAVANESE ISSENTE									1
1	ELIE A LATHIDA S.II	BOVING PARAINST UENZA I VINUS			1						!
THEMA THU									İ		
PRAPE PISE			22:52	207.74	130-461					Ī	!
PVCL) PISB	OTED PRECURSOR		361.331								
BUAZAT MIB		BOVING PARAMETURING A VINUS									i
	E Al Dela CIMIDAIT	BOVING RESPURSION SYNCYTIAL VIRUS (STRAIN ASSISTED)			1.						
PRINT BROWN	MA FOL FRANCE AND PARTY	SACRES SERVICE TO STANKE WALLS (STEATH AS 1900)	5	102 16	2						
IVCL! BRSVA	FUSION GLYCOPROTEIN PRECURSOR	BOVOR ALTER A STATE TAKE THE CHAIR LICENAMIA A STOOL	25.72								
PVALAZ BRSVA	MATTUX GLYCOPROTEIN M2	BOVOR MENTAL OF THE STATE OF TH	210.365								
ALSON WALES	MATRIX PROFESS	BOVING RESPONTORY SYNCYTIAL VIRUS ISTAMIN ASTRAIN	ļ	100	14. 441	1	100				
WAR INA	THE PERSON OF VICTOR IN PARTY IN PARTY IN COLUMN TO SERVICE AND ADDRESS OF THE PERSON	BOYDUR BETPERSTORY STACFTLAL VIRUS (STRADA COPEMIAGEM)	•								
VC.	POSICE CONTRACTOR OF THE PARTY	ANY DE DESPERATORY SYNCYTIAL VIRUS (STRAIN COPEMIACEM)	2								ļ
PVCLO BASVC	MADE SUID ALE CATION POLICE	STATE STATE AND AND VILLE VIRIAL ACTUADA BOOK	3	34.70	200					i	İ
PVCU BASM	TEN PREC	BOARS RESTRICTED STREET STREET	10.53						İ	İ	
SENS NO VOR	ENV POLYPROTEIN	CAS BL 6 MURDR LEUKPHA VINUS	1	311.160	31.16	136.310	637.630				į
VIVE	RMV POL YPROTERI	CHACAMZEE IN BACAMODE FICHER T VIRUS									
The same		CHEGOLOGE DESCRIPTION VINUS									İ
200		CHALPANZES BLOCKNODE/ICIENCY VIAUS (SIVICEZI)	342-269								İ
POL SINCE		CHARLES AND	5.34						Ì		
PVE3 CILIVIX		COLUMN AND STREET STREET STREET STREET STREET STREET	100								
30.15		COLLON ALL MARIN (SHOVE) FAVOLUMENTO (STRONG MARINE)		100	101.1014						
		DENGUE VILLS TYTE I (STRAIN SONGAPORE STITIO)				1010	1117,1143				
The second	Separate Sep	DENGLE VOLUS TYPE 3 (STRAM 1644))				-	***	1	Ī		
1000		PROJECT VILLE TYPE S (STRAD) 16401-PDK5))	1300.15			-	_				
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N. N. N.	CENCACE POLYPROTEIN	DENCINE VIRUS TYPE 3					•	-			
STATE OF THE PARTY		DENGUE VINUS 177E 4									
		DOCT HEPATITIS & VIRUS (DROWN STANGINI DUCK ISOLATE 33)									
TOTAL MARCH		DESCRIPTION OF STRUCTURAL STRUCTURAL	2.13				1	-	İ		
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TOTOL INTOM	DNA POLTMEJANE	TEACHER STREET STRAIN BOY. D.	103:133	_		1876-1903					
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711 CE 13V	VOUCH PROTED/BRILL!	EPSTEDS DATA VICTORIAN PRINCIPAL									
700	INTOTATION PROTED BOLD!	EPSTED-BARR VIRUS (STRATH DVI.4)		-::		ļ					
	THE PERSON NAMED IN COLUMN TWO INCOMES AND PARTY OF THE PERSON	EPSTED BALL VINUS (STRAIN 095-0)									
	THOSE DAY REAL PARTIES.	EPSTEIN HARE VIXUS (STRAIN 895 4)	409.436								
700	HYPOTHE INCAL PROJECT SICING	ALTERNATION OF THE CORP. C.	101	89:08							-
PG 11 EBY	INTOTICE HEAL PROTEIN BOLF		169.030			-					
PVCA EL	MAJOR CAPSID PROTEDI	EPSTEIN-BARD VINOS (2) INAIM 873-13									
Van 6 Enve	OPROTED	EPSTECH BACK VIRUS (STRAIN 893-8)				1					
	CHANGE OF THE CASE OF THE CURSOR	(DITED: DAIL VIRUS (STRAIN 895.1)									
7	ROSI	EPSTEIM-BAAR VIRUS (STRAM BPS-1)				1					-
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ļ	PROB INTEGRAL NEADIRANE PROTEIN	EQUING HERPESVINITS TYPE I (SIRAIN ADAP)									
	CAPSID PROTEIN VP16	ERPESVINIS IVE	16-61								:
PYCO3 MSVEK	GENE 3 PROTEIN	EQUAC SERVES VIRUS TYPE I (STRAIN KENTUCKY A)	=======================================						i !		į
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١	Mai Cary Est Color	BELLEVIEW BOARDONE CONTRACTOR STORY AND STORY		ļ		İ		Ī	!	İ	
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15	LANCE CONTINUE VALON PROTECT	A 2051ER VIRE				<u> </u>		<u> </u>		
	THE STREET STREET	VALIFEL A POSTER VIRUS (STRAIN DUNIAS)	200		1		1	<u> </u> 		1
MAN WAY	COM IS NECESSARY PROJECT	State of the state of the state of	200							
M.S. V.V.	PROB DNA REP CEME & PROTEIN	VALUE A COLUMN TOTAL STATE OF THE COLUMN TOT	305.122		<u> </u>					
ON J. F.L.	CL VCOPLOTEIN GPV	A-2051ER \INGS					1	<u> </u>		١
	Cartes No. or De Ball	VARICELLA 20516A VIRVS GIRAIN DUNIAS)				1		<u> </u>		
200	ı	CARLEST A PROPERTY COMES OF PARTY SALES	=		-	_				
PYER VEVD	PROBABLE DNA PACKAGING PROTEIN		21.12		-		_			
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NUM NOVA	DAY PACTAGASE	WOODCHAICK IMPATILIS VINIS I			1		1	<u> </u> 	 -	
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LAND THE PARTY	LANA TUCTOR PAGE	Constitution of the second of	22.5	= :				1		
PERCH WHY	DNA POLYNGRASE	WOLLDAN TECHNIS VINCE	111.341	210.110						
POPOL WAYS	DNA POLYNERASE	WOODCHACK IEPATIIIS VINUS			-		<u> </u> 		 -	
Total Property	DAY POLYNORASE	WOODCHUCK HEPAILLS VIRUS &				1				

TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS

			П			١.		1000	Т	AREAI	ARCAS
PCCENE	107117814	S. C.	10380	J	4		11.77	1168-1202	i		
PTLENAMOR		PICKETTSIA RICKETTSII	٦	340-798					Т		
PLYOR BICE!	120 KD SUMFACE EXPOSED PROTEIN		3.53			Т	Т	Т	17761 0461	1534.1531	1723.1750
	13 KD ANTIGEN PRECURSOR		241.268	460-487 6	607-634	754-781	179-1150				
	LAND ANTICEN PRECIMENT (CELL SURFACE)	NOKETTSIA NUKELLISII	8	2131-2168					1	Ī	
3				+-	120-147				1		
	March and March	OBILIS	1	T							
TIKE UEN	CO COLUMN TO COL	NO.									
A CONTRACT		ESCHENICHIA COM							1		
PEOPLE ECOL	O KU DANEL PREMON	PROTEUS MORABILIS	٦		Ī						
PEODE PROPE		15	~	076-000							
PLSKE ZYDAG				218-240							
PAPED BACSU	공		262-502								
CO GOOM	28		205-233								
	AUDITION TO THE P		450.437								
2	SUBJECT VOICE	STAMPLOCOCCUS AUREUS		100 313							
PAACA STAAU	- AMILANE I COSE	BACTLLUS SP									
PAAT BACSP	SPARTATE AMINO	COL	351-378								
PAAT ECOLL	ASPARTATE AMINOTRANSPERASE		176-203								
PARC ECOLI	ABC PROTEIN		13.126	170-204	209-273						
V DV L	ABORTIVE PHAGE RESISTANCE PROTEIN ABIC	LACTOCACTOS CACTOS	127.154								
	THE AMECRIPATIONAL REPRESSOR ACCR	ACKOGACTEMUM TOMETACION	100.412								
ACLA ACT	The state of the s	ESCHENICHIA COLL									
VACEA ECOL	PACEA ECOLI ISOCIEMINE LI MANE	BACELUS SUBTILIS	48:73								
PACON BACSI	ACONITATE HTDRAINS	FECHERICHIA COLI	41-66	017-040							
PACON ECOL	ACONITATE INDIATASE	AT CALICENES EUTROPHUS	15-112								L
PACOR ALCEI	ACETOIN CATABOLISM REGINO	100 1000	4.31								
182	ACYL CARRER PROTEIN	ENCHANGE OF THE PROPERTY OF TH	213-247	L							
	A PRECURSOR	ESCHENICALIA	1830-881	L							
	COLUMN A VINA BECOME	ESCHENICHIA COLI	93	136.361			L				
NO.	A CALL LANGE BEING BOOTEN!	ESCHENICHIA COLI	200					_			
PACIN' ECOL	COULTAVIN MESAS		31.18								L
PACTS STRCO	PUTATIVE RETUNCTE PENCHEN PRECIDIO		87.	210.00			L				L
PACTA LISMA	CTD-ASSEMBLY I		1129.3163								L
PACVS NOCLA	A ACV SYNTHETASE	PACELUS SUBTILIS	136-170			1					 -
PADAA BACSU	METPHOSTILES TEX	BACH 1 US SUBTILIS	108-425	454.48	357.330	100			1		L
PADDA BACSU	TP-DEPENDENT N	PACE LUS SUBTILLS	257-284	10.00				-	-		
A USON BACSU A	TP-DEPENDENT N	-	284-511								
ACD INVA	ADDITION TO THE STATE OF THE ST		398-125	-	L						
SACIO ALIANA	NOCH DEPENDENT		298-325	-	Ŀ						1
AND CLOAD	A NADH-DEPENDENT BUTANOL DEHYDROGENASE B	_	653-680	179.BC	L						-
	POWER DENTOR	_	371.308	-		L	L				
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PADPI MYCHE		MYCOPLASMA PNEUNIONIAE	1337:13			1	L	-		L	L
PADPI MYCH	zΙ	RICKETTSIA PROWAZEKII	200.70			1	1	-	-		
PADT RIGHT	N.A.	AEROMONAS HYDROPHILA	274-303			-	-	-	-		L
PAERA AEM	LEAOL YSDN PLECT	STREPTOCOCCUS MUTANS	419-483	597.611				1	-		L
PAGAL STRUM	L'HA-GALACTUS	PSELIDOMONAS ATLANTICA	\$?	╗		\downarrow	1				ļ
PAGAR PSEAT	BETA-AGAILASE PR	READMAN OCOCCUS AUREUS	139-159	163.192			-	1	1	1	-
PAGE STAAU	ACCESSORY GENE	CORPUSAL SATERACION ITALA	19.46	_						1	1
MAIL YELL	τ.	TO A DOLLAR OF THE	3.30	466-493	501-530					1	1
TOOK HILLS	~	ENCHANCES COL	1.15	608-635	L						-
1	ASPARTOKDIASE		266-312	-	L						1
	TACARTATE KINASE DALPIA AND BETA SUBUNITS	911	5		-	_	L				1
	COARTAIT KDIA	┑	286.316		-						4
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PALCO PARA	_	Г		110	1	-	-		_		Ц
WITH LEG	_	PSEUDOMONAS OLEOVORANS	7	Т	1	-	+	-	-		
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PREMISE DICTYGGLOMUS THERMOSHILLAN 19734	C-PACO AMINOPEPTIDASE			†							
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ALTOCAMPILAGE PRECINSOR	SELECTION AND THE THE BUSINESS OF THE COMPANY OF TH			Τ	459.486						
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U.D.H.A.APTALE PRECINESOR BACILLUS SUBTRUS (16)-101	ALPHA-AMMASE PRECURSOR		•	37.474							
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STEEP TO A PURE LANDIA 171-150	ALPHA-AMYLASE PRECURSOR	FUROGENES	П	12.642							
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THE OCENTAGE BOOK-BOOK PROTEIN ALPHA CHAIN AZOTOBACTER VINELANDII 99-112	MITROGEN FLXATION PROTEIN ANFA		22.239								
THE COCENAGE BOWLOON PROTEIN BETA CHAIN AZOTOBACTER VINELANDII 196-100	THOGENASE MON-MON PROTEIN ALPHA CHAIN		<u>=</u>								
VEGE PROTEIN VIRBO ANGILLARIAN 91-10 165-20 VECT PROBLES TO LINEER POLYPETIDE FYBECHOLSTHON 11-10 165-20 HYCOBILISOME 10 KD LINEER POLYPETIDE SYNECHOCOCUS SP 17-46 318-613 HYCOBILISOME LINEER POLYPETIDE SYNECHOCOCUS SP 17-46 318-613 HYCOBILISOME LINEER POLYPETIDE SYNECHOCOCUS SP 17-79 318-613 HYCOBILISOME LINEER POLYPETIDE SYNECHOCOCUS SP 12-79 318-613 HOSTALES LINEER POLYPETIDE SYNECHOCOCUS SP 12-79 318-613 HOSTALE CYTCOROME OXIDASE SUBURIT I EXCEDIORANA ARROPALA ARROPA SALIGIDAS 111-141 17-144 ALIALDE PROTEASE ECLETION PROFEIN APID PREDIOMONA ARROPA CALCINOSA 111-141 17-144 ALIALDE PROTEASE ECLETION PROFEIN APID PREDIOMONA ARROPA CALCINOSA 111-141 17-144 ALIALDE PROTEASE ECLETION PROFEIN ARE PREDIOMONA ARROPA CALCINOSA 111-141 17-144 ALIALDE PROTEASE ECLETION PROFEIN ARE ESCIENTION ARE ESCIENTION ARE 111-141 17-144 ALIALDE PROTEASE ESCIENTION PROFEIN ARE ESCIENTION ARCHAUSA CALCINOSA 111-141 17-1	STROCENASE DON-DON PROTEIN BETA CHAIN										
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1746 1747	HYCOBILISONE 120 KD LINKER POLYPEPTIDE										
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UKTL HYDIOPEROXIDE REDUCTASE C32 ROTENSALJONELLA TYPUMAUNIM 62-49	PHYCOBILISONG 130 KD LINKER POLYPEPTIDE		2.3		1						
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AMBNO ACID ACETYLTTANSFEASE LYS.ARG-GINN-BINDING PROTEIN (I.AO) PRECURSO ESCHEDING COLU PROSEHOSIBUGIATE I CARBOXYVINYL TANISTER STANDYCOCCUU AUTEUS CHOUSIAATE SYNTHASE ESCHEDICIA COLU SALMONELA TYPHU	ROBABLE ARGINDICORNITHINE ANTIPORTER	PSEUDOMONAS AERUGINOSA	П	186-420							
LYEARGONN-BORDOG PROTEIN (LAO) PRECURSO ESCHENCHA CÓLI PROSEHOSIBIZIANTE LEARBOXYVINYLTEANISER STÁPHYLOCOCCUS (UREUS CHONSHATE SYNTHASE ESCHENCIAL COLI SALMONELLA TYPHI	ANDNO-ACID ACETYLTRANSFERASE	ESCHENICHIA COLI	83-109								
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CHONISMATE SYNTHASE ESCHENICIA COLI	PHOSPHOSHIDCIMATE I CARBOXYVINYL TRANSFER	STAPHYLOCOCCUS AUREUS	021-98								
TOWNSTRIANT SYNTHASE	CHORISMATE SYNTHASE	ESCHENICIÓN COLI	64.95								1
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	ACCREGATION SUBSTANCE PRECURSOR	ECONTRIBICION CONT	27.150	:							
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1	ASPARADINE SYNTHETASE D		116-141								
	INSTRUMENTAL PROPERTY ASM.	ESCILIATION CO.	12.5								
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PASPA SERMA	ASPARTATE AMMONIA	DACH LINE ICHENIFORNIS	252-288		!	:		:			
PASPO BACL	LASPARAGINASE	COMING CHINSANTIGINI	168-218								
NO ERWCH	LASPARAGINASE PRE	CAMINA CHES COLLEGE CO	94-10								
A CONTACTOR	CLUTAMINASE-ASPAR	ACINE LOBACIEN OCO	154-301								
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	A B C. PANOS LICCONATE SYNTHASE	ESCHERICHIA CUCI	367.114		L						
		METHAMOSALICINA BAJKEN	17	201.245							
VV I WEINY	THE STATE STATE	STAMM OCOCCUS AUREUS		76.6							
PATER STAND	TOTEN INC. ALT. DISTOR THE ANCHOR TONG ATPASE A	ENTEROCOCCUS FAECALIS	2								
KY EMILY	OI ASSUMEDITED	ENTEROCOCCUS PAECALIS	200.010								
KS ENTRA	OTASSIDACOFFEA	SALMONELLA TYPHIMUMUMI	303-330			\downarrow	-	ļ			
THE SALTY	AG(3+) TRANSFOR!	cynerotococcus sh	333-260				+	ļ			
The STAGE	ATP SYNTHASE A CHAD	VIBRIO ALGINOLYTICUS	2:3			1		1			L
PATTE VIBAL	ATP SYNTHASE A CHUIN	ANABARNA SP	9.76	2							<u> </u>
TPA ANASP	ATP SYNTIASE ALTIA CITAIN	PACIFIE MEGATERIUM	4-36	453.480							
PATPA BACME	ATP SYNTHASE ALPHA CHAIM	ESCHEMICHIA COLI	486-513				1	1	-		L
IPA ECOLI	ATP SYNTHASE ALPHA CHAIN	ENTEROCOCCUS FAECALIS	4-16	\$ 2 2		1	1	1	1		
TA ENTRA	ATP SYNTHASE ALPHA CHAIN	LANCOR A CALL ISEPTICUM	362-409				1	+			L
PATPA MYCGA A	A ATP SYNTHASE ALPHA CHAIN	Parcel Angelon Control MODESTUM	6-36			_		1	1		
TPA PROME	S ATP SYNTHASE ALPHA CHAIN	AUG-DOCUMENT CAL BURBUNA	165-200	459-416					 		l
TO A MORE	I ATP SYNTHASE ALPHA CHAIN	THOUGHT TOTAL AND	110.145	\$62.589							
A TANK ACT	ATPASE ALMA CHAIN	SULFOLOBUS ACIDAL ALIANOS	7								1
100	ATP SYNTHASE ALPHA CHAIN	SYNECHOCOCCUS SY	1	162.389		-	L			_	4
	ATT CONTINACE ALPHA CHAIN	SYNECHOCOCCUS SY		5			-	L			
IFA STREE	ALCONOMINATION OF THE PART CHAIN	SYNECHOCYSTIS SP			+	-	-				
TA STATE	ALF STRUCKS AL DUA CHAIN	INGRAMOPHILIC BACTERUM PS-3	9	1	1	+	+	-	L	L	
TA TEP	AIF STRIPAGE ALCONOMINA	VIBRUO ALCIMOLYTICUS	200		+	1	-	-			L
TA VIEW	AIP SINITAGE AND COLOR	ANABAEWA SP	200-301	200	$\frac{1}{4}$	1	+	-	-		L
PATPE ANASP	P ATP STRUMASE BEING COMM	MACOLUS FOUNDS	163-190				1	1	-		L
TIPE BACK	ATP SYNTHASE BEIN CHAIN	LAYCOPI ASMA GALLISEPTICUM	375-402			-	$\frac{1}{1}$	1	-	ļ	L
PATPB MYCGA	IA ATP SYNTHASE BEIN CHAIN	BHODOGODI LUM RUBRUM	339-386			-	4	1	1	1	-
PATTE RHORU		CIT SOLOBLIS ACIDOCALDAMUS	161-191	L				1		1	ļ
PATPS SULAC	ATPASE BETA CIVI	S SOURCE OF THE SE	381-408				4	4	1		\downarrow
PATTE SYNFI	ATP SYNTHASE BET	SINGUICACO SE	291-318	301-408				4		$\frac{1}{4}$	1
ATTA SYLD	ATP SYNTHASE BET	STRECTOCOCOS ST	181.408	L	-						4
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SANA COTA	ATP SYNTHASE DEL	ANABALINA SI	41.90	3	-	\mid	-			4	4
TOTAL MATERIAL		BACGLUS FIRMUS	113,150		-	-	_	_			4
TATE BACK	ATP SYNTHASE DEL	BACELUS MEGATERUM		-	-		-				4
ATTO BATE	ATP SYNTHASE DEL	ENTEROCOCCUS FAECALIS	100	118.149	-		-				4
ATPO PROMO	AD ATP SYNTHASE DELTA CHAIN	PROPIONICENIUM MUDES I UM	134.183	Т	-	L	_	L		4	4
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PATPE BACFI	ATP SYNTHASE EPSILON CHAIN		27.60	+	+	1	1			I
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PATPF MYCGA		ISEPTICUM		10.18	1			_		
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PATTE SYNDS			1	28-122			+	-		
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STAN CALL			176-310				-			
		COLI	253.283		_			-		
2	THE STATE OF THE S	LISEPTICUM	Г	92.140	_					
TAIRU MYCCA	ALL STRITINGS CAMPING CHAIN		270.297			-		_		
PATPG RHOXU	ATP STRIBLASE GAMMA CHAIN		280.307							
PATPG SYMPI			Т	100 000				_		
PATPO SYNY3	ATP SYNTHASE GANONA CHAIN		T		1					
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PATPX BACFI	ATP SYNTHASE BETA CHAIN		2	136-36		<u> </u> 	1			
PATPX RHORU	ATP SYNTHASE B' CHAIN	JBRUM	٦			1				
PATPX SYNP!	ATP SYNTILISE B' CHAIN		7	21-155				+		
PATTEX SYNDS	ATP SYNTHASE B' CHAIN		818	1						
PATPX SYNYS	A1P SYNTHASE B' CHAIN		20-13	1				+		
PATPZ BACME	E ATP SYNTHASE PROTEIN!	ושור	14.62		1		+			
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PAVEB PSESO	AVRULENCE B PROTEIN	PSEUDOMONAS SYRUNGAE		207-177	+	-				
PBA71 EUBSP	7-ALPHA-HYDROXYSTEROID DEHYDROGENASE		66.07	1	+	+	-	-		
PBA72 EUBSP	1.ALHIA-KYDROXYSTEAOID DEHYDROGENASE	EUBACTEUUM SP	(C-9)	t	\dagger			+		
PBACH HALPON	HALORHODOPSIN	HALCHACT ERIUM PALOBIUM		1			 	+		
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PBAES ECOLI	PBAES ECOLI SENSOR PROTEIN BAES	GALACTIAE	T	118.204	267-306 34	141-185 487-524	362-589	1014-1041	<u> </u>	
PBAG STRAG	IGA FC RECEPTUR PRECURSUA		١.	Т	Ť	Т	Т		L	
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STATE OF THE PARTY	BAY PROTEIN	ESCHENCHIA COLI	\$ ≅	-	-					
PRCO ECOL	+		6-35							
PBCHBI CHOCA	METHYL TRANSFELL		1000-1033			_				
PBCID NIOCA			9						_	
PBONS CLOPE	BACTERIOCIN BONS	CLOSTRUDIUM PERFRINGENS	8.2	\$85.646						
PBCPA PROAE	_	PROSTNECOCHLONIS AESTUARII	3							
PBCSC ACEXY	CELLULOSE SYMTH	ACETOBACTER XYLINUAL	131-138	1055-1012						
PBCSD ACEXY	CELLULOSE SYNTH	ACETOBACTER XYLINUNI	10.37							
PBENA ACICA	BENZOATE 1,2-DIOX	ACINETOBACTER CALCOACETICUS	130-217	1						
PRETT ECOL!		ESCHENICHIA COLI	20.230	1	1		1	-		
PBEXA HAED	BEXA PROTEIN	HAEMOPHILUS INFLUENZAE	┪					1		
PBEXC HAEDI	BEXC PROTEIN	HAEMOPHILUS INFLUENZAE	✝	286.33	1	1	+			
PBEXOD HAEDN	BEXD PROTEIN	HAEMOPHILUS DIFLUENZAE	67.50		1		1	\downarrow	1	
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BOAL CLOTU			245-272	1	Ì	Ì	T	Ī			
DOAL KLEPH			105-132				T				
PBGAL L'ACDE		רחצ	<u>_</u>		1			T	Ī		
BOAL STRIR	BETA GALACTOSIDASE		39-86	179.206				Ì			
BOAL SULSO	SETA-GALACTOSIDASE		139.156								
BOAM LEULA	BETA GALACTOSIDASE SMALL SUBUNIT	RECUS	106-140		İ	1	:	:	į		
PROAM SULSO	BETA-GALACTOSIDASE		1	418-445	٦						
PROILA CLOTM	DETA-GLUCOSIDASE A		239.286	315.409	554-581	631.665					
MCO D WILL	THERMOSTABLE BETA-CLUCOSIDASE D		Т	\$36.363				٦			
	RETA CHICURONIDASE		ı								
			Т	416.46.	617.709	118.765					
		2	Т	Т	Т						
	ACC DIVI		3					•			
PBINI STAAU	LASE DIN		163-197	1							
	SOL TASE	CTABAYI OCOCCUS AUREUS	163-190								
PBINE STANU		BACH 115 SPIIAERICUS	33-60								
		DACH LIE CHIAFRICUS	145-172								
PBIOB BACSH	BIOTIN SYNTHETASE	ESCAPE ICHIA COLI	130-157								
PBIOB ECOLI	- 1	BACH LIS SPRAFBICUS	144.171								
PBIOD BACSH	DETHIOBIOTIN STATINASE	SACH LIE CEBEIN	111-16	115-305							
PBLA! BACCE	BETA-LACTAMASE PRECURSOR, TYPE I	SACRETOR OF THE TENTAN	152-179	204-231							
PBLAI HAEIN	BETA-LACTAMASE ROB-1 PRECURSOR	MAEMORNICOS MY LOCATES	18-63	201-228							
PRI AZ BACCE	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS CENCUS	19.61								1
PRI AS BACSP	BETA-LACTAMASE PRECURSOR, TYPE II	BACILLUS SA	15.0	95.129							
PRI A1 BACOS	BETA-LACTAMASE PRECURSOR, TYPE !!!	BACILLUS CENEUS	9								
	BETA-LACTAMASE PSE-4 PRECURSOR	PSEUDOMONAS AERUGINOSA	77.	700-227							
	RETA-LACTAMASE PRECURSOR, TYPE II	9ACILLUS CEREUS					L				
	RETALL ACTAMASE PRECURSOR, TYPE II	BACTEROIDES FIXICILIS	2	176.103							
BRI AC BACKE	BETA-LACTAMASE PRECURSOR, TYPE I	BACILLUS CENEUS		51.5							_
PRI AC BACL	BETA-LACTAMASE P	BACILLUS LICHEMUTORMIS	191.221								
PBLAC PROPE	BETA-LACTAMASE PRECURSOR	PROFESS ME CABIS	5	740-367							
PRLAC PROVU	BETA-LACTAMASE	PROTEUS VOLUMUS	8								
PRI AC STIAL	BETA-LACTAMASE PR	STREPTOM TES ALBOS O	21:12								
PRI AD KLEPN	BETA-LACTAMASE PR	KLEBSIELLA PREUMUNIAL	20.02	98-136	L	L					
PBLAI STANU	PENCEL DYASE REPR	STAPHYLOCOCLOS AGRECOS	20	235-261							1
PRI AD ECOL	BETA-LACTAMASE P	ESCHERICHIA	181.18				L				_
PRIAP ECOLI	-	ESCREDICHIA CULI	28	35.53							
PRI AR BACL	REGULATORY PROT	BACILLUS LICHENIFORMIS		122.161	134.361	211-112	\$63-539				4
PRIAE STAND	REGULATORY PROTE	STAPHYLOCUCLUS AUREUS									4
AGENT TARPA	BASIC LENGRANE PI	TREFOREST FALLIDOM	2		L			L			
DESCRIPTION OF STREET	MALTEDRUG RESISTA	BACILLUS SUBTILIS	19								
PRINTA PARPU	BENZENE 1.3-DIDXY	PSEUDOMONAS PUTIDA				L					
PRINZE PSEPU	BENZENE 1,3-DIOXYC	PSEUDOMORAS PUBLICA	1			L	L	L			4
PRINZO PSEPU		PSEUDOMONAS PULIDA	163.23	262-290	211.35	391-425	3.53				4
PRPC3 DECAM	-	DESOLPURCUODOS AMBIA ALCAS	360.387	113.340		L		L			
PRRAR PSEAE	CARAGEA PROTEDY	PSEUDOMONAS AEKUGINOSA	3		-				L		
PRIAE PSEAE	_	PSEUDOMONAS AERUGINOSA	2		\downarrow						Ц
PREAD PSEAE	BRAG PROTEIN	PSEUDOMONAS AERUGINOSA	716.466		ļ						
PRTH ECOL	VITAMON BID RECEDI	ESCHEMICHA COLI	5	1	L	L			L		_
PRTIE ECOL	VITAMON B12 TILANSI	ESCHEUCHIA LOLI	100				L				Ц
PRVGA BORPE	-	BONDELELLA PERIOSSIS				L	L			Ц	Ц
		BOXDETELLA BRONCIUSET (ICA	116.143		L		-				
PBVCB BORPE	ERIPLASMIC PROTE	BORDELELA PENTOSSIS	30.66	302-329		L	L		Ц		4
PBVGC BOLD	E SENSOR PROTEIN BVGC	BOWEITELA PERIOSSIS		т	\$01.531		L		Г		
PBVGS BORBA	A VIRULENCE BVGS PROTEIN PRECURSOR	BOXDETELLA BRONCHISETTICA	300	Т	Т	115-842	T	869.998	1159-1207		
PRYA CLOBO	ROTTH DRIDG NEUROTOXON TYPE A PRECURSOR	CLOS TILDICIA BUT ULINUM		3.	Т	007.128	Т	1004-1031 1058-1089		_	_

1000	100.000	Prokarvolk Seasonces	Г		П	\mathbf{I}	Γ	_	П		
FILE NAME			H	L VZEV		AREA	AREAS	AREA	<u> </u>	VBCA!	ARTA S
PRXC1 CLOBO	BOTUL INUM NEUR		<u> </u>	3	1	Т	7			1	T
PBXD CL080	BOTULINUM NEUK		\$ 8	526-576	727.770	٦	-1	٠,	000	1	T
PBXE CLOBO	BOTULINUM NEUR		154-701	36.38	26.75	٦	Т	_	A	1	Ī
PBXE CLOBU	BOTULINUM NEUR		<u>2</u>	36.36	704.753			4101.744		1	
PBXG CLOBO	BOTULINUM NEUROTOXIN TYPE F PRECURSOR		969-710	200	192.919	1013-1040	37-175	0171-6810	1	Ť	
PCS30_NGCAE	CYTOCHROME CS50		2	111 000	101	704 764	(1).(4)		\dagger	T	T
PCADA BACTI	PROBABLE CADMINA TRANSPORTING ATPASE	BACILLUS FIRMUS	200	20,000	241.60	т				T	ĺ
PCADA STAAU	ROBABLE CADMI		201.70	417.441						Ī	
PCADC ECOL	TRANSCRIPTIONAL ACTIVATOR CAUC		301.340	416.40	\$10.55	619-646					
PCASA YERPE	FI CAPSULE ANCH		200							Ī	
PCAPA BACAN		BACILLUS ANTIBACIS	2							Ì	
ACAPS BACKE	CAPB PROTEIN	BACILLUS AN INCACIS	100 376							Ī	
PCAPP ANAMI	PHOSPHOENOLPYRUVATE CAUBOXYLASE			781 691	11.				T	Ī	
PCAPP ANASP	PHOSPHOENOLPYRUVATE CARBOXYLASE	ANABAENA SP			77.					T	
CAP COAG.	PHOSPHOENOLPYRUVATE CARBOXYLASE										
KAP ECOLI	PHOSPHOENOLPYA		70.6						1	Ì	
PCARA BACSU	CARBAMOYL-PHOSPHATE SYNTIASE	BACILLUS SUBTILIS							İ	Ī	
PCALL BACSU	CARBAMOYL PHOSPIKATE STRITIKASE		1777								
CAM FOR	CAUBAMOTIL FROSTIA IE STRI MASE LANGE CITA	Afriketis	Т	87.114							
LAI2 SIANO	CHLORAMITERIC	STANKS OCOCCIS ALBERIS	T	67.114						Ī	
PCATO STAND	COLUMNICAL ALE ITLINANS EXASE	ACTUALIZACION CALCOACETICUS	11-65								
Y VCC	CATECHAL LAW	MACHINE ATTENDED TO THE TAKEN PILLING	440.470								
S V V	PERUALINASE CAL	ECCEPTION FOR I	29.60								
TAIN ECOL	CALALASE TUT	reus	453.480								
	100 March 100 Ma	RIUN	25.51	\$10.00							
	CAPACACE UPI		13:30								
CAT CALCO	CHE ORANDHEMICOL ACETYL TRANSFERASE	CAMPYLOBACTER COLI	=								
CAT GOD	CHA ORANO HEDATIC	N. I.	81.13								
PCAT ECOL	CHECKALOPHENIC		911.5								
PCAT PROM	CHE CORANGHEDICOL ACETYL THANSFERASE		92.119								
PCAT STADY	CHILORANDHEMICOL ACETYL TRANSFERASE	STAPHYLOCOCCUS INTERNITIOUS	=								
PCAT STRAG		STREPTOCOCCUS AGALACTIAE	-								
PCBME COXOLU	CRIE PROTED	COXIELLA BURNETII	96.50								
KORT THEN	CALBOXYPEPTIDA	THE LANGACTINGANY CES VULGARUS	200							1	
100 Y	TWA MULEOIDTLINANS EASE	escurpocorio con	10.00							T	Ī
PLOS STATE	TOTAL PROTECTION	SYNECHOCOCCUS SP	217.756	311.112	445.486						
THE THEFT	CYCLOMAL TODES	THERMOANAEROBACTER ETILANOLICUS	201.201								
A DOM		BACKLUS NACESANS	439.466	616-643							
PODG! BACK	CYCLOMAL TODES	BACELUS MACERANS	210-231	436.466	913.642						
PODGT BACCI		_	217.244	442-412	159-65						
PODOT BACL	CYCLOMALTODENT GLUCANOTRANS PRECURSOR		217.244	215-255	\$94.647						
PCDOT BACOH	I CYCLOMALTODEXT CLUCANOTRANS PRECURSOR		10-01		·						
PCDOT BACS	CYCLOMAL TODEXT GLUCANOTRANS PRECURSOR		210.237	433-462	915.642					Ī	
PCDOT BACS	CYCLOMAL TODEXT GLUCANOTRANS PRECURSOR		409.47								
MODEL BACS	~	BACILLUS SF	20.20	79-66	10.00				Ì	T	
SOVE 500	CTCLOMALICOLATI GLUCAMOINAMS PRECUASOR				3						
STATE OF THE STATE	CTCLOMALIONEAT GEOCANOTRANS PRECIESOR		77							Ī	
POOL PACE	CYCLOMAL TODEXT CLUCANOTINAS PRECURSOR		212.238							T	
1	CALLOMAL 1005	_		364.134						T	ĺ
T T T	COLINE I PROTE	SHIGELLA SONNE	15.3	284.335	411.440						
	CON ICIN ES	ESCHERICHTA COLI	334.366								
TOP FCOL	COLICINE	ESCHENCHIA COLI	334-368								
MOEAN ECOL	COLICIN E6	ESCHENICHIA COL!	334-368								
PCEAS ECOLI	COLICIN B	ESCHENCHIA COLI	283-341								

PCCENE 11	107617814	Probaggite Sequences	ANIAL	ONE A L	7	777	1				
	PROTEIN	MIA COLI	=		1	1	i				
DOS GAS	COLICIN D		16-227			1		T			
-	COLICINI		Т	133:300			-	1		i	: :
	COLICINI		216-258								1
т		CHROBAC LEAST CLASSICS	10.00								
Ļ	SOPENICILIAN NEPAERASE		26.99			415-452					
Т	COLICEMIA PROTEIN		68.93	185-287	330-413	25.65					<u> </u>
Τ		PALITA.	29.89								
CELA ACENT	UTO TRIBYLY TRANSFERASE		76-103								
	MOTENCELA			1							
	CFAN FINGRIAL SUBUNIT A PRECURSOR	ESCHEDICHIA COLI	138-167	388-456	\$.50	T					L
Т	CFAN FINGRIAL SUBURIT C PRECURSOR		133-160								ļ
	CFAN FUGDIAL SUBURAT D		Г	344-271							1
	GAN FORBUAL SUBURIT B	ESCIEDURIA CULI	38.5								
1	10 KD CHAPERONDA	_	10.19								
	10 KD CHAPERONIN		44.01					-			
THE STATE OF	IS KD CHAPERONIN	CHLAMYDIA TRACHOMATIS	17.6								1
-	DED CHAPERONIN										4
Т.	NIN CHAPERONIN			T							
Т	A LIN CUA DEPONING								L		
DHIS LEGISLA	TO AN ORANGE OF THE PROPERTY O		*								
STATE MESS	The Care Course	THERMOPHILIC BACTERIUM PS-3	6.60						L		
CHIS TIER!	TO CAN EXCENSE	TIC BACTERIO		41.	777.367						
CHEG ACTES	60 KD CHAPTACHIA		2	2	30.5					L	
PCHAS AGRITU	60 KD CHAPEKUNIN	ACTENUM	2							L	
PCHISO AMOPS	40 KD CHAPERURIN	BACH LUS SUBTILIS	26.33 26.33	3					ļ	L	L
PICHED BACSU	60 KD CHAPEKONIN	HORRELIA BURGDORSEN	135-163	3						Ļ	_
DEMOS OFFICE	40 KD CHAPERONIN	RELICELLA ABORTUS	117.144	36.56							L
PCHIS BRUAB	60 KD CHAPERONIN	CHE AMYDIA PWELDHONIAE	-					1			-
PCHEO CHE PA	60 KD CHAPEKUNIN	CHEANTDIA TRACHOMATIS	ē					1		L	L
PCHEO CHETA	66 KD CRATERONIN	CHROMATIUM VINOSUM	2000	***	107				_		Ц
NO CORN		CLOSTAIDIUM ACETOBUTYLICUM	717-917							L	_
20 C OV	SO RU CINVERNATIO	CLOSTRIDIUM PERFRINGENS	100								
200	SO KU CHANESTONIN	COXTELLA BURNETII	77.00								Н
	SCHOOL STATE OF STATE	HAEMOPHILUS BUCKEY!							L		1
NAME HAND	SO KU CHATERONIN	LEGIONELLA MOCDADEI	1			1	1				L
	TO CONTRACTOR OF THE PARTY OF T	LEGIONELLA PNEUMOPHILA	7		32.5				L		
2001	160 KD CHATENONIA	MYCOBACTERIUM LEPRAE	2	ê e	1		1	-			L
NO MACE	SO KIN CANADA SANA	MYCOBACTERUM TUBERCULOSIS & BOVIS					ļ		L	L	L
SEC.	т	PSEUDOMONAS AERUGINOSA	8		77.	1		ļ		L	L
NAME PER AL	60 KD CHARLAND	INTERNAL LEGUNANOS ARUNI	9	321-326	8		1	ļ	-	-	-
	10 KU CAVENORUS	NOKETTSIA TSUTSUGAANSHI	10.130	81.10	8	1	1	1	-		L
S S S S S S S S S S S S S S S S S S S	O TO CHARLES OVER	SYNECHOCOCCUS SP	2			\downarrow					L
200	September 2019	SYNECHOCYSTIS SP				1	ļ		L	_	L
CARS SAND	S CONTRACTOR OF THE PARTY OF TH	THERMOMELIC BACTENIUM PS.)	30.		1	1	1	-	-		H
ON ON	7	STREPTOMYCES ALBUS G					-	-	-		L
NE SE	Т	VIBILIO HARVEYI	7				-	-			L
SEA PO	A MINORAL MANAGEMENT	BACELUS SUBTELIS	3	340		1	-	-	-	L	H
NODA BACS	CHEMOTOR PROTECTION CHEA	ESCHENCHIA COLI	*			\downarrow	1		-		H
100	CHEMOLOGICAL PROPERTY	SALMONELLA TYPHINIUNIUNI				1	1		-		L
A TAL	COLMOI AND TROIT	BACELUS SUBTILIS			\downarrow	1	1	-	1	L	-
DOES MACS	CHEMIC BONDING	ESCHENCHIA COLI			1	-	1		L	-	L
NO EN	Concessor and the concessor of the conce	SALMONELLA TYPHINOPULMI		1	1		1	-	l		-
MOEW SALT		ESCHENCION COLI	2	1	1	1	1	-	-	<u> </u>	Ľ
MORY EXOC	CHEMOLOGICAL PROPERTY	SALMONELLA TYPHINURUMI		13	1	-	1	-	-		L
	CHUTDIASE AL PREC	BACRILUS CIRCULANS			1	-	-	-			
94.14		AL CLOMONAS SP		-		-	L				
		VALUE DAVID OF THE PARTY.									

PCCENE	110717014	Prohamotic Sequences	:				AUVACA	Aura Saura 7	AREAT	ARFAR	AREA
FILE NAME		ORGANISM]		1			Ţ			
MOHID BACCI	CHITINASE D PRECURSOR	BACILLUS CIRCULANS	_[1		Ī	Ī	
PCHIT SACEA	CHITINASE	SACCHAROPOL YSPORA ERYTIIRAEA	11.24					Ī			
POUT STRUL	CHITINASE 63 PRECURSOR	STREPTOMYCES PLICATUS	2 7 7 7		Ť						
PCHOMU BACSU	HORISMATE MUTASE	BACILLUS SUBTILIS	50,176		T	T	-	İ		 -	<u>.</u>
PCHOD BREST	HOLESTEROL OXIDA	STEVIEW STEVENS STEVENS	70.104	T		Ì					
PCHTA VIBOR	HOLERA ENTEROTO	VIBRO CROLEGOE	T	107.101		T	T				
PCINA AGRIU	ETA-(I->3)GLUCANE	ACRORACTED IN TIMES ACIENT	2								
PCHVE AGRIU	RECEPTOR PROTEIN CHUE PRECUASUR	CHICANTER EREININ	415:462								
PCB CITY	TIKOLYSIN PROTEIN	ECONOMIA COLI	6.53								
PCIM ECOLI	OLICIN I RECEVIOR	DATE OF STREET	178-405			T					
CISA BACSU	PUTATIVE DINA RECOMBINASE	ACTURE ALITA ATION	W1.171			T					
PCISY ACIAN	CITICATE SYMPLASE	BACH LIN COACH ANS	14.51								
PCISY BACCO	CITILATE SYNTHASE	BACILLOS CONCOLATAS									
PCITA SALTY	CITRATE-PROTON SYMPORT	SALMURELLA ITRIBICALIONI				İ	Ì		ĺ		! !
KCTIN KLEPN		KLEBSIELLA PNEUMONIAI:	77	Ì		İ	Ť	-	T		
MOTHS WITH		SALMONELLA DUBLIN	7			1	Ī				
SALES SELEC	CITALTE-SODIUM SYN	SALMONELLA PULLORUM	277	-		1	İ				
PCLCA PSEPU	CHLOROCATECHOL I,	PSEUDOMONAS PUTIDA	9:10	i		Ì	Ì				
PCLDI ECOLI	CHAIN LENGTH DETE	ESCHERICHIA COLI	┪				1	T			
PCLD2 ECOL!	CHAIN LENGTH DETE	ESCHEMICHIA COLI	1	7.	Ī	Ì	Ì	Ī			
PCLD SALTY	HAIN LENGTH DETE	SALMONELLA TYPHINIUMI	J	717.1		1	1				
PCLOS CLOHI	ALPHA-CLOSTIUPAIN PRECURSOR	CLOSTRIDIUM HISTOLYTICUM	1								
DOJ YOU	ATP-BINDING SUBUNIT CLPA	ESCHENCHIA COLI	655-695			1	1				
PCLPA RHOBL	CLPA HOMOLOG PROTED	RHODOPSEUDOMONAS BLASTICA	٦				1				
POLITIE BACHO	CLPB HOMOLOG PROTEIN	BACTEROIDES NODOSUS	7	42.476	558-505		1				
LION ECOL	CLP8 PROTEIN		╗	55.58			1	1			
MOZA X4.04	CLPX HOMOLOG PROTEIN		٦	132-350							
POLYX ECOLI	ATP-BINDING SUBUNIT CLPX	ESCHENICHEN COLI	~ ~				1				
PONIS ECOL	T. J. CYCLIC NUC T. PHOSPHODIES TERASE PRECURS	ESCHENICHIA COLI	20.73				1				
PCODA ECOLI	CYTOSINE DEAL/DNASE	ESCHENICHIA COL!	65-129								
PCOMI BACSU	A COMPETENCE PROT	BACILLUS SUBTILIS									
PCOMO BACSU	J COMPETENCE REGULATORY PROTEIN	BACELUS SUBTILIS	17-1					Ī		ľ	
PCOPE STANU	COP-4 PROTEDN	STATE OCCUDE AUTEUS	66.5				T	Ī			
PCOPB PSESM	COPPER RESISTANCE	PSECUCIALISM STRUNGAE						I			
COLA ECOLA	MAGNESIUMCOBALT TRANSPORT PROTEIN CURA	CALINOVER I A TYPUNG BUILD						Ī			L
PCORA SALTY	MAGNESSUM/COBALT		9					Ī			
PCOTE BACSU	SPOKE COAT PROTEIN E	BEADVELTZOBITE JAPONICIA	180-407					Ī			
TOX BEACH	CATION OF COMPACE BOI VEETING I	PARACOCCUS DENITTURICANS	383-410								L
PCOXI PADE	CTIOCHACHAE COMMASE POLITICALINE	RHODOBACIER SPICKEROIDES	in Table								L
PCOXI BACE	OVERAGE ACCEMBLY FACTOR	BACILLUS FIDMUS	19-91								
NO.	I OYDASE ASSEMBLY PACTOR	BACILLUS SUBTILIS	49-76								
PCP B NEIGO	CRYPTIC PLASAID PROTEIN B	NEISSEALA GONORAHOEAE	12.99	602-591							
NCPSB ECOL	MANNOSE 1-PHOSPIL	ESCHENICHIA COLI	309.336								
MOSS SALTY	Т	SALMONELLA TYPHOMUNUM	311.338				1				
PCPXA ECOLI	SENSOR PROTEIN CPXA	ESCHERUCHIA COLI	254-281								
PCPXG STRSO	CYTOCIDEONG PASO 105CI		157-184								\downarrow
PCPXU SACER	6-DEOXYERYTHRONOLIDE B (DEB) HYDROXYLASE		333.360								
PCPXON BACSU	U CYTOCHOOME P450 109	BACELUS SUBTEIS	240-283								
PCPXW ANASP	PROBABLE CYTOCHROME P450	ANABAENA SP	911.15								
PCLL7 BACTI	27 KD CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	133-187								\downarrow
PCR17 BACTM	1 27 KD CRYSTAL PROTEIN	BACII LUS THUMNGIENSIS	13)-117								
PCR41 BACSII	I 9 KD INSECTICIDAL TOXIN	BACII LUS SPIIAFRICUS	176-308								\downarrow
PCR42 BACSH	I 9 KD INSECTICIDAL TOXIN	BACIII US SPIAFRICUS	200.92								
PCR43 BACSH	ALP ENSECTIONAL TONIA	BACH I US STRAEMOUS	307.314	243.330	470-461						
PCR70 BACTO	TO NO CREST AL PROTEIN	BACH DE TAR BACHENES		2	27.464						L
PCR70 BACTO		MACILLUS INDININGIENES									

PUCKNE	107117814	Probanyaile Sequentes	AREAL	ARIA	$\overline{\ }$	10110	17117	3000	7 7 77	4	3
	ROILIN	A CHAIN THE INCIENSIS		7	\$ F						
PCATO BACTT	NE KD CRYSTAL PROTEIN		93-133		£ 200 200 200 200 200 200 200 200 200 20						
PCRTI BACTK	70 KD CRYSTAL PROTEIN		111.76	113.414							
TRIE BACTI	13 KD CRYSTAL PROTEIN		1111	191-214	552-593						
PORT BACTK	TO KD CRYSTAL PROTEIN	BACILLOS INOMINIONES	308-335	\$02-529							
PCR77 BACT!	TKD CAYSTAL PROTEIN	BACILLOS (MONINGERIA)	001-01								
CLEC ECOLL	ENSOR PROTEIN CREC	ESCIENCIA COL	===								
Н	DOVER MEMBRANE PROTEIN CRED	EXCREMENTA COM	Γ	127.154							
LOOP ECOL	CATABOLITE GENE ACTIVATOR	ESCHERCRIA COLI &	Γ						j		
•		SHIGELLA PLEANEN	100	27.154							
VALUE CALLY	CATABOLITE GENE ACTIVATOR	SALMONELLA TYPHINIUNIUNI	T								
Τ		KLEBSIELLA AEROGENES									
	WIVTOENE DEHYDROGENASE	ERWINIA HEABICOLA									
PCRTI EXWILE	THY LUCKE DEN LONGERANDE	AHODOBACTER CAPSULATUS	39-416								L
	PHYTOENE DEHTOROG	RHODOBACTER CAPSULATUS	3	334.361			;	!	:	•	
PCRTJ MIOCA	CRTJ PROTEIN	DACH FOR THURSINGS	331-355	175.303	_	İ	!				
CAYS BACTA	132 KD CRYSTAL PROT	DACTILL DE TIMBERGIENSIS	130-771	163-891	1053-1080					1	ļ
PCRYS BACTB	130 KD CRYSTAL PROT	DACTION THIS PACIFICAL	736-770	16.06							1
CRYS BACTE	133 KD CRYSTAL PROT	BACILLOS INGUINACIONES	218-252	127.107	175-802						1
CRVS BACTI	NO KD CRYSTAL PROT	BACILLUS TITUTURGIENSIS	111.111	165-892	1053-1050						
PCRYS BACTK	N KD CRYSTAL PROT	BACILLUS TITUIGNOIENSIS	716.770	16-068			_		:	•	_
PUBLIC RACTS	INDIED CRYSTAL PROTEIN	BACILLUS THURINGIENSIS	10.00	2	1041.1080		· •			_	_
1	CANCELL TIME OF STAL PROTEIN	BACILLUS TITURINGILINIS		80			j				
2	AND COVERA PROTEIN	BACILLUS TINUMUGIENSIS			100	774.803				_	L
CATI BALLE	CAN CANCEL AND THE PARTIES.	BACILL US THURUNGIENSIS	217:23								_
CITY BACTI	DO FOUND AND AND AND AND AND AND AND AND AND A	BACKLUS THURTHGIENSIS	137.71	9						_	L
CAYT BACK	Date Carsing Property	BACILLUS THUMINGIENSIS	396-770	20.0			1		-		-
PORTU BACTA	IS KOCKYSTAL PROTEIN	BACH LUS THURINGIENSIS	117-251	20.22	134-80					-	ļ
PCKYU BACTI	DO KD CRYSTAL PROTEIN	BACTI LIK TSUTENSIS	110.77	866-1193	1034-108					1	1
PCRYU BACTK	PCRYU BACTK 131 KD CRYSTAL PROTEIN	BACH LINE THE PROPERTY.	111.711	168-1192	1053-1080					1	1
PCRYV BACTA	IN KD CRYSTAL PROTEIN	BACH LIFE THE PAGENSIS	110-131	345 772	819.810					1	1
PCRYV BACTI	115 KD CRYSTAL PROTEIN	DACH LIFE TAITEMENTS	136.770	16.001						1	1
PCRYV BACTK	11) KD CRYSTAL PROTEIN	PACIFIC TANBOACIENSIS	1745-779				_			1	+
PCRYW BACTA	INDIKED CRYSTAL PROTEIN	MACHINE THURINGLENSIS	408-650	969-699	6192.618					1	1
PCRYW BACTR	133 KD CRYSTAL PROTEIN	TATE TO THE TATE ASIS	97:110	111.254	605-633	10.00	3		1	4	1
PORTX BACTK	139 KD CRYSTAL PROTEIN	EPONE BOOM COLL	\$ 77	i% ;%	1905	144.378				1	1
PC\$33 ECOL!	PCS33 ECOLI CS3 PtLJ SYMTHESIS 43 KD PROTEIN	EXTENSION COL	-1-8	2.5	208-242					1	+
PCS33 ECOLI	CS) PLLI SYNTHESIS 48 KD PROTEIN	Common com	20.43	34.108			L				4
DOS MEN	CSS PILLS SYNTHESIS 33 KD PROTEIN	ESCHEDICHIA COLI	10.00	184.611			_				4
PCSG HALHA	CELL SURFACE GLYCOPROTEIN PRECURSOR	HALDBAC I ERIUM HALDBICK	2	16: 66		L					-
PCSG HALVO	CELL SURFACE CLYCOPROTEIN PRECURSOR	MALUBAC I ENDM VOLCASSI	19.107		L						-
PCSG NOTIFE	CELL SURFACE CLYCOPROTEIN PRECURSOR	METHAMOI MEANIUS FER 1003	201.05	ļ							4
PCSO METSC	CELL SURFACE CLYCOPROTEIN PRECURSOR	NETHUNG DELANCE SOCIADIOS	9.7.					L			4
DOZE BOOM	CS1 FOCBALAL SUBUNCT B PRECURSOR	ESCENCHIA COCI				L	-	L			
KTITA GLOVE	B COA-TRANSFERASE SUBUNIT A	CLOSTRUCTOR ACETOROLITICOS	134.208		_	_					4
AGD WIN	COA-TIANSFERASE SUBUMIT B	CLOS FROIDE ACETOROLITES OF	101.01			L		L			-
PCTILB NEDATE	DANEEL MEMBELLINE PROTEDY CTR.B	NEISSENG PIENING HOUS	1	134.151	8	117.351				j	-
ACK PACK	CYTOTOXIN PRECURSOR	INSERDOMONAS ACADOMICOS	2	16).219		-		L			4
NOT WAY	COLICTY V SECRETION PROTEIN CYAA	ESCHEDICINA COLI			-	-					_
NAS ECOL	OLICON V SECRETIO	ESCHENICIBA COLI			1010.1044	1		L	-		
TO THE PARTY	CELL WALL	BACKLUS BILEVIS		9	Ť		-				L
	CHITER CELL WALL PROTEIN PRECURSOR	BACILLUS BREVIS			Т	1	1		-	ļ	L
	A CYCLY A TRE CYCLA	BOIDETELLA PEATUSSIS		60.76		1	1	-	-	-	┞
	ADDMINITE CYCLASE	YEASINIA INTERACEDIA			1	-	 -	-	1	-	Ļ
		BOADETELLA PERTUSSIS	2			1	 	+	-		<u> </u>
7		BORDETELLA PERTUSSIS	~ ·	1	1	+	1	1	\downarrow		ļ
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		BONDETELLA PERTUSSIS	213.34	4	$\frac{1}{1}$	$\frac{1}{1}$	1		1	-	ŀ
2		MHODOBACTER CAPSULATUS	2		1	1	1	1	-	-	-
	THE ANCHOR T PROTED	ESCHENICHIA COLI	2	3	+	1	+	1		-	╀
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FILEMANE	PROTEIN	STANDARY CARE CO	Т	т	Т	1	_				
PCYMO ACISP	CYCLOHEXANONE MONOOXYGENASE		170-200								
CYNT SYND?	CARBONIC AMIYDRASE		2.50		l	Γ	H				
CYNX ECOLI	CYNX PROTEIN		=			-					
CYOB ECOLI	CYTOCHORDING O UBION		107.141						_		
CYPH SYNP	PETIDITION CINEDAM		101-13								
CYSA ECOLI	SULTATE PERMEASE A PROTEIN		90:					!			
KY88 ECOL!	CYS REGULON TRANSC	The latest and the la	8.			-					
PCYSO SALTY	CYS REGULON TRANSC		164.19	Ī							
CYSE ECOLI		110000	97.7								
CYSE SALTY			100	T	t			_	Ī		
PCYSO ECOLI			7	1	1	\dagger		İ	Ī		
CYSO SALTY	SINCHEM SYMPHASE	INICATOR	77.60	1		$\frac{1}{1}$		t	Ī		
CYSN ECOLI	SULFATE ADENYLATE TRANSFERASE SUBUNIT I		64-91		\dagger	+	\dagger	$\frac{1}{1}$	Ť		
CYSW ECOLI	SULL'ATE PERMEASE W PROTEIN		201-12	1	+		1				
CANS WSY	SULFATE PERMEASE W PROTEIN		٦	┪			+	†	Ì		
CACA ALCEU	POTON ALCON ICATION EFFLUX SYSTEM PROTEIN CZCB		П	0.7.0	364-391		\dagger	T			
CZCD ALCEU	CATION EFFLUX SYSTEM PROTEIN CZCD	OPITUS	139.169		1	+	+	†	1		
DAG MACKU	PEMICHLIN-BONDING PROTEIN 5" PRECURSOR	S	10.103	1			+	1			
DADA ECOLI	ID-ANITHO ACID DENYDROGENASE		127-154	1							
DAGA ALTHU	NAU- LINKED DALANTHE GLYCINE PENNEASE	LOPLANKTIS		1	1		1	1	1		
PDANOT ECOL!	DALCK PROTED		1	20.5		+	1				
POAPA BOOL	DOWNORODOPICOLINA			₹. 1				1			
DATE BACKU	NA PROTEDICYSTE	BACELUS SUBTILIS	7			-		1			
1000	NA ANCHONG PROTEIN		12-19								
PDBN CLOPA	ONA BINDONG PROTEI	TEUMANUM	13-53			1	1	1			
OCAM PORT	DECARBOXTA SE PROENZYME		146-173	Ì							
DOM CORCE	DIAMMOPDICE DECARBOXYLASE	CUN	134-161			-	1				
POCDA PURAE	DIALENCY DAELATE DI	RUGINOSA	2.5	Ì		-		1			
DOS ECOL	CLUTAMATE DECAMBOXYLASE BETA		₹			1	1	1			\downarrow
POCHS ENTAE	HISTIDONE DECALBOXYLASE	res	=			1		†			
DOM KLEN	HISTIDDRE DECANDOXYLASE	5		1	\dagger		t	\dagger	T		
DOTHS MORN	O HISTIDINE DECAUBOXYLASE	MORGANELA MORGANII		1	1		†	\dagger			1
DCD BACSU	DIPEPTIDE TRANSPORT PROTEIN DCIAD	BACILLUS SUBTILIS	777		1	+	\dagger	1	Ī		
DOLY HATA	POCLY HAFAL LYSINE DECAMBOXYLASE	HAPMA ALVEI	7	07. 07.	1	Ť	T	+			
DCOA KLEPN	OXALDACETATE DECARBOXYLASE ALPHA CHAIN	KLEBSELLA PNEUNONIAL	107	107.760	1	-	\dagger		I		
PCOA SALTI	OXALOACETATE DECARBOXYLASE ALPHA CHAIN	SALMONELLA TYPHIMUROUNI	Т		1	\dagger	†				
PDC08 EALTY	OXALOACETATE DECAMBOXYLASE BETA CHAIN	SALMUNELLA TTPIUNUONI	27.44		T		T	t			L
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POCTS TODA	NAMEPORT SENSOR	TOTAL STATE OF THE	Т	15.15	1	t	T	T	Ī		L
PDEAD ECOLI	_	ESCRETOLINA COCI	Т	777	1	1	T	Ì			L
POEAD KLEPN	ATP-DEPENDENT IN	REPURE CON 1	Т		\dagger	\dagger	İ	T			L
PDEDA ECOLI	DEDA PROTEIN	EXCENSIVE COLI	Т	34,140	161, 101	\dagger	T	1			
PDEGS BACSU	SENSOR PROTEIN DEC	BACILLUS SUBTILIS	Ţ,	Τ		Ì	T	\dagger			L
PDEND MORSP	HALOACETATE DEHA	RECUESICITA CO.	14.14	I	1		T				Į
PDEOC ECOLI		BEET TOWN OF OF ENVIRONMENT	117		T	l	T				
PDHAL PSEOL		PACTICINE CITETATION	721.55	T		T	T	T			L
PDHAS BACSU	ASPARTATE SEMAL	CONTRACTEDING CHITARCIAL	2	112-139	T	t	Ì	T			
POHAS CURICA		ECHERICKIA COLI	329.256		Ī	l	T			L	
DOS SAID	ASSACTA LE SEMINA	VIBRIO CHOLERAE	306-336				Ī				L
TOWN COUNTY	_	BACILLUS SPHAERICUS	149-176								
TOW WITH	т	BACILLUS STEAROTHERNIOPHILUS	121-76								
PORT PACE	Т	CLOSTRUDIUM DIFFICILE	116-163								
204 TEPAS	Т	PEPTOSTREPTOCOCCUS ASACCHAROL YTICUS	247.274	145.180							
PDIES SULSO	CLUTANATE DENTO	SULFOLOBUS SOLFATARICUS									
POPEA CORGL		CORYNEBACTERIUM GLUTMICUNI	168-215	329-336							
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CHAPTER CHAP	HOK! STRVN !	'ASE	CH ACFORUBEA	168-195	1	j	1					
117.140 199.214 199.				917-76			1	Ì	Ì			
STATEMENT BENTWOOGENAME WITHOUT INFE WEITHOUT WITH STATEMENT WO NATED WITH STATEMENT W		٦	•	117.344			1		1			
### PRINCIPLY ##		٦		٢	90-334		1					
### PRINCE BENTON CORNAGE (SUBJUIL 1 PRE CONTRACTOR SUBJUIL CONTRACTOR		JETHANOL DESPYDROCENASE SUBUNIT I PREC		Ť	90.234				Ť			
	100	JETHANOL DEHYDROCENASE SUBUNIT I PREC		18:33								
ACCOUNTY ACCOUNTY ACCOUNTY ACCOUNTY ACCOUNTY ACCORDANCE ACCOUNTY ACCOUNT	1000	AFTITION DEHYDROGENASE SUBUNIT I PREC		1								
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MANUAL PRICE PRINCOGENASE DICTLITS SPINSUCUS 419.19	SHOW BACSU	HOMOSEAINE DEHYT	GLUTNICUM	105-132			1					L
VACTOR ENTRY ALCHER BETTAMOGENASE VALLED STREAM	BION CORCL	ACHAOSERUME DEHYTO		212-219								L
AVACE GENTOROCELALE EL LA CONDUCTER STRUCKITA 19-10 19-1	200	HENN ALANDE DE		402.512		,						
COURTER PURPOGENIES OF 105 SIBUNIT AMAREA C'LINDRICA 131-140	_	THE PERVISE FLAVOPROTEIN SUBUNIT		Т	130-168							
ACTORIST HOLOGOPHINE STATEST HOLOGOPHINE 191-100	DHSA EULL	SUCCESSION OF A SUBSTITUTE AS	IICA	Τ								
A	DEISS ANACY	SQUEE HTMOGETANE AS AN AND AND AND AND AND AND AND AND AND		8								
	Ī	SOLUBLE HYDROGENASE, SMALL SUBURIL	(IETHYLOPHILUS	439-466				Ī				L
100 100	ATT THE THE	THE THY AND ED		584-611								L
POLYGINE NOTES PACTED A PACTED A	1000	PROPARTE ATP-DEPE		(6.9)	114.141		_					1
DECOMBRIGE DESTORGGENASE PSEUDOMONAS PUTION 11-15 11-1	THE PLOTS	MOST ATTOM MOSSING		9								
Individue Entropoletics Color (ii) AZOTOGACTER VINELANDIII 11-15 11-15	DIVE BALSO	THE PROPERTY OF THE PARTY OF TH			***							
Incomparison	DED PSEN	DOM DROLLFOAMING DOM (E1)	ZO:	2								
LTOANDING DEPTYONCEANASE CONFORMS STATELLUS SUBTILIS 131-191	DCDH AZOVI	LIPOANIDE DEHTURUSERASE COFU (ES)		82-124								L
Image: Color Col	DE DH BACST	LIPOAMIDE DEHYDROGENASE LUPU (EJ)		13:109								_
DIATA POTERN R	DI DAL BACKL	I DOAMIDE DEHYDROGENASE CONP (EJ)	BALLILOS COLORES	104-135								ļ
DHYPRICE DOLANGE DENTORGCENASE PSEUDOMONAS PUTIDA 401.50 DHYPRICE DOLANGE DENTORGCENASE PSEUDOMONAS PUTIDA 401.50 DHYPRICE DOLANGE DENTORGCENASE PSEUDOMONAS PUTIDA 401.513 DHANA PROTEIN BACELLUS SUBTILIS 112.10 201.213 131.10 DHANA PROTEIN BACHLUS SUBTILIS 112.10 111.11 131.30 111.11 131.30 DHAA PROTEIN BACHLUS SUBTILIS 112.10 111.11 131.30 141.11 131.30 DHAA PROTEIN BACHLUS SUBTILIS 112.10 111.11 131.30 141.11 131.30 DHAA PROTEIN BACHLUS SUBTILIS 112.10 141.11 131.30 141.11 131.30 DHAA PROTEIN MATCORCUS LUTEUS 112.10 141.11 131.30 141.11 131.30 DHAA PROTEIN PROTEIN 12.50 111.11 131.30 141.11 131.30 DHAA PROTEIN 12.50 12.50 12.50 12.50 12.50 12.50 DHAA PROTEIN 12.50 12.50 12.50	200	DILIVIA OF POALATIDE DELIVIDA OCENASE	ESCHENCHIA COLL	134.151	223.275							1
PAGE PAGE	2	SHANDED FHYDROGENASE	PSEUDOMONAS PLUUMESLEPS	8								1
DRIAK PROTEIN DRIAK PROTEIN 16-190 16-11	DOM NOT	DISTURCE CONTRACTOR	PSEUDOMONAS PUTIDA	2								
DRIAK FROTEIN BACELLUS SUBTILS 116-100 116-110	DIADN PSEPU	PHENOL HYDROATE	BACHLUS SUBTILIS	447.374								
DRIAGE PROTEIN BACELLUS SUBTISTS 111-110	DINA! BACSU	DNAK FRUIEUR	BACHLUS SUBTILIS	130-46								
	DNA2 BACSU	DNAK PROTEIN	BACILLUS SUBTILIS	316-380							L	L
STATE STAT	DNAA BACSU	DNAA PROTEIN	BORREL LA BURGDORFERI	183-216	248.273							_
	DNAA BORBU	DNAA PROTEIN	RINCHOGERA APHUDICOLA	33.188	1	201:161						L
MAY PROTEIN MICROCCCUS LUFEUS 191-115 21-110	DHAA BUCAP	DNAA PROTEIN	F CHELICHIA COLI	366.400							L	
15.00	DNAA ECOL!		SUCESCOUS LUTEUS	385-415								L
NACOBED NACO	DINA MICLU	DNAA PROTEIN	COUNTY CAPACOL UNI	3:	75-112	274-310	350-369				1	1
NACA PROTEIN PREUDOMONAS PUTIDA 199 419	DNAA LOYCCA	DNAA PROTEIN	MI COLLAND AND AND AND AND AND AND AND AND AND	365.399							1	1
1917 1917	DANA PROM	DNAA PROTECN	FROIEUS MINORILIS	398-439								+
STATE OF THE PARTIES STATE OF THE PARTIES		NOTION A PROTEIN	PSEUDOMORAS PULIDA	1	36.110	145.180						4
CALLONARIE CHALANTOLATIS 112-151	DAY SES	TANK A BEOTECH	SPINOPLASMA CITRU							L		
STATE FROM STATE STA	POWAA SPIICE	-	CHEAMYDIA TRACHOMATIS								L	
SALMONELLA FORTER SALMONELLA TYPHINATEUM 12-109	POWAS CHA.TI	DNABLUKE PROTEST	FSCHERICHUA COL!	12.10			1					L
1940.0 PROTEIN 1940	PDNAB ECOL	DINAB PROTEIN	CALLACTURE LA TYPHINURUM	13-109					1		-	1
SACELLUS WEGATERIUM 401-514 401-514	PDNAB SALTY	DNAB PROTEIN	ESCURBICHIA COLI	146.190						1	1	ļ
DNAK PROTEIN BANCELLA DATE 117:594 DNAK PROTEIN 171:594 171:594 DNAK PROTEIN 241:213 211:546 DNAK PROTEIN 241:213 211:546 DNAK POTEIN 241:213 211:546 DNAK POTEIN 241:213 271:530 DNAK POTEIN 241:213 271:530 DNAK POTEIN 271:530 271:530 DNAK POTEIN 271:530 271:530 DNAK POTEIN 271:530 271:530 DNAK POTEIN 271:530 271:530 DNAK POTEIN 271:530 271:530 DNAK POTEIN 271:530 271:530 DNAK POTEIN 271:540 271:530 DNAK POTEIN 271:540 271:540 DNAK POTEIN 271:540 271:540 PROMABLE SIGNAL RECOGNITION PATICLE PROTEILUS SUBTLIS 114:44 PROMABLE SIGNAL RECOGNITION PATICLE PROTEILUS SUBTLIS 13:44 DNAK POLITION PATICLE PROTEITUS SUBTLIS 13:44 DNAK POLITION PATICLE PROTEILUS SUBTLIS 13:44 DNAK POLITION PATICL	PONAC ECOL	DNACPROTEIN	THE PARTY OF THE PARTY.	497.524	341.511							4
BRUCELLA ONIS BULCELLA ONIS 111-346	PUNAK BAOK	E DNAK PROTEIN	BACILLOS MCOATERON	\$12.594	L	L					1	+
DIVAK PROTEDH BAUCELLA OVAK FROTEDH	SALAN BORR	JINNAK PROTEDI	BUNGLIA BURUNA L'A	348.335	\$17.546			_				4
CLOSTINDINA PER RINGENS 499-330	Olin Jane	VINNAK PROTEDI	BRUCELLA OVIS	141.588			-				4	4
CLOSTBDIAM FER ENGTENS 665.337	STATE BALL		CAUCOBACTER CRESCEMIUS			-						
CLOSTADILM PER ELVCENS 121-529			CLOSTICINA ACETOBULTULUM		-		-	-	L			
NEGLETIC NETTICAL NETTICAL NETTICAL NETTICAL NETICAL	POWAK CLUA		CLOSTRIDIUM PENFRINGENS	26.96		1					L	L
MYCOBACTENUM TUBERCULOSIS 50:379	PDNAK CLOP	DNAK PROTEIN	METHANOSARCINA MAZEI	22.52				-	1	ļ		L
STREPTOMPTOCOLOR 19-21 1	PONAK MET	ADVAK PRUIEIN	MYCOBACTENIOM TUBERCULOSIS	\$02-228				-		-		L
DINAR PROTEIN ESCHEAGGIA COLI 114-141	PDNAK MYCI	TUDHAK PROTEIN	STREPTOMYCES COELICOLOR	45-73	533-572			1		1	+	+
	POWAK STRC	DNAK PROTEIN	ESCHERICHTA COL!	114-141		_				1	1	1
DINA LIGASE	PONTA ECOL	REGULATORY PRO	Z VMOMONAS MOBIL IS	658-712					1	1	1	ļ
TRANSOUCTION PROTEIN UNIT 1 PROGRAME SIGNAL RECOGNITION PARTICLE PROTESTUFFOLOBUS SOLFATARICUS DIA POLYMEANSE III, CHAIN FARTICLE PROTESTUFFOLOBUS SOLFATARICUS DIA POLYMEANSE III, ALPHA CHAIN ESCHEUCHA COLI DIA POLYMEANSE III, ALPHA CHAIN	POKLI ZYMON	DINA LIGASE	STREPTOMYCES PEUCETIUS	24-51			$\frac{1}{1}$			-	1	╀
PAGNABLE SIGNAL RELOCATION PARTICLES SUBTILIS INA POLYMERASE III ALPINA CHAIN ECCHEACH FOR YELVASE III ALPINA CHAIN INA POLYMERASE III ALPINA CHAIN ECCHEACH FOR YELVASE III ALPINA CHAIN ECCHEACH FOR YELVASE III ALPINA CHAIN	PDNIL STRUE	TILANSDUCTION PR	THE STATE OF THE SOLFATARICUS	104-172						1	1	\downarrow
DNA POLYMENASE III, ALPINA CHAIN ESCHEUCHDA COLI	PDOCK SULS	PROBABLE SIGNAL	BACH LUS SUBTILIS	× 15	417.444		-			4	1	+
DNA POLYMENSE III, ALTHA CHAIN	PDP1A BACS	DNA POLYMERASE	ECCHERICHA COLI	33.104	L					\downarrow	+	+
ATA THE PARTY OF T	POPJA ECOLI	DNA POLYMERASE	PACCULATION VONDA FRATIGRAEA	130-257							-	$\left\{ \right.$

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PCGENE	107157814	ORGANISM	H	ARIA1 AREA1	AREA	281.43	CARCE SAREAS	44541	AREA!
PDPJA SALTY		SALMONELLA TYPHINIURIURI	┪		1				
PDP3B BACSU	DNA POLYMERASE III	BACILLUS SUBTILIS	\$11.219			+	1		
POPJB BORBU	DNA POLYMERAS	BORRELIA BURGDORFERI				+	1		
PDP3B BUCA	DNA POLYNGERASE	BUCHNERA APHIDICOLA	┪	96.350	1	1		1	
POPJB MICLU	DNA POLYMERASE	MICROCOCCUS LUTEUS	101.218		$\frac{1}{1}$	1			
PDP3B MYCCA	DINA POLYNGRASE	MYCOPLASMA CAPUCOLUM	0.00		-			-	
PDPJB PSEPU	DNA POLYNGRASE	PSEUDOMONAS PUTIPA	T	30.177 273.310					
ביים	DNA POLYAGIASE III, BETA CHAIN		٦	Т			-		
PDP3X BACSU	DNA POLYNCERASE	BACILLOS SUBILLIS	491.741						
POPC1 ECOL	_	ESCHERICHIA COLI	100		ļ		-		
בסבל בנסרו	DNA PRDKASE TRAC-4	EXCREMENTAL COCI	70.120		-				
NOTE ONTO	_	BACILLIS CALGOTENAY	201.215						
POPOL BACCA	_	STREET COCCUS ENCERACIONES	Т	101.424 1571.500	645.672				
NATES TO TO	DNA POLYMEKASE I	THE TOUCHUS TREATIONS	Т	1	Т				
PDPOI THEAD	_	INCIMUS AQUATICUS	Т						
POPOL THEFL	DNA POLYMERASE	I HELMINS ACIDA II C. U.S.	270.766				-	 -	
PDP02 ECOU	DNA POLYMERASE II	ESCHERICITA COLI	26. 376						
POPOL FYREU		PYROCOCCUS FUNDISUS	Т	277	71.6 1.75			+	
PDPOL SULSO	_	SULFOLOBUS SOLFATARICUS	Т	T	1	_	1		
POPOL TIELL	DNA POLYMERASE	THE LACOCCUS LITORALIS	1	221-384 842-470					
PDPP_LACLA	DIPEPTIDAL PEPTIDASE IV	LACTOCOCCUS LACTIS	110-131		-				
POPP LACE	DEFPTOYL PEPTU	LACTOCOCCUS LACTIS	110-133				1		
rors Ecot	DNA PROTECTION	ESCHENICHIA COLI	٦						
PDRING STREO	DEOXYMIBONUCLE		╗	291-316					
PDINA STRUE	DAUMORUBICON RE		286-313	1			1		
PDYIN STANU	OBYYDROFOLATE	STAPHYLOCOCCUS AUMEUS	┪	7			1		
PEUB BACCI	GLUCAN ENDO-1, 1-BETA-GLUCOSIDASE AT PREC	BACELUS CIRCULANS	_]	T	T		199		
PEAE ECOLI	ATTACHING AND EFFACING PROTEIN	ESCHENICHIA COLI	1	76:-676 (11:46)	041-140	Т	2	+	
PEBGR ECOLI	EBG OPERON REPRESSOR PROTEIN	ESCHEDICHIA COLI	201	1		1			
PEBR STANU		STAPHYLICCUCUS AUTEUS	97-00				T		
VECHE MOCA	ENOYL-COA HYDIK	CONTRACTOR CALATOR							
PECTO ECOL	CHAPERONE PROTEIN ELPD PILELUKSON	SUCCESSION CONTRACTOR	91.51		-	Ì			
PEDO ZYDOGO	PHOSPHOGLUCOPALE DESTURATASE	STREET STORY STORY STORY	T	110.144					
PEDRY STAND	EPIDEUMAL CELL DIP INH PAECURSON	DESTRUCTOR ACTION OF THE PROPERTY OF THE PROPE	١,				-		
2 2 2	ELUMONIUM FACTOR 1	HALORACTERINA HALORIDA	186-213		-				
1	PLONGA FINAL FACTOR 1	ARTHANOCOCCIS VANNIEL II	408-436				 - 		
VALUE AND	Т	081	 -						
TATE AND A	ET ONDATION FACTOR 2	THERMOPLASMA ACIDOPHILUM		49.76 220-247					
PEEC ANANI	FI DWGATION FACTOR G	ANACYSTIS MIDULANS	112.150						
PEFO ECOL	ELONGATION FACTOR G	ESCHENICHIA COLI	234.261						
PEFO LIYOLE	_	MYCOBACTERUM LEPRAE	211-259 330	110-157					
PEFO SALTY	ELONGATION FAC	SALMONEL LA TYPHIMURURI		_					
PESO STOL	EL ONGATION FAC	SPORULINA PLATENSIS	334.334 481.51	-811					
PEFO SYNY	ELONGATION FACTOR O	SYNECHOCYSTIS SP	16.41						
PETTI STUDY	ELONGATION FAC	STREPTOMYCES PAANOCISSINIUS	121.251						
PETTS STUDY	ELONGATION FAC	STREPTOMYCES RANIOCISSINUS	221-258						
PETTS STICK	Ť	STREPTOMYCES RAMOCISSIMUS	228-255						
PETS ECOL		ESCHENICHIA COLI	~						
PETS STICE		SPROPLASMA CITU	П	134-161	Ц				
PETTY BACTR	ELONGATION FACTOR TU	BACTEROIDES FRAGILIS		329-256					
PEPTU BACSU	ELONOATION FAC	BACOLUS SUBTILIS		230-257					
PETTU BUTCE	ELONGATION FACTOR TU	BURUHOLDERIA CEPACIA	26.55	_	-				Ī
PETU CALTA	ELONGATION FACTOR TU	CHLAMPDIA TRACHOMATIS	218.245	1	4	1	1	-	
PETU DEISP	ELONGATION FACTOR TU	DEDVONEMA SP	230-257	1	+	1	+	1	
PETU FLES	ELONGATION FACTOR TU	FLEXISTIPES SINUSALABICI	302:127		1	1	$\frac{1}{1}$	+	I
PETU KALMA	A ELONDATION FACTOR TU	INTOAKTULA MIANISMIUNTUI	16-31	-	$\left \right $	1		-	

1714000	1015-1781-4		AREAL	ABEAL	AREAL	100	200	1			
-	MALOGO		Т								
TOTAL	STONE ATTOR TU		076.666	Ī							
	TOWN TOWN THE PARTY OF THE PART		-	i	į :		:				
PEFTU MYCHO	ELONGATION PACTOR TO	¥.									
FTU MYCLE	FLONDATION FACTOR 10		270-147								
TANK THE	III DINITATION FACTOR TU		1 5.4								
	EL OUGATION FACTOR TU	-	910.010								
200	T WOLLY STORY										
т	TO THE PROPERTY OF THE PARTY OF	MCINOSA									
	PSEUDOL 13IM PAECONOMIA PRECISIONE		6	;	•						
PELTI ECOLI			7:18	_							
LT ECOL	T. ABILE ENTEROTOXIN A CITAIN PAIL LINXIN	NA CONTRACTOR OF THE PARTY OF T	338-364			İ	1	Ī		!	
100 00			100								
	STATE OF THE PARTY OF TAKE CONTROLLEY OF										
FENTO ECOL	ENIERCEACING STATE	SAT MONETLA TYPHINIUMUM	٦				010.00				
PERMI SALTY	ENVM PROTEIN	STORE COLUMN COLUMN	2:40	25:23	\$30.022	7					
AND CTARS		SIAMILLOCUS CIDEN	_					i	1	:	:
	THE PROPERTY OF THE PROPERTY EPIC	STAPHYLOCOCCUS EPIDERAILUIS	ī	1 100							:
7	TO SELECT SECTION OF THE SECTION OF	STAMYLOCOCCUS EPHNICAMINIS			i	1		!	:		
PEPUP STAEP			101-0							-	
PEMY STAEP	HYPOTHETICAL 167 KD PROTEIN IN EPIX 3 KENDE	STATE OF STATE STA	001::3	1							
44.46	LYPOTHER TICAL PROTEIN IN EPIA S'REGION	SIAMILLACOURT	1			L				ا	
	000 000 000 000	ESCHERICHIA COLI	Ì								
M ECO.	OI F.BINDAN	SACCHARDPOLYSPORA ERYTIIKAEA	_								
PENS SACEA	SENSORY INCASSOR	ECCUPATIONS COL.	2.64	071.10						_	
PEREA ECOLI	ELYTHONAYCIN ESTE	STATISTICS NOT A CHARLE ACAD A CONTRACT OF A	9.36	967.934	= 7						
MERVY SACER	ERYTHOLONOLIDE SYNTHASE, MODULES & AND &	SALCHANOTOLI SI CICI ETT	36.155								
		STREPTOMYCES SCABILES									
PESTA STRUK		PSEUDONIONAS FLUORESCENS	107-110								L
STE PSEST	AAM ESTELASE	STATE OF THE ALIE ALIE ALIE	76-117	135.206							L
SETCI STAND		STAMPLECUCOS ACALOS	76-117	155.206							
		STAPHYLOCOCCUS AUREUS		70,							
PETG STAND	COLUMN A PROCESSION	ISTAPHYLOCOCCUS AUREUS		30.00							L
PETCS STAND	ENTEROTOXIN TYPE C.3 PRECURSOR	ET A MAY OF OCCUS AUREUS	26-46	165-192				\downarrow			L
PETIXA STAAU	ENTEROTOXIN TYPE A	SA SECTION OF THE PERSON OF TH	309-236								1
1400	EPSD CON-TOXON, TYPE	CLOSINGMACINA	101.10	173.207	L						
	BATTEROTOKIN TYPE B	STAPHYLOCOCCUS AUREUS	3				L	_			
	PRINTED TOTAL DIRECUSOR	STAMMLOCOCCUS AUTEUS	27.75	911				L	-		
	PARTICIPATION TYPE E PRECITE SOR	STAMPALOCOCCUS AUREUS	2						L	<u>_</u>	
PETXE STAND	ENTEROIDAN INCOME LANGE LANGE	SALLACINELLA TYPHINIURIUNI	116-130				-				L
EUTC SALTY	ETHANOL AMINE AMMONIA-LI NAS. LICH	FCCMFAICHIA COLI	63.89					+		-	
FVCA ECOL	PUTATIVE TRANSCRUTTON REGIETOR	E PAGE LOUIS COLI	45.70	249-276	431.458	126-553	179-130		1		1
PEVES ECOL	PUTATIVE SENSOR PROTEIN EVUS		116-753								1
TACK BOWL	FXODEOXYPUDOMUCLEASE V	ESCREDUMA COCI	10.103		L	L	L				
	STORY VAR TRANSPORT EXES PROTEIN	ESCHENICHEA COLI				-		L	-		
	GIG RY JA JOHN JOHN	RECOGNISM MELILOTI	2		\downarrow						L
EXOA MINDA	SUCCINCETCAN BIOSTINITIES	STREPTOCOCCUS PNEUMONIAE	218.254					1	-	\mid	L
EXON STRUM	XODEOXYMBONUC	Same Abril NA LATER IN OTT	236-270	327-361				4			1
STATE SOUTH	EXOF PROTEIN	KILL USING THE SAME	353.370		L	L	_				
A PART BURN	HICEBOOK YCAN BIO	NOZOBIOM MELECOII		30,00	150-101	-			_		
	GISCHARGE VEAN BLOSTATHESIS PROTEIN EXOP	ANEZOBRUM MELILOTI						-			L
PEXOF IUDIC		ESCRENICHIA COLI	Ş	<u> </u>		-		+	-		L
AND ECOL	FATT OXIDATIONS	RECEIPTION COLI	230-247				\downarrow		-	ļ	ļ
PFADL ECOLI	FATTY ACID TRANSP	Programme CO. 1	1233-155	(\$7-12)	507-541	_					1
PEART FOOL	OUTER MEMBRANE P	ESCHERCIAN COL	7.5								1
	Т	ESCHEMONIA CUE			100	210.747	-	L	L	L	
1	Assembly and a second	ESCHENCIAN COLL	100-194	180-473	370-062		-	-	-		L
HAND BOOL		PKNEENCHOA COLI	23.51					-	1	-	1
PFANE ECOLI	CHAPERONE PROTEIN PARE PACCOCC	SCOURS NOT COLI	104-131	 			-	4			1
PFANG ECOL	FANG PROTEIN PRECURSOR	EPOTEBICIDA COLI	193-141	L	L	_					
PFANH ECOL		Course Course	273	200	L						1
PFAOR PSET		Pacubolicana Productives	64.93			_	L				4
US JOAN MANA	1=	WOLINELLA SUCCINCOCACA	1		L			L			
200		ESCHERICHAN COLI		100	-		-	L		L	H
	7	PSEUDOMONAS SP	4		011		-	-		Ŀ	L
PLON PARAM	TOWNS TO DELIVER OF THE PERIOD	ESCHENICION COLI	200-315	2	ġ	-	-	-	-		-
אבטים ביכור		ESCHEDICHTA COLI	331-561	_	-		$\frac{1}{1}$			-	ļ
PFECA ECOL		RECOVERICHE COLL	1310-237		_			$\frac{1}{1}$			+
THE BOW											
			1	ļ	-	Ĺ	F	_	_		

PCGENE	107117814	Sequences		S YARY	T CANA	ABYA 4	AREAS	AREA 6 TAREAL	AREAL	AKIA S
FILE MANIE	PROTZIN	UNICOCOLIS AUSTRIC	Т	1	Т		Г	-		
MEND STAND	POSSIBLE PROTEIN FEMB		2							
PENA SYNT	FERREDOXIN-NADP REDUCTASE	F SCHEMICHIA COLL	136.203							
MENC ECOL			13:34	281-308						
WENE ECO.	ENDIC ENTERORACTION TRANSPORT PROTEIN FEPO		28-155						1	
200	ENDEDOVOL HETEROCYST	•	1-19					1		
STATE AND A	ERREDOXIN-LIKE PROTEDNIN NU NEGION	ANABAENA SP '1	¥ .					7076		
PHAS BORPE	TLAMENTOUS HEMAGGLUTININ		138-1138	1128-1138 1359-1316	2007-2114	7841-780		1	<u> </u>	ļ
PPHAC BORPE	ALMOLYSIN-LIKE P	USSIS	342-169				†	1	<u> </u>	1
PEREA ECOL	COMMATE HYDROGE		16.4)	30.314	#01-42B					1
PEHUA ECOL	EALLCHOOME-IRON		451-415				1	+		1
MAN ECOL	PROTEIN FHUB PREC		227-234						 	1
PENTE ECOL	OUTEA-MEMBRANE RECEPTOR	ESCHŒRUCHIA COLI	587-614					1		1
PFIB SPICE	FIBRIL PROTEIN	SPIROPLASMA CITIL	161-193	126.367			i	-		
100 E	CELL FILAMENTATION PROTEIN FIC	ESCHERICHIA COLI	2 - 2				Ì		 	_
MIC SALTY	CELL FILAMENTATION PROTEIN FIC	JUM	2:-3					-		
PRINC BORDE	OUTER MEMBRANE PROTEIN FINC PRECURSOR	russis	201.23	26.50	618-043				<u> </u> -	
PFINC ECOL	CHAPERONE PROTEI		2			80				1
PERO ECOL	FUND PROTEIN PREC		22.23	6	376-30	207-700				
PFDGE ECOLI		ESCHENICHIA COLI	761-691					1	<u> </u>	
PEDAY SALTY	FINIBILIAE Y PROTEIN	IIMURIUM			91. 72.				1	1
FWZ ECOL	FINDRIAE 2 PROTEIN			2	27.00					1
PEDGZ SALTY		SALMONELLA TYPHIMIUNI	R					-		-
PINO ECOL		ESCHENCHIA COLI	2					<u> </u>		-
PFUCA NOU		ACKETTSIA RICKETTSII	201							
MIXC AZOCA	FIXC PROTEIN	AZORHIZOBIUM CAULIMODANS	2					1		
PFIXE AZOCA	SENSOR PROTEIN FIXI.	AZONHIZOBIUM CAULINODANS								L
PFIXE BRAIA	SENSOR PROTEIN FL	BIADTIQUE UNITARIONI							-	
PFLA1 BONBU	TAGELLAR FILANE	BONDELIA BORGOODEN	61.63	23.124				-	-	_
PFLA! HALHA	LAGELLIN ALI PREC	MCTUANCOCCIO VOLTAE	100	3				_		
MINI METVO	FLACELLIN BI PAECUASON	METHANOCOCCUS VOLTAE	35.55							
PLAN ME IVO	LAGELLIN BY PRES	HALOBACTERIUM HALOBIUM	30							
ALLA MALIA	LACELLIN BI PAC	METHANOCOCCUS VOLTAE	5.36					_		
WLAS METVO	TAGELIN BY PREC	HALOBACTERIUM HALOBIUM	36.90	137.180						
	ELAGEIL ON BI PREC	HALOBACTEMUNI HALOBIUNI	36.63	134:181						
200	TAA LOCING 22 9 KL	BACILLUS SUBTILIS	33.149	153-186						
DE CANCO	LAGELLINA	CAMPYLOBACTER COL!	15-13	164-161	497.535					1
PELAA CAMIE	TAGELLINA	CAMPYLOBACTER JEJUNI	330-366	36.57	200.5					1
PFLAA METVO	FLAGELLIN A PRECURSOR	METHANOCOCCUS VOLTAE	<u>?</u>					1		1
PFLAN PSEAE	FLAGELLIN	PSEUDOMONAS AERUGINOSA	7	=	2				+	
THAN NOG	FLAGELLIN	RHIZOBIUM MELILOTI		17.97	186-381					1
PFLAA SPIAU	FLAGELLAN FILAM	SPRIOCHAETA AURANTIA	2079	310,384					-	ļ
PEAN TREPY	FLACELLAR FILAMENT PROTEIN PRECURSOR	THEONEWA PAIL IN IN	241.270							
THAN THEY	LACELLAR PILA	CAMPYLOBACTER COLI	144-191	497.535						
	TCACCLER OF	CAMPYLOBACTEA JEJUNI	220.266	110-313	500.510					
TANK CAMPE	STAGE IN	RHIZOBIUM MELILOTI	66.113	177.210	228-255	160-391				
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	FI AVODOXIN	CLOSTRUDIUM NO	16.52	L						
NA PA	_	CAULOBACTER CRESCENTUS	291-318	16.188						4
PETA BACKL	FLAGELLIN	BACELUS SUBTELIS	102-129	328-328						
PFI GG BACSU	FLAGELLAR BASAL	BACILLUS SUBTILIS	65-86							
PFLGK SALTY	FLAGELLAR HOOK	SALMONELLA TYPHIMUMUM	12-50	133.360	456.540				1	
PFLGL ECOLI	Τ	ESCHENICHON COLI	6:03 0:03	239-266					+	-
PFLGL SALTY		SALMONELLA TYPIUMURIUM	6	907-X72						1
PELIED ECOLI	FLAGELLAR TRANSCRUTIONAL ACTIVATOR FLID	ESCHEDIONA COLI			1					-
PFLIA PSEAE		וויייייייייייייייייייייייייייייייייייי								

		Proharyotic Sequences	1	VALUE OF THE PARTY		AREAS	AREAS	AREA	VIII.		
1	07817816		Т	Г	195.339	431-466					
FILENAME	CABLLAN		Ī	Τ	136-198						
_	FLAGELLIN	LERAE-SUIS	I	Т	Т	212.219	112.299	176-403			
PELIC SALCH	FLAGELLIN		T	L	Т						
_	PLAGELLIN	SALMONELLA PARATYPHI-A	Ī	T	701.76						
_	FLAGELLIN			Т	200						
_	FLAGELLIN	SAL MONELLA TYPHIMURIUM	-	J		011.101	13.164	125.575			
PILIC SALTY	FLAGELLIN	CENS	T	Т	10,103	116.20	5979				
_	FLAGELLIN		٦	Т		101					
I	FLAGELLAR HOOK-ASSOCIATED PROTEIN	HINTORONI		2	£7:52						L
	PLACELLAR MOOK-ASSOCIATED PROTEIN .		6-35								L
•	PLAG HOOK-BASAL BODY PROTEIN PLIE	PACO 116 CIRTINIS	137.361	2							
PEI E BACSU	FLAGELLAR M-ADMO PROTEIN	CENTUR	г	197-324	361.388			-			
	PI ACELLAR MADING PROTEIN		414.520								1
	PLACE LA MANAGE PROTEIN	MURION	3								
7	A A CELL AS CONTINUE DECITEDA FLLIC	BACULUS SUBTILIS							_		_
MINO BACSU	PLACELLAS SWITCH BROTTEN EL IO	ESCHENICHTA COLI			Ì	:	:		_		
J	FLAGELLAL SWITCH PROTEIN TEST	NACH LUS SUNTILLS	19.46	2			1				L
FFLIII BACSU	PROBABLE FLIII PROTEIN	BACH 1 115 SUBTILLS	7.37								
PFLU BACSU	FLAGELLAR FLU PROTEIN	CALLES OF TABLES OF THE PARTY O	33.118	į			:	•	·	:	!
VI 11 CA1 TY	FLAGELLAR FLU PROTEIN	SALMONE LESS TO THE PARTY OF TH	30	117.14							1
PEI IK NACSU	PROBABLE FLIK PROTEIN	BACILLOS SOUTIES	16-71	78-105	109-136						1
ACT II BACKII	FILIT PROTEIN	BACILLUS SUBTILITS	105.132	L	L	L					<u>- </u>
PACE PROPERTY	FI IN PROTEIN	ESCIENCHIA COCI	11.101								1
1	1. PACYETA	SALMONELLA TYPHIMURIUNI									1
VILL XALIV	The resultant	BACILLUS SUBTILIS							L	L	
PFLDA BACSU	FLIM PROTEIN	ESCHENCHIA COLI	231-278			+			<u> </u>		_
אונמי בכסרו	FLIM PROTEIN	CAULOBACTER CRESCENTUS	2				1			L	L
PELIN CAUCK	FLAGELLAR MOTOR SWITCH TO	ESCHENCHIA COLI	29.00							L	
FLUS ECOLI	FLAGELLAR PROTEIN PLIS	SALLMONELL A TYPHIMURIUM	9.46	97.				-			-
FLUT SALTY	FLAGELLAR PROTEIN PLIT	PERITOGONAS AERUGINOSA	10-67	2			1		1	ļ	L
PFM12 PSEAE	FUABILIAL PROTEIN PRECURSOR	E CONTRACTOR COLI	5.32				1		-	1	L
PEMIA ECOLI	TYPE I FEMBRIAL PROTEIN, A CHAIN PRECURSOR	ECTIFEICHIA COLI	11:38								ļ
PFMIC ECOLI	TYPE-I FORBRIAL PROTEIN, C. CHAIN PRECONSOR	ACTINOM/YCES VISCOSUS	248-282	32-379	9-44	1	1		-	-	-
PEMI_ACTVI	FORBILAL SUBURIT TYPE I PRECUASOR	FSCHERICHIA COLL	14:141				1	-	\downarrow	1	-
PENSE ECOL	I FDGRILAL PROTEIN 917 PRECUASOR	BACTEROIDES MODOSUS	10-13				1	1	-	ļ	-
PENAS BACHO	FINBRIAL PROTEIN PRECUASOR	BACTEROIDES NODOSUS	107-134			4		1	-	ļ	-
PFIMA! BACNO	FUNDALAL PROTECY PRECUESOR	PACTERONDES NODOSUS	107-134			-		1		1	-
PFLAS BACHO	PENAS BACHO FEMBRIAL PROTEIN PRECURSOR	RACTEROMES NODOSUS	110-133					1	 -	ļ	-
PFILAT BACH	FEMBRIAL PROTEIN PRECURSOR	BACTEROMES MODOSUS	133-150						-	1	ļ
POW BACK	S FORBILL PROTEIN PRECURSOR	BACTERORES MODOS116	107-141	L	L				1	1	+
PENAF BACK	FRANKL PROTEDN PRECURSOR	BACITACIDES INCOSOS	95-122						4	1	\downarrow
NOVE HALVE	DEMONIAL PROTEDY PRECUTSOR	BACTEROIDES PUDOSOS	10.14		L		_				$\frac{1}{1}$
DAY I	STAMBIAL PROTEDY PRECURSOR	BACTEROIDES NUDUSUS	1				-				4
	THE THE PROPERTY PROTEIN PRECURSOR	BACTEROIDES NODOSUS			ig	-	-		L		
PACA CANA	PENANTAL PROTEIN PRECURSOR	PSEUDOMONAS AERUGINOSA		100	1		-	-	-		
		BACTEROIDES MODOSUS	3		-	-	-		L	H	Ц
	POSSIBLE FINDRIAL	BACTEROIDES NODOSUS			\downarrow	+	-		L		
2		ESCIENCIA COLL	77-174		1	+	-			L	L
100 EOO	PIT PURCHASINA	MEISSERIA MENTINGITIDIS	ě		1	1	+	1	-	-	-
POC NEDGE		NEISSENIA GONDRINOEAE	66-97				-	-	1	-	ŀ
PROG NEGO	FINGRICAL PROTECT	MORAXELLA HONLIQUEFACIENS	100		-	+	$\frac{1}{1}$		-	-	-
POOL MORNO	FINGRIAL PROTEIN	PSEUDOMONAS AERUGINOSA	3	3	1	1	+	1	+	-	\vdash
PEND! PSEA	FORMAL PROTEIN	PSEUDOMONAS AERUGINOSA	è		1	+	+		-	-	\mid
MOD PSEAE	FDABKAL PROTECT	ESCHERICHIA COCI	3	22		1	+	1	-	-	-
PRISI ECOL	CSI FOUNTAL SUBO	ESCHEDICHIA COLI	\$	\downarrow	1	1	1	1	1	-	ļ
Photos Econo	IN INCOME AND	20.50			37 165	1	443.686	32.55		\mid	
A SALIN		STAPHYLOCOCCUS AUREUS			┰	Т	Т	Т	Т		-
PENBA STAND	_	ESCHEDUCHIA COLI	2	1	$\frac{1}{1}$	+	+	-			Н
אמר בנסר	FOLITON YOUNGENTA	LACTOBACELLUS CASÉ!	2 2	\downarrow	+	+	+	1	-	L	H
3		2 C T E T E E E E E E E E E E E E E E E E	1	-							

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and or other	1	Prohamotic Secures				П	_	П	П	
FILENAME	ROTEIN		\Box	AREA JAB	ABEA1 ABEA1	7	AREA'S SAREA'S	Т	N N	AREA
PFRDA ECOLI	UNARATE REDUCTASE FLAVOPROTEIN SUBUNIT		≊	-						· i
PERDA WORSE	LIMARATE REDUCTASE FLAVOFROTEIN SURUNIT	NOGENES	1.35	487-514						
PERT MYXXA	TIDING MOTHLITY REGIL ATORY PROTEIN	MYXOCOCCUS XANTHUS	27-51	478-505						
200	CALLA TE TETT AUVINORS ATE LICASE	ACETUR	061-(91		_		-			
	CONTACT ANGEBACE	AUTOTROPHICU			-					
PETER BAPELL	ELL DIVISION PROTEIN FTSA	BACILLUS SUBTILIS	26-110							
PETSA PCOLI	CELL DIVISION PROTEIN FISA	-	301-331	175.418						
PETEL ECOL	CELL DIVISION PROTEIN FISS	ESCHERICHIA COLI	16.4							
PFTS. PCOLI	CELL DIVISION PROTEIN FISH		63.90							
PETEN BOOK			131-168							
			278-305			_				
1000			310.760							
PFTSY ECOL	CELL DIVISION PROTEIN PLST	COCHEMICAL COLI	3,1							
PFUCA ECOL	L-FUCOSE OPERON ACTIVATOR		ç	-		1			1	
PFUNA BACST	FUNALATE HYDRATASE CLASS I, AEROBIC	HERMOPHILUS	290-317							
PFUNG! BACSU	FUNALATE HYDRATASE	BACILLUS SUBTILIS	414.445				:	:		
PELIE VERPE	FURBIC INTAKE REGIN ATION MOTEIN	YERSINIA PESTIS	4.130	<u>-</u>	_	_	_			
			103.130							
2	ULIC J-FRUS DERTUROVERASE A	9 2		\mid	-					
PGIPI ANAVA	GLYC J-PHOS DEHYDXOGENASE 3			1	$\frac{1}{1}$					
PGJPJ ANAVA	GLYC 3-PHOS DEHYDROGENASE 3	ANABAENA VANJABILIS	162-139							
POJE ECOLI	GLYC)-PHOS DEHYDROGENASE C		•		1				Ì	
POJP BACAGE	GLYC 1-PHOS DEHYDROGENASE	KIUM	49-76	175-762						
POID BACKII			49.76							
OWENE SIDE	GLYC J-MOS DEHYDROGENASE	131	259-286	-						
POTE TATELAL			290-328							
	Ī	BACH I HE STEADOTHERMOPHII HE	Т	241.268		-				
	TOTAL STANDARD OF INCIDENCE		т							
	ALUCASE & FRUSTRA I BIT I DECITATION ASS			1						
PC&PD ZYDOAO	JUCOSE4-PHOSPHATE 1-DEHYDRUGENASE		741-601	+	1	+				Ī
POACA PSEFL	CYANIDE CONTROL PROTEIN	•	507-11		1					I
POAL! SALTY	GALACTOKINASE		Т	-	1				1	
POAL? HAED	GAL-I-PHOS URIDYLYLTRANSFERASE		I	239-269	-					
POAL? LACHE	GAL-1-PHOS UNIDYLYLTRANSFERASE	2	104-316		+			-		
PGALE SALTY	GALACTOSE OPERON REPRESSOR		10-10							
POALR HAED	GALACTOSE OPERON REPRESSOR		607-70		1				1	Ī
PGAL_PSEFL	DE D-GALACTOSE I-DEHYDROGENASE	JORESCENS	271.27							
PCC10 ECOCI	GTP CYCLOHYDROLASE U		٦			1			1	
PGCH2 PHOLE	GTP CYCLOHYDROLASE II	LEIOGNATHI	_	246-273						
PGCSH ECOLI	GLYCINE CLEAVAGE SYSTEM H PROTEIN		10-37							
PGCSP ECOLI	GLYCINE DEHYDROGENASE		216-246					1		
PCCVA_ECOLI	GLYCINE CLEAVAGE SYSTEM TRANSACTIVATOR		60.94							
PGENK_ECOLI	PROTEIN K				_	_				
PGENI BACSU	SPORE GERMMATION PROTEIN I	BACELUS SUBTELIS	П	182-216 350	350.384					
PGEN BACSU	SPORE GERMINATION PROTEIN III PRECURSOR		193-123							
PGENE BACSU	GERMINATION PROTEIN GENE		13-40							
PGGIZ STAHA	ANTIBACTERIAL PROTEIN 2		î,							
PGGI3 STAHA	ANTBACTERIAL PROTEIN 3	HAEMOLYTICUS	6-33							
PGIDA BACSU	GLUCOSE DIMEBITED DIVISION PROTEIN A	BACELUS SUBTELIS	136-423							
PGEDA ECOLI	CLUCOSE DAMBITED		\$33.564							
	GLUCOSE INMIBITED	PSEUDOMONAS PUTIDA	339.566							
	GLUCOSE INVEBITED	BACELLUS SUBTELIS	19-96							
PGIDB PSEPU	GLUCOSE DAMBITED DIVISION PROTEIN B	TIDA	25-52							
PGLCP SYNY3	GLUCOSE TRANSPOI		200-322							
PGLDA BACST	GLYCEROL DEHYDR	THERMOPHILUS	20-79		H					
PGLGA ECOLI	_	ESCHENICHIA COLI	256-283							
PGLGC ECOLI	_		114-141							
PGLGC SALTY	_		14.141							
PGLMS ECOLI	GLUC-FRUC-6-PHOSAMMOTRANSFERASE	П	209-343							
PGLN1 METTL	_	METHANOCOCCUS THERMOLITHOTAOPHICUS	\$8-6\$		1	_				

	Probacyoule Sequences	П	╗	П	_		7		4 0 6 7	ABEAG
AT DECISION		4	Z Z Z	7	1	2			3	
THE WINE SYNTHETASE	ANABAENA SP	<u>~</u>	1				T			
TASE.	TILIS	=		1						
THE ANALYSIS CONTROL ASE	OBUTYLICUM	43.440								
THE AND SANTHETASE		=					T			
2 UT AMINE SYNTHETASE	OLTAE	200			Ī	T				
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ALUTAMINE SYNTHETASE			Ī				T			
GLUTAMINE SYNTHETASE	1		-		:					
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NITROCEN REGULATORY PROTEIN P.II										
NITROGEN REGULATORY PROTEIN P-11	(Q.A.TUS	9				Ī				
NITROGEN REGULATORY PROTEIN P.II	SYNECHOCOCCUS SP	ī								
IND IREINY VI TRANSFERASE	ESCHERUCHIA COLI	_	21:5							
THE TRICK OF TRANCEE ASE	SALMONELLA TYPHINGRIUM						1	!		
		001-01	433-4640	761.70						
CONTRACTOR DIVIDONO DE CITE NO DE COLETA COMPANION DE COLETA CONTRACTOR DE COLETA COMPANION DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE COLETA CONTRACTOR DE CONTRACTOR DE CONTRACTOR DE COLETA CONTRACTOR DE CONTRACTOR DE CONTRACTOR DE CONTRACTOR DE COLETA CONTRACTOR DE CONTRACTOR DE CONTRACTOR DE CONTRACTOR DE	ESCHERICHIA COLI	126-153								
CLUTANTIAL BEHAVEAGE OPERON PROTEIN GLAD	THERMOPHILUS	7.74								
CELLIABLIC PLANTS BUTCH DELICATION OF THE COLUMN CELLIAR CELLI		194-230								
MILTO MACCOL CATCO-THOS DESIGNATE		66-014								
CONTRACTOR INTERESTINATION DESCRIPTION	9	235-274								
OF TOTAL OF THE PARTY OF THE PA		16.93								
		8.95								
OLYCEROL KINASE		Ē								
GLICEROLI-MOSTRA E NEGOLOF NO PERSON	CCAR ICHIA COLI	297.124								
	CUICELD A SI EXMENT	267.124								
		15.5								
		8								
	SCHERICHIA COLI	110.346								
TOTAL COLD PROJUCTO TOTAL STATE STATE TOTAL TOTA	ESCHERNORA COLI	130.159								
	BRADYRHIZOSIUM JAPONICUM	3.0								
	CAMPYLOBACTER JEJUNI	176-403								
ACTIVE WYPUT SEEME HYDROXYNGTHYLTRANSFERASE	HYPHONDCROBIUM METHYLOVORUM	:8-55				Ì				
PGMG7 BACSU COMG OPEAGN PROTEIN ?	BACILLUS SUBTILIS	9	?							
CLUCONOKINASE	BACILLUS SUBTILIS	236.23								
PGPID CHATE VINUENCE PROTEIN PCPI-D		33	i							
PGPID CHETR VIRILENCE PROTEIN PGP 1-D										
VIRULENCE PROTEIN										
VALUENCE PROTEIN		8	0.7.61							
VIRULENCE PROTEDY	CHELAMYDIA TRACHONIATIS	8								
VIRULEINCE PROTEIN	CHEANTDIA TRACHONIA IIS									
	MCKETTSA TRUMACCATI									
_	BACKLUS SUBTILIS									
	CONTRACTOR ACTIONS	19.61								
CAPELLICE PROTEIN	BACH LIK RESON	(1)	200.007	140-113	1015-1062					
PORTA BACON COLANGE DATABLE ASSE	BACELUS BREVIS	2.3	~	201.15	1136-1153	1213-1240	2162-2119	2559-2586	2019-2346	1606-161
COCOCC DESCRIPTION OF THE COCCUS	ESCIENCIÓN COLI	339-366	174-301							
COLUMN TANGEN	ESCHENIONA COLI	100-134								
COLOR PORTE CULTATIONNE REDUCTASE	PSEUDOMONAS AERUGINOSA	10.0								
STARYA TION-DIDUC	BACOLUS SUBTRIS	14-101	265-296							
₹	ERWDRA CAROTOVORA	251-215	\$16.543	619-615						
_	ERWINIA CHRYSANTHEMI	159.302	107.338	118-188	989-669					
PROTEIN D PRECURS	KLEBSELLA PNEUMONIAE	259-786								
	EAWDIA CAROTOVORA	129-367								
PGSPE ELWCH PROTEDY E	ELWINIA CHRYSANTHEMI	136-367								
_	KLEBSELLA PWEUMONIAE	33.36								
Т	PSEUDOMONAS AERUGINOSA	25.18	26.16							
7	PSEUDOMONAS AERUNIMOSA	1146-153	107.167			1	$\frac{1}{1}$			1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

PCGENE	107117014	Proharyadit Sequence				-	-	-	-	-	
EILE NAME			ARIAL	1	AKIA 2	APEAL	AKEAN AR	AREA & ABI	SKAI	ARIA 6	AMEA 9
PCSP XANO	PROTEIN F	XANTHOMONAS CAMPESTIUS	230-237			1	+	1	1		
VIET AFRICA	PROTEIN NEWSTON						<u> </u>	 	1	1	ļ
PGSPI ERWCA			9			İ	+	Ŧ	+	<u> </u>	-
MGSPJ KLEPN	PROTEIN J PRECURS	KL EBSIELLA PREUMONIAE	140-167	ĺ	Ī	İ	ł	+	\dagger	t	
PGSPK EAWCA	PROTEINE		200			1	-		ł	\dagger	Ī
POSPK EAWCH	PROTEINK		20:33				-		İ		
MONTH KIEN	-		12.99				_				
AGY PSEA		J\$A	2								
KSM ENWCH	PROTEIN			246.384	131.358						
KGR. XAKO	PROTEDIL	MS	16.73	297.124							
	ROIEM M	EXWIND CAROTOVORA	٦								
COO ENCH	PROTEIN D PRECURS		<u> </u>	448-475		Н					
	COLUMN TO A MARTIN AND THE CONTROL		Т	ĕ	П	=:	=:	1495-1529	j		
	ALLICOS TE I MANSEE		ī	2	\$8.48\$		477.1474	<u> </u> 	<u> </u>		-
STEE STEEL	GLUCOSTIL PANSFERASE:	STREPTOCOCCISAGITANS	207.150	11. 01.		- Г	┑			1	
KOTTE STEAM	CLUCOS M. TRANSFE		Τ	200	Ŧ	W-740	169-34	 	+	+	
POTFS STREED	CLUCOSYL TRANSFEI		2	436.463	E	T		1	t	İ	
PICTURE METTE	OSSIBLE G-T MISMA	IN THERMOFORMICICUM	Т	10.13			-	<u>].</u>	t	\dagger	
MOUVA BACSU K	CAS SYNTHASE	Г	L	L	50:10		<u> </u> 	<u> </u>	+	<u> </u>	1
POUA ECOLI	GMP SYNTHASE		Т	Т		t	T	1	<u> </u>	$\frac{1}{1}$	
PGUS BACCI	BETA-GLUCAHASE PI	BACILLUS CIACULANS	164-191			\dagger	<u> </u>	<u> </u>	\dagger		Ī
NGUB BACLI	BETA-GLUCANASE M	UNIS	35.56			-		l	\dagger	\mid	Ī
PGUB BAOK	BETA-GLUCANASE PRECURSOR	BACULUS MACERANS	136-160					<u>l.</u>	H	\mid	Ī
PCUM BACK	ENDOGLUCANASE A		П						H		
CON TACSO			П	76-40)							
	DANCE IN MAKE BRECH BROW	BOLTELVISION FIBRISOLVENS	T	457.495	1						
KGBO TIGEL	ENDOGE UCANASE	A ETIECA	70.30	1							
POUNT BACS	ENDOGLUCANASE C PRECURSOR		77:107	148 178		1	$\frac{1}{1}$	+	1	+	
NOUND BACSU	ENDOGLUCANASE P	BTILIS	T	Т		\dagger	+	+	+	+	T
PGUND FIBSU	ENDOCEUCANASE 3	CINOGENES	\$42.586		Ī	\dagger	1	\downarrow	+	$\frac{1}{1}$	1
POUR THEFU	ENDOGLUCANASE E.		308-342					1	\dagger	\dagger	
POUNS THEFT	ENDOGLUCANASE E.	IA FUSCA	П				-			$\frac{1}{1}$	
A COLUMN	ENDOGLUCAMASE A PRECUISOR		┑	1975							
PGUNA PREFI	ENDOGE UCANASE A	PRETINOMONA EL LIORESCENA	200	1					H	H	
PGUNA RUDAL	ADOCE UCANASE A			1	1		1	+	+	1	
PGUNA RUDGI	TELLODEXTRUNASE	FACIENS	2,4-301	T	1	†	1	1	+	+	Ī
PGUNB BACKA	ENDOGLUCANASE B PRECURSOR		33.450			\dagger	1	$\frac{1}{1}$	\dagger	1	Ī
PGUNB CALSA	ENDOCHUCANASE B	UN4	П	444-478		\mid	-	<u> </u>	+	t	Ī
NO.	DEDOCE UCANASE B	CELL ULOMONAS FIMI							+	ł	
CON COLOR	-		1	266-300					Н	H	
PGUNC CELFI	ENDOGLUCANASE C		200		Ì	1		+	+	1	7
PGUNC PSEPL	ENDOGLUCANASE C				1	+	1	+	+	1	
PGUND CLOCE	ENDOCLUCANASE D	N	13770	T	Ī	+	+	+	\dagger	\dagger	
ופתאם פרסכו	MDOGLUCANASE D		Т	271.394	T	T	+	+	+	\dagger	T
PGUNE CLOTH	MOOGLUCANASE E		П	П	284.311	\dagger	+	+	+	\dagger	T
PCUNK CLOTA	ENDOCLUCANASE H PRECURSOR	ELLUM	П	435.452			L	_	+	+	Τ
POUNS ENWICE	ENDOGLUCANASE PRECURSOR			113-149			-		+	+	Ī
PCINT CLOIM	FUTATIVE ENDOALUCANASE X	CLOSTUDIUM THERMOCELLUM							\vdash	-	
PCUN BACTO	DOGLUCANASE		286-126	33:540	1					Н	
PCUN BACS	ENDOGLUCANASE PRECURSOR		11.14	T	Ť	\dagger	+	+	+	+	
PGUN BACS6	ENDOGLUCANASE PRECURSOR		Т	301.328	199 (29	\dagger	$\frac{1}{1}$	$\frac{1}{1}$	+	\dagger	T
			1	7		1		$\frac{1}{1}$	┨	$\frac{1}{2}$	7

PCGENE (107a) 78a4		Probaryotic Sequences			_		, , , , ,	, , , , , ,	1000	100	A B 7 A
PILE HAME PROTEIN		ORGANISM	4	N N	4	1	Ŧ	T	т		
CORBITOL 4-PHOSPIL	TE 1-DEHYDROGENASE	ESCREDURIA COLI	3				İ	Ī	<u>:</u> -	:	:
POVPI HALJIA OAS VESICLE PROTEIN, PLASMID	MID	HALOBACTERIUM HALUHIUM			Ī	Ī		Ì			Γ
PGVP3 HALHA GAS VESICLE PROTEIN, CHROMOSOMAL	MOSOMAL	HALOBACTERIUM HALOBIUM	990				1	Ī	1	\dagger	
PCVPA APIEL GAS VESICLE PROTEDY		APHAMIZOMENON FLOS-AQUAE	7	8			†	T	+	t	
PGVPA FREDI GAS VESICLE PROTEIN		FREMYELLA DIPLOSIPHON	2	8			1			T	
PGVPA HALME GAS VESICLE PROTEIN		HALOBACTERIUM MEDITERRANEI				T	Ì	Ī		İ	
PGVPA_MICBC GAS VESICLE PROTEIN		MICROCYSTIS SP II	8	į	<u> </u>		1			:	:
POVPA PSEAN GAS VESICLE PROTEIN		PSEUDOANADAENA SP	-	3		Ī			t	T	Ī
POVPC APHEL DAS VESICLE PROTEIN C		APHANIZOMENON FLOS-AQUAE	3						İ		
POVPC HALHA GAS VESICLE PROTEIN C		HALOBACTERIUM HALOBIUM	20.24						-	Ť	1
POVYC HALME GAS VESICLE PROTEIN C		HALOBACTERIUM MEDITERIKANEI	139.169						1		
PCVPD HALLIA GVPD PROTEDY PLASMID		HALOBACTERIUM HALOBIUM	110-143						-	i	
VPO PROTEIN		HALODACTERIUM MEDITERRANGI	10.147								
COTO MANE COTO TOTAL		MALORACTERINA MALORITAL	1	135.169							
VYP FRUIEIN, FLAS		UAL DEACTERING MENTERS AND	13.47								
POVP HALME GVPP PROTEIN		TALORACTE STATE OF A S	07.								
VPF PROTEIN		TATOMACHER DATE OF THE PROPERTY OF THE PROPERT	18.61								
PCVPG HALHA GVPG PROTEIN, PLASMID		TALCORACTE NOT THE TALCORDS									
PGVPG HALME GVPG PROTEIN		TALCONCIENCE MEDITENATE						Ī		T	
PGVPH HALHA GVPH PROTEIN		HALOBACTERIUM HALUBIUM	2							t	
POVPI HALME GVPI PROTEIN		HALOBACTERUUM MEDITERUANEI	?							T	
PGVPK_HALMA GVPK PROTEIN		HALOBACTEJUDA HALOBIUNI								T	
PGVPK HALLAGE GVPK PROTEIN		HALOBACTERUM MEDITERIANEI	ñ. 2	7					†	1	
PGVPK HALSA GVPK PROTEIN		HALOBACTERUM SALINARIUM	11.38	50.77					1	1	
PGVPL MALLAS GVPL PROTEIN		HALOBACTENUM MEDITERRANGI	44.78								
MATCHE MAYOR AN IAM MAYOR		HALOBACTERIUM HALOBIUM	113-140						-		
COLUMN TAN DE LA PROPERTIE DE		HALOBACTEMUM MEDITEAUANEI	3.30								
CONTRACTOR OF THE PROPERTY OF		HALOBACTERUM MEDITERRANEI	8.88	23:130							
ACCES DATES TOWN OVER A CE STRAINED A		BACILLUS SUBTILIS	180-407	429.499							
DAY CAPACE CIRCLE		CAMPYL DBACTER JEJUNI	267.310	161.408	452.439	S69.549					
TOTAL CAME DAY OF SEE CHIMITA		F CCHF LICHIA COLL	266-293	469.497						l	
POTICA ELOCI DAN OLIMASE SUBGISTA		KLEBSIELLA PNEUMONIAE	6. 8.	448-496	\$18.545						
NA CYPACE CIBIL		MYCOPLASMA PNEUMONIAE	5						-		
POTEN MYCHA GAA GIRASE SUBURILA		STAPING OCCUS AUREUS	129.136	346.173	430.479	647.674	89.61				
MA CYRASE SUBUR		PACIFIC CIRTIES	91.710								
DNA CHRASE SUBUR		BOAREITA RICCOORFERI	134.181						-		
POWER SCOTT THE CONTRACT BY		ESCHEDICHIA COLI	616-64)							T	
AND OF A SECOND		UAL OFFIRM Y CP	210.257								
POTENTIAL DIA CITACAS SUBURIT B		AVCORT ASMA PNETOACHAR	349.783							T	
UNA UTRASE SUBUR		MICOLOGICA COMOBBIOGRA		***						T	
POTE NEICO DIA OTRASE SUBURIL		PERSONAL PRINCIPA		484.311					l	T	
DINA OTRASE SUBUR		SECONDARY CITY			010.000		90,000		İ	T	Ī
DNA GYRASE SUBUR		STRUCKSMA CITM			2007	200	2			T	
╗		SIAPHTLUCCCUS AUREUS	27.76	16.167						1	
PROHA ECOLI 1-ALPHA-HYDROXYSTEROID DEHYDROGENASE	DEHYDROGENASE	EXCHEMINA COLI								1	
_		ESCHENCHIA COLI	8	23.5						1	
LIPOPROTEIN E PREC		HAEMUPHILUS INPLUENZAE	3							1	
PHEMI CHEM GLUTAMM-TINA REDUCTASE	SE	CHELOROBIUM VIBRIOFORMES	232-259							1	
GLUTANM-TRNA RI	SE	ESCHERICHIA COLI	289.316								
S-AMBHOLEVULING	ACID SYNTHASE	RHODOBACTER SPHAEROIDES	73.100								
•	SE (SALMONELLA TYPHUMURUM	389-316	344.371							
	SE	SYNECHOCYSTIS SP	163-198	150-177							
-	ID DEHYDRATASE	METHANOTHERMUS SOCIABILIS	131-158								
PHEMA BACSU PUTATIVE UROPORPHYTUNOX	HYRUNOGEN-III SYNTHASE	BACILLUS SUBTILIS	10.13								
	4-III SYNTHASE	ESCHEDICHÍA COLI	311-338								
PIENDA ECOLI HEMM PROTEIN		ESCHEMICHIA COLI	147-174							Ī	
PHEMA YEAEN HEMIN RECEPTOR PRECURSOR	O.R.	YEASING ENTEROCOLITICA	334-361								
PHENCY ECOLI PUTATIVE METHYLTRANSFERASE	KASE	ESCHERICHIA COLI	3	105.219						1	
PHEMY BACSU HEMY PROTEIN		BACILLUS SUBTILIS	217.262								

PCCENE	1000175.4	Prahaceatic Commence									
FILENAME	PROTELIN		AREAL	ABFA 2	ARFA 3	ARFA 4	ABFA S	ABFAG	107.	100	9 10 4
PHEME BACSU	ERROCHELATASE	US SUBTILIS	98:336							Т	1
META ANASP	ETEROCYST DIFFE	ANABAENA SP	114-211	357.198	\$21.565						
PHEXA STRUN	DNA MISMATCH REP	STREPTOCOCCUS PNEUMONIAE	426-460								
WEST STON	DNA MISMATCH REPAIR PROTEIN HEXB	/E	470-497								
TO STATE OF THE PERSON AND ADDRESS OF THE PERSON ADDRESS OF THE PERSON AND	98.125										
A LANGE	MULL PROJECT	ESCHENICHIA COLI	9-19								
MEO CON		ESCHERICHIA COM	169-176	į							
PHIFC HAFIN	I IATION PROTEIN	HACADOM IN THE STATE OF THE STA									
PHIST LACEA	ALCIA MORPHORY	INCREMENTAL US INTLUENCAL	9		447.474						
PIUSA ECOL			2 2								
V IVV PARA	B.C. A. CABBOYALINE SIBOTINE		25-159								
PHICE LIFTUR	P. P. CARBOXANDE RIBOTIDE		9	181-228							
74 175 75111	T-PA CAMBUCAMIDE NEOTING		115-142								
	P.S.A CAUGOXAMIDE MINOTIDE	URUM	651-521								
Muss LACLA	AMIDOTIANSFERASE HISH		7.14								
	TAY TROIEU			143.169				-			T
PHIS6 SALTY	HISF PROTEIN	TINUM	99-66	142.169							I
THISY ECOL.	IMIDAZOLEGI. YCEROL-PIIOSPHATE DEHYDRATASE ESCHENCHIA COLI		161-199								T
PHIST SALTY	IMIDAZOLEGLYCEROL-PIIOSPHATE DEHYDRATASE		161-199								Ī
PHISE ECOLI	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE		290-317								
- 1	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	CANII	174.201								Ī
YHOSH LACEA	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE		161.18							T	Ī
PIUSE SALTY	HISTIDINGL PHOSPHATE AMINOTRANSFERASE		293.320							Ì	Ī
PHISQ SALTY	HISTIDINE PERMEASE MEMBRANE Q PROTEIN	HIMURIUM	•.35							T	Ī
WEST ECOL	HISTIDINOL DEHYDROGENASE		393.434			Ī				Ī	Ī
LINSX LACA	HISTORIOL DEHYDROGENASE		976	264-303						T	
PIGSX MYCSH	HISTIDINOL DEHYDROGENASE	S	201.329	199.430							T
PIOSA SALTY	MISTIDINGL DEHYDROGENASE	2	393-434								Ī
PLA SIAKU	ALTRA-REMOLTS SIN PRECUESOR	STAPHYLOCOCCUS AUREUS	12								Ī
1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	HARMON VEN SEPRETTON BEATERN CHROLOGOLIS	ESCHENCIA COL	T	76-103	161-224	234-261	153.380	458-492	334.381	E2:73	Ī
PHLY4 BCOL	HEADLY SDV D CHROMOSOMAÍ	TOO VIDOR TOO	┪	7							
PHLYA ACTE	JEWIN YON		=		┪						
PHLYA ACTSU	HEMOLYSDA	T	7	T	_	٦		П	846-914		
MEYA ECOLI	HEMOLYSIN A, PLASINID		1		T	П	П		846-924		
PHLYA PROM	HEMOLY SIN PRECURS		7	101.0/	┑	П	T	7	643.729		
			Т	Т	000000						747.714
PHLYA SERMA	HEMOLYSIN PRECINSOR	SEALATIA MARCESCENS	T	Т	1	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	8	21		_	133
			15	ī	T	Т	9	99.06	8	- 12 - 12 - 12 - 12 - 12 - 12 - 12 - 12	1249-1280
MEYA VIBOR	EMOLYSON PRECURS	Ī	_	638.663	\dagger	Ť		1		1	1
PIETO ACTUL	HAEMOLYSIN SECRETION PROTEIN	LEUROPNEUNIONIAE	14-61			T		T	1	1	T
THE ELOCA	HALMOLYSIN SECTETION PROTEIN, PLASHID		315.5		<u> </u>				T	\dagger	1
TO SERVICE	MACANI VEN ACTIVATION PROTESS			600-543					Ī		T
MA YR CERVA	MEMOR YOU ACTIVATION PROTEIN BECOME	redieus volcadus		487-514						T	T
	HENOLISM ACTIVATION PROTEST SECTION										Ī
NO VC	HELDE VEN P			413-447	438-524						
A CA DIA	HELDI VON CETTE STION PROTECT A PRO	ACTUMOBACILLOS PLEUROPNEUNIONIAE	<u>2</u>							T	Ī
HE YO ECOL	1 HEMOLYSIN D. MASMID		Т	7							Ī
MEY KALIS	HALOLYSD PRECURSOR	1000	7	<u> </u>	223-331						Γ
PHOACH DESWH	4) 2 KD PROTEIN IN HOAC OPERON		9		1						
MOD NETKA	HITH ORNOW DESTYDROGENASE		91.00	1	1						
PHOYS SELVAN	DHA-BINDING PROTEI			1	1	1					
PHOLA ECOL!	PHOLA ECOLI DNA POLYNERASE IR DELTA SUBUNIT		Ţ	166.111		Ì	1				
PHOKA BRAJA	REG PROTEDY HOXA	JAPOMICUM	_	177	\dagger	\dagger	1	T	Ť	+	
PACON NOON	HOXS ALPHA SUBUNIT		Τ		<u> </u>	T	T	1	1	+	
THOUSE ALLED	MOND PROTEIN	ALCALIGENES EUTROFILUS	76-110				†	T	\dagger		Ī
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PCGENE	107117814	Proharyothe Sequences		\Box		П			1-1		
ELLE MANIE			4	7537	AREA S	1	1	ANEAS AAREA!	П	A STATE	1
PHOXX BILAJA	OXX PROTEIN	BRADYRHIZOBIUM JAPONICUM	8	Ī	1		İ	İ	İ	i	i
7. DEIX	TEXAGONALLY SUR	DEINOCOCCUS RADIODURANS	2	: 		Ī	İ	İ	Ì	İ	1
PIIPRT LACLA	PHOSPIIONIBOSYL FRANSFERASE		╗	6			İ	Ì	Ť	1	
PURDO STRCO	IGNA FACTOR INDO		8					Ì		1	
PHOUSE BUSCO	EGULATORY PROTE	EARUN	7			1	1	1	1	1	
PIGUH PSESY	OTER NENDRANE P	PSEUDONIONAS SYRINGAE	2	100		1	1	T	Ť	1	Ī
HOUS PSESH	ROBABLE REGULAT			Ī		Ì	İ	Ì	İ		
PHS18 CLOAB	I KD KEAT SHOCK P	3	0	i	-	1	•		_		
PISTO HALMA	HEAT SHOCK TO KD P	=	÷.::					_			
MISTO MYCLE	IN:AT SIKKK TOKOP		1	= 1		:	:	 [:	1	-	_
PHISTO MYCPA		PARATUINIRCULONS						-			
PHING ECOLI	HEAT SHOCK PROTEIN C62 5		21.348	415.50							
PHTRA ECOLI		ESCHERICHIA COLI	21.400			ĺ			1	-	1
PATE SCOT			ŀ	\$34.476			İ		Ī		-
	CENTON AND PARTY	out on the	ł					Ī	Ť	İ	
			1	1	1	İ	<u> </u>		!		
A MALSA	SEMSORY MODULESIN	ALIMANIEM			i		_			-	_
PIEUTP BACSU	HUT OPERON POSITIVE REGULATORY FROILIN		1	-			1	j	j	j	
PHYT LACIE	HELVETICINI	TELVETICUS		18.13							
PHYCA ECOL!	FORMATE HYDROCES		13.100	104.13							
PHYDO ECOLI	RANSCELPTIONAL A	ESCHEMICINA COLI	341.178								
PHYDO SALTY	RANSCRIPTIONAL R	HINDUNI	251.276								
PHYDH ECOL	ENSOR PROTEIN HY	ESCHERICHIA COLI	912-339	160-187			-				
PHYLE PSESN	INYDANTON UTILIZATION PROTEIN B		T			l		Ī	İ	Ì	Ī
PHYSIC PARKIN	WYDAMTON ITTEL IZA		6.40	10.00		Ì		İ	T	İ	
		TIMOAF	8	207.111			Ť	İ	T	T	
T TOO I WATER	ALE PROSECOVATE CONVERSION PROTEIN		Т		T	Ť		T	T	İ	
١.	Cee NOLVE CON SOIL		Ţ.	433.440	127 713	414.441	1 080	1000	349.701	100.75	110.00
	ILE NOTE OF THE		T		Т	Т	т	Т	Т	Т	
		A SOCIED ASSESSED	7	Т	1	Т	Т		Т		T
. Ł	ICE MUCLEATION PRO		T	1	Ŧ	100	Т	7	116-911	987-1006	Ī
ונפי וצפון	ICE MUCLEATION PROTEIN	PSEUDOMORAS PLUORESCENS	Ť	٦	П	╗	729.781	73-632	1	1	
- 1	ICE MUCLEATION PROTEIN		7	T		(M.40)	1	1			1
PICEN XANCI	ICE MUCLEATION PROTEIN	VESTRUS	_	22.52	202	1248-1275	1	1		1	1
PICS SADI	INTERCELLULAR SPREAD PROTEIN		T	431.467				1			
PD3 BACST	DUTIATION FACTOR D.2	TE KAIOPHILUS	П	20. 10g				1	Ì		
PUT BACSU	INITIATION FACTOR IS-2	2	╗	127.76							
PUT ECOL	DOTIATION FACTOR IF:3			835-862							
PD3 ENTEC	DATIATION FACTOR IF-2	ENTEROCOCCUS FAECIUM	239.627								
PUT BACST	DATIATION FACTOR IF.3		1								
PF) ECOLI	DATIATION FACTOR (5.3)		٦	20.0							
PUT KIEPN	DATTIATION FACTOR D-3			76-01							
PUT MACHE		GNTANS	Ξ								
PIF3 PROVU	ENTTATION FACTOR G-3			69							
PE) SALTY	DISTIATION FACTOR IS-3	ממא		70.97							
PIET SERVICE	DATTATION FACTOR IF-3										
PICA NEIGO	IGA-SPECIFIC SENDIG ENDOPEPTIDASE	HOEAE			098-((1	1034-1058	1333-1404	1483-1331	_	L	
PIGGB STRSP	Ī		46-76	120-150	155-222						Γ
PICCO STRSP	INCO BENDENC PROTEE			120-150	195-225	170-797		-			
PILVH ECOLI		ESCHERICHIA COLI	13.61	130-147							
PEWH SALTY	ACETOLACTATE SYNTHASE	URUM	47-81	120-147		ľ	l				
PRW LACLA			20-75			İ				l	
PDGB SALTY	DAPS PROTEIN		115-2112						l	l	Γ
PDO ACICA	BHOSINE S-PHONOPHE	ALCOACETICUS	166-193						T	İ	
PING BACSU	E-5-MONOPHOSPHATE DEHYDROGENASE		П				r		H	T	
PINA BACTI.	DOWNE DIMERTOR A PRECUISOR		103-130								
PDGA LISMO	DIERNALIN A	LISTERIA MONOCYTOGENES	•	161-188	196-232				H	H	
PRO LISMO	DATEMALIN B PRECURSOR		Ť	П	2						
PINVA YELEN	IMAASIN	TENSIMIA ENTEROCOLITICA	201-535		1		1			1	7

PCCFME	107.196.4	4									
THE MANE	PROTEIN	ORGANISAL	AREAL	ABEA 2	ABFA 1	APFA	ABFAG	ADEAA		Т	
PUPA7 SHIFT	W KD ANTIGEN	SHIGELLA FLEXMEN	Т			_	т-		Т		2000
PUA SHIT	1	SHIGELLA FLEXMEN	8 13 8	437.475	493.557	596-630					Ī
PIPAB SEIDY		SHIGELLA DYSENTERIAE	20-55	71.169	480-507	23.53					T
PIPAB SHIFL	62 KD MEABRANE ANTIGEN	SHIGELLA FLEXMEN	21.53	71.169	480-507	\$23.556					
PIPAC SHIDY	41 KD MEAIRRANE ANTIGEN PRECURSOR	SHIGELLA DYSENTERIAE	21.53	13-161	173.300	324.378					
FIFAC SHIPL	43 KD MEABRANE ANTIGEN PRECURSOR	SHIGELLA FLEXNEM	28.57	113-161	173.300	324.373				T	
TOWN SHOP	14 P.D. MENBANE ANTICEN I'AD	SUCCELLA DYSENTE MAR	٦	391-318							
ACTION ACTION	PERU PENDICALE ANTICEN	SHIGELLA FLEXNEN	4	259-286	291-318						
	Por Providen	MIGELIA DISENTEUAE	175.702								
PIPT BEREE	INCH PROTEIN	SHIGELLA FLEXNEN	20								
Mary Front		PSEUDOMONAS SYUNGAE	٦	143-173							Ī
2000	WHICH THE PROTECT BEFOREOUT	ESCHENCHIA COLI									
200	VANUE PROFESSION PRELUXSUR	VIBRIO CHOLERAE	212-239	336-377						Ī	
PIROS VIBOR	VIKULENCE REGULATORY PROTEIN INCO	VIBRIO CHOLERAE		67-97							I
PIER STREET	MON-KEGULATED MOTEIN A	SYNECHOCOCCUS SP	167.194					Γ			
PICEL CUITY	INSERTION CLEACH ISOLISIN FAULT INSE	SHIGELLA DYSENTERIAE	96-15								
PISE ECO!	DATE TONE FACTOR IS DOUGHT THE	SHIDELLA DYSENTEUAE	6.31								
PICE CHIT		ENCHANCIAL COLI	122-149								Ī
PIXE CHICO	DATE TION OF ENGINEER PROTECT IN INCH	MUCELLA FLEXNER	=								Γ
PISPI BACKII	e le	SHIGELLA SONNEI	┪								Ī
PISP BACPO	INTRACELLULAR SERINE PROTEASE	BACILLIS SUBJECTS	┪	197.224	233.200	1					
PISTA ECOL		PROPERTY OF THE PARTY	2		Ī	1					
PISTA SHISO	ISTA PROTEIN	CHICKLI A COMME				1					
PIUTA ECOLI	FEALC AEAOBACTIN RECEPTOR PRECURSOR	ESCHERICHIA COLI			100	1					
PIAG BACSU		BACILLUS SUBTILIS	Т	,	100	1					
PK6P2 ECOLI	6-PHOSPHOFRUCTOKINASE ISOZYME 1	ESCHERICHIA COLI	0.1.0	Ī		Ì		Ī	1	1	Ī
PKAD BACSU	ADENYLATE KINASE	DACILLUS SUBTILIS	111.215			Ť	İ		<u> </u>		Ī
LYO TYCIY	ADENTLATE KINASE		116-21)		Ī		T			\dagger	Ī
PKANU STAAL	KANAMYCIN MUCLEOTIDYLTRANSFERASE		96.69						1		
PKDGT ECOL	-KETO-)-DEOXYGL	SCHEDICLIA CON .	8								
PKDGT EAWCH	2-KETO-3-DEDXYGLUCONATE PENAGASE		10.07		1						
PKDTA ECOLI	J-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANS	ESCHERICHIA COLI	144 104			1	1				
PKGTP ECOLI	ALPHA-KETOGLUTARATE PERMEASE		21.10		1	Ì	1	1			
PKGUA ECOLI	GUANYLA TE KDIASE		162.110			1	1	1		1	
PKHSE BACSU	HOMOSERINE KINASE		49.76		T	\dagger	\dagger	1	1	1	1
PKHSE FNEDI		NO	52.79			T		Ť	1	1	I
TOTAL BACCI	AMINOCALYCOSIDE J. PHOSPHOTIANSFERASE	NS.	12.39					T	T	\dagger	T
PROVE ELUCI	RUM I INVISCULTIONAL REPRESSOR PROTEIN		228-255		T			Ī		1	1
PKPYK BACKT	PYNOVATE KOMAKE		113.148							\dagger	
TACA STAIN	POWER AND ACA CINING	HILUS	111.174				T		T		
PLACA STUMO	SOMERASE LACA SI	STATE OF COUNTY AND CONTRACTOR	3								I
PLACE STRUM	TAGATOSE & PHOSPI		30		1						
	6-PHOSPHO-BETA-GALACTOSIDASE		7		1	1	1				
PLACI ECOLI	LACTOSE OPERON REPRESSOR		١	1	1	1	1				
	LACTOSE OPERON REPRESSOR		195.229		Ī		1	1	1		
	PHOSPHOTRANSFERASE REPRESSOR	2	2.2	T	T	\dagger	†	†	†	†	1
_	PHOSPHOTRANSFERASE REPRESSOR		5		T	T	t	†	†	t	I
TACT LAGE	LACTOSE PENGEASE	11	196-230		T	f	\dagger	†	+	1	T
٦,	MAN TOWNER BESCHESON	U.S	Ē	517		l	t	T	\dagger	1	T
	ENDO-1 1/4LBETA-CHICANA CE PRECINCON	KLEBSELLA PREUMONIAE	337.364								T
PLASI PSEAE	OHOLL SYNTHESIS PROTEIN LASI	2	13:159							<u> </u>	T
	PROBABLE LEUCOCIN A INDAUNITY PROTEIN	LEUCONOSTOC GELIDITA	201	†					Н		
PLCNC LACLA	LACTOCOCCIN A SECILETION PROTEIN LCNC		163.180	716 696		1		1			
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INTERCRETATION ANTIGGED ANT	CW CALCIUM MESTONSE ECCUSIONEN				190.00		1	1		1	
International Content	NA ANTICEN			co-367			1	1	1	1	
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LACTATE BEINDOCENARE SOCIETIES SYCTOMICS 14-27 14-17 17-10	Kilnase			ī	907-641					1	
LACKATE DEPRODUCEANIE SOCIETION HEADER 1913				Τ	39.306					1	ŀ
The principle of the proposers Part Pa			144.374								
Land Reproposable Land			Г	116.66				-			
LACTATE DEPTROGENARE INTEGRACETORY 13-14			Т	140-267							
LACTOR INTEGRATORY 1972			22.49								
LACTOR DEPRODUCEMENT (14719AL MUDOCTORIES) LACTOR DEPRODUCEMENT (107.311								
LUCTOR ESPYDOCENASE LISTEDIAL MONOCY FLOCATION 15-10 1						Ī			ĺ		
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The SEPTION OF CRANGE THE MAN ACTUALITY SHOWN OF STATE S		EUMONIAE	210-017					1	Ì		
THE PARTICULAR PRECURSOR SECTION PRECURSOR PRE					╗	Т	7		t		١
EACH POINTER 19.90	-incom	SACILLUS ANTIBUACIS	Ī	2	╗	٦	╗	201.70	1		
17.00			33-50						1	1	
CONTRACTOR CON		SACILITIES CITETATION	3.30								
1500 OF TABLE 1500 OF TABL			417-464								
1507071AALATE BENTRAKE LACTOCOCCUS LACITS 11-215	SYNTHASE		†	70,7				Ī			
	SYNTHASE		1					Ī			
	DEHYDROGENASE	SACILLUS COAGULANS	36:12					1	1		
150 150	DEHYDROGENASE.	CLOSTRIDIUM PASTEURIANUM	185-212								
International Recursion International Recursional Recursion International Recurs	DELIVORATACE P	ACTOCOCCUS LACTIS	П								
FORTING PROJECTOR CANDIDATE CAND	EVE LANGE VOTA RICE	AACH LIS SUBTILIS		676-703	344.334	785-822		1			
PARE PARE	L REGULATION I PROTEIN CEST	CEMPAIA CAROTOVORA	146-173								
PARE 1		ACRA VELLA CO	16.53								
IF ASE PRECINSON NAMEDIAL COLI 19-20 1	IPASE 1	MUKAXELLA SF		T							
INTERPRECINSOR ESCHERICHIA 19-20		MORAGELLA SP									
Interpretation		ESCHEMCHIA COCI	6.8								
ITASE PRECUISOR PISTUDDALONAS PLUDAKUSCENS 16-146 513-146 11-146		BURKHOLDENIA CEPACIA	(DZ						1		
1945E PRECURSOR 1945ED 1	IPASE PRECURSOR	PSEUDOMONAS FLUORESCENS	5						T		l
INTERFECTION INTE	IPASE PRECURSOR	PSEUDOMONAS SP	176-203								
19,220 1		STAPHYLOCOCCUS AUREUS	10-146	\$12-546							
155-1275 155-1275	ATTACK OF CITETAL PRECITE SOR	SALMONELLA TYPHIMURURI	193-220						7		
EUROPA STRUTH BINDING TRANSPORT ROTTEN LIVE ESCHELICHIA COLI 13-30 15-31 1	COUNTY AND THE PROPERTY OF	EAL MONET I A TYPHIM IN IN	195.222								
United acid Transform Front Fig. 19-191 19	NOING PROJEIN PRECUASOR	ALEXANDER A COMMEND OF	10.								
EULICAL EMBORAS NOTERN PRECURSOR ESCHENCHIA COL	AMINO ACID TRANSPORT PROTEIN LIVE	SALMUNCLLA ITTIMUNIUM	97.16						Ī		
EURIGESTATE 192-222	AMINO ACID TRANSPORT PROTEIN LIVE	ESCREMENTA COCI									
EUGINE SPECIFIC BINDING PROTEIN PRECUASOR ESCHENCHIA COLI EUCINE SPECIFIC BINDING PROTEIN PRECUASOR ESCHENCHIA COLI EUGINE SPECIFIC BINDING PROTEIN LYM ACTINOBACILLUS ACTINOBAYCE TEMCOMIT ANS 111-14 113	LEUALE/VAL-BINDING PROTEIN PRECURSOR	CITROBACTER PREUMULI	777.541						T		
EUCINE SPECIFIC BINDUNG PROTEIN PACCURSON ESCHERCHA COLI 191-121 191-131 191-141 191	LEUMLEVAL BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	103-222							Į	
131-148 131-149 131-	L FUCINE. SPECIFIC BINDING PROTEIN PRÉCURSOR	ESCHERICHIA COLI	195-222								
EUROTOXIN ACTINOBACILLUS ACTINOB	AND ACTO TRANSPORT PROTEIN LIVE	ESCHENICHIA COLI									
EUROTOON SCRETCH PROTEIN PASTEURELLA HAEMOLYTICA 51-99 179-716 145-712 409-416 455-442 449-309	THE PROPERTY OF THE PARTY OF TH	ACTINOBACILLUS ACTINOMYCETEMCOMITANS	113-147	113.213	198-443	111-151	191-620	655-711			
EUKOTOKN SECRETION PROTEIN ACTINGBACILLUS ACTINGNIVEERKONITANS 403-514	MAQ4044	PASTELIRELLA HAEMOLYTICA		179-216	345-372	409-436	455-482	496-530	_	11-131	133-926
LEUKOTOSTA SECRETION PROTEIN LTC MOTEIN	LEUKUIOAIN	ACTINOBACII I IIS ACTINONIYEETENCONITANS	417.514								
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17.0 PROTEIN	LEUKOTOXIN SECRE	TASIEURELLA DALMOLT IILA									L
INTERPRETER		ACTINODACILLUS ACTINONIYCE HENT UNITANS									ŀ
INTERPROTEIN	LKTC PROTEIN	PASTEURELLA HAEMOLYTICA									$\frac{1}{1}$
LKTD PROTEDH PASTEUTHELLA HAENOLYTICA 184-289 147-144 14	LKTD PROTEIN	ACTINOBACILLUS ACTINONIYCETENICONIITANS		202-142	28.70	264-36				-	
ATP DEPENDENT PROTESSE LA TOPP PARCETYLGLUCOSAMORE ACYLTRANSFERASE INCRESTISII TOPP NOTEIN SIGNAL PEPTIDASE SCHEMICHAR COUCH INC. TOPP COUCHE SIGNAL PEPTIDASE STAPHYLOCOCCUS AURISIS ISTROCTOM STATINIT PRICINSOR STAPHYLOCOCCUS AURISIS ISTAPHYLOCOCCUS AURISIS ISTAPHYLOCOCCUS AURISIS	LKTD PROTEDY	PASTEUMELLA HAEMOLYTICA	134-289								
UDP-N-ACETYL GLUCOS AAMTE ACYLTAANSTEANSE NICKETTSII 129-259 LEOPROTEIN SIGNAL PEPTIDASE SCHEMICH COLL LIPOROTEIN SIGNAL PEPTIDASE STAFFLYLOCOCCUS AUNIEUS 104-101 LEINOROTEIN SIGNAL PEPTIDASE STAFFLYLOCOCCUS AUNIEUS 104-105	ATP.DEPENDENT PR	ESCHENICHIA COLI	121-148								
LIPOPROTEIN SIGNAL PEPTIDASE SCHERICHIA COLI LIPOPROTEIN SIGNAL PEPTIDASE STAPHYLOCOCCUS AURIENS LIBIROCIDIN F SUHLINIT PRECINSOR STAPHYLOCOCCUS AURIENS LIBIROCIDIN F SUHLINIT PRECINSOR	IMP.N.ACETYLGLUK	NCKETTSIA NCKETTSII	229-256								
LIPOPROTEIN SIGNAL PEPTIDASE STAPHYLOCOCCUS AURIEIS 119-161 15/16/CDA SUBLINI PRECINSOR STAPHYLOCOCCUS AURIEIS 161-193	I POPROTEIN SIGNA	ESCHENCHIA COLI	10-37								
STAPHYLOCOCCUS AURILIS		STAPHYLOCOCCUS AURIUS	134.161								
		STAPHYLOCOCCUS AURILIS	161.195		!						
Controlled a section of the section		CTAPHINI OCCUPING ALIBITIS	101.01	İ	: :						

PCCENE 1031/314	Prokaryotic Sequences	П				п				
ME REDIEM	DRCANISM	٦.	AREAI	ABEAZ	AREA	AREA 1	VANA	V TVJAV	ARGAL	ABEAS
ALKANAL MONOOX	KRYPTOPHANATON ALFIREDI	Т								
ALKANAL MONOOX	PHOTOBACTERIUM PHOSPHOREUM	/17-111	147-167					1		
PLUXB_VIBHA ALKANAL MONOOXYGENASE BETA CHAIN	VIBIO HALVEYI	3						1		
JXC_PHOLE JACYL-COA REDUCTASE	PROTOBACTEMUM LEIDKWATHI								1	
PLUXC PHOPO ACYL-COA REDUCTASE	PHOTOBACTERIUM PROSPROZEDA		I					1	1	1
PLUXC VIBIL ACYL-COA REDUCTASE	VENDELLANDIE INGINERENE	0.00						1	1	I
AL ACRED ACTIC-CON REDOCTASI.	BIOTOBA CTERINA PROCESS	T,	375					T	t	I
PLUXD PHOLE ACYL HAMSPERASE	WINDS AND AND AND AND AND AND AND AND AND AND	Т						1	1	
PLUXE VIBRA LUCIPERIN-COMPUNENT LIGASE	PRIOTORACTERINAL FINGUATHI	145.172	T					1	1	
NON-EL LORE SCENT	PHOTORACTERINA PROSPHOREIN	Т	99-126	T	Ī		Ī			
PROPERTY OF ANY	Vasio Fischeri	Ţ,			T				T	T
_	VISSO DABOTO	5								
MANUAL MANUAL PARTIES BOTTOM INT	Viento Fredriker		T							ĺ
OLDER CYNTHERIC DE	VIEWO TISCHER	10.01					T			
OLONG STRINGS13 FR	PHOTORACTERITAL PRIOSPICORITAL	38.13	63.180				Ť		1	
VIEW VIEW BEGIN ATORY PROTEIN	VINE OF VINE VEVI							1	T	
PLYBI PHOLE ALKANAL MONOCYCENASE BETA CHAIN	PHOTOBACTERION LENGUATH	768.705							T	ĺ
ALKANAL MONOOXY	PRIOTOBACTERIUM LEIOGNATHI	311.335								
B.ENZYALE	BACILLIS SUDTILIS	917						1	1	
т	CLOSTRIDIUM ACETOBUTYLICUM	811:18						Ī	l	Ī
PLYSP ECOLI LYSINE-SPECIFIC PERMEASE	ESCICERICIIIA COLI	142.176								
AMIDASE EMIANCE	BACILLUS SURFILIS	13.02	150-177	467.513	\$55.518					
TB ECOLI LYTB PROTEIN	ESCHERICHTA COLI	210-237								
PLYTC BACSU AMIDASE PRECURSOR	BACILLUS SUBTILIS	_	115-252							
IR BACSU (MEMBRANE-BOUND PROTEINLYTR 💃	BACILLUS SUBTILIS		139-303							
PHILL STRPY IN PROTEIN, SEROTYPE IT PRECURSOR	STREPTOCOCCUS PYOGENES	П	114-156	191-300	П	П	107-911			
П	STREPTOCOCCUS PYOGENES	Ī	20-13	75.702	Ξ.	<u> </u>	190-457			
Ι	STREPTOCOCCUS PYOGENES		269-337							
PASS STREET INTROCEDING SERVICES & PRECINCOL	STREFFOUNDED FTOURNES		20.70	100.133	019-76				1	
7	STATE TOUCKERS					1			1	
PAINTE FATAF MALTOSE BINDING PROTEIN PRECURSOR	ENTERONACIFE ACEDICINES	19					Ì		1	
LE ENTAE INNER MEMBRANE PROTEIN MALK	ENTEROBACTER AEROGENES	9			Ī		\dagger		1	Ī
PHALT ECOLI MALT REGULATORY PROTEIN	ESCHENCHIA COLI	852.879					T	Ī		Ī
LX STRPN MALX PROTEIN PRECURSOR	STREPTOCOCCUS PNEUNIONIAL	Т	180-207					T	T	
PAIANB DACSAI 1,4-DETA-MIANNOSIDASE A AND B PREC		П					İ	Ī		Ī
	CALDOCELLUM SACCHAROLYTICUM		929-265	1332-1345	13%-1333					
PAIAON DACST MALATE OXIDORESENCESE	BACILLUS STIAROTHI RACOTHU US	26-23								
APPRIORICE ACTION	EXCISEDIOUS CO.							1		
MUNICIPALITY OF THE	NOV. HINDS		5		Ī			1	1	
PALCES FOR I LACER PROTEIN		Т					†	1		Ì
PACED ECOLI INCED PROTEIN		١,	234.361	104.144		1	1	1	1	
METHYL-ACCEPTING		Т			Ī	1		1	T	
METHYL-ACCEPTING		38.30				Ī		İ	t	Ī
PAICPS SALTY METHYL-ACCEPTING CHEMOTAXIS PROTEIN II	SALMONELLA TYPHIMUMUNI	308-306	Ī		Ī		T	T		I
WETHYL-ACCEPTING		316.315						Ī	T	Ī
PAICP4_ECOLI METHYL-ACCEPTING CHEMOTAXIS PROTEIN IV		3:18	164-191	277.304			T			Ţ.
PA CALICA CHEMORECEPTOR MCPA		160-287	369.403	\$16-543						
PC_SACTY CHEMOTAXIS CITRATE TRANSDUCER		314-348		-						-
PMCPD ENTAE CHEMOTAXIS ASPARTATE TRANSDUCER		2	П	П						
PS ENTAL LINEMOTAUS SENDING TRANSDUCER	ROGENES	1	28.208	117.351	418-523					
MURA ECOLI SPECIFIC RESINCTION ENGINESA	METHANOSARCINA BARKERI	17.71					1	1		
PHORA METVA METHYL COENZYME M NEDUCTASE T		617	1	Ī				1	1	1
NA METVO METHYL COENZYME M REDIXTASE	METHANOCOCCIN VOLTAR	200.710			1	1	1	1	1	
			1	1	1	1	1	1	1	7

1107.170.4	Proharyotic Sequences	Т	1964	AUGA L	ABEA A ABEA 9	Т	ABEA 6 ARFA?	AREAI	AREA?
FILE NAME PROTEIN	ORGANISM	1	┰	1	_	7		Ι.	
BETTE METHYL. COENZYNE M NEDUCTASE	METHANOTHERAIUS FENVIOUS	3,1.3%							
ETVO METHYL-COENZYNE NI REDUCTASE	METHAMOLOCCUS VOLIME			-	-	-			
COLI MCRC PROTEIN	ESCHENCHIA COLI					-	-		
GETVO REDUCTASE OPERON PROTEIN D	METHANDCOCCUS VOLTAE		Ť			-			
OLI MALATE DEHYDROGENASE	ESCHENCHIA COLI		T				-		
THE MALATE DEHYDROGENASE	ALETHAMOTICE AND FEM VIDUS		Ī						
PRIDIT SALTY MALATE DEHYDROGENASE	SALMONELLA TYPHINIUMUNI	T	110,484	903,1010			-		
OLI MOL PROTEIN	ESCHERUCHIA COLI	T	Т						
BIOS YNTHESIS PROT	ESCHERICHIA COLI	7	1	+	+				
METHICILLIN RESIS	STAPHYLOCOCCUS	721-122			1		-		
	EPIDEMMIDIS & AUREUS	╗					-		
STATE STATE ANETHER IN BESISTANCE MECRI PROTECT	STAPHYLOCOCCUS	419-495	<u>\$</u>	1					
	EPIDERMIDIS & AUREUS					$\frac{1}{1}$			
A THEORY OF A CONDON TO THE THEORY	METHYLOCOCCUS CAPSULATUS	214-248							
PACING METCA METHANE MONOOATGENASC COMPONENT A	LAFTHAY OCHAIS TRICHOSPORIUM	331.348				-			
CITA METHANE MONCOATUENASE COMPONENTA	ECACEMENTAL COLI	133.367							
COLI SHCHC SYNTHASE	ENCHANGE OF THE PARTY AND THE	150.126		ľ		-			
TILL PROBABLE HG TRANSPORT PROTEIN	SHEFTONICES LIVINGS	144.165			-				
PAGERA BACSA MERCURIC REDUCTASE	BACILLUS SF	Т	311. 116	Ī			_		
MERCURIC REDUCTA	STAPHYLOCOCCUS AUREUS	Т		1	1				
MERCURUC RESISTA	STAPHYLOCOCCUS AUREUS	10-01	1	1	1				
CVSTATHIONING	ESCHEALCHIA COLI	136-363		1		1		ļ	
PARTY FOR I CASTATHIONINE BETA-LYASE	ESCHENCHIA COLI	36)-380				1	1	1	I
TVETATUIONING BE	SALMONELLA TYPHIMURUM	1.29					$\frac{1}{1}$		Ì
	FSCHERICHIA COLI	448-483							
PAGE ECOLI METHONINE STRINKSE	FSCHERICHIA COLI	371.398	943-676						
METHIONINE STRIFT	ECCHEBICITIA COLL	118:312							
TANSCAUPTION AL	ESCUEDICUIA COLI	63.80	312.380		-	-			
PAIGLA ECOLI GALACTOSIDE-BINDING PROTEIN	AACH LIN CINETIL PC	65-122							
SEPTUM SITE-DETE	PACIFICAL COLUMN COLUMN	621:00		ľ	-				
COL! MIOC PROTEIN	7	15.15					_		
LTA 17 KD MEMBRANE PROTEIN PRECURSOR (+	104-133			_	-			
PHIP LEGAL OUTER MEMBRANE PROTEIN HIP PRECURSOR	7	1	38.184						
NTFA RAWA ADENING WANGTHYLTRANSFERASE	7		T						
TAAU TRINA ADENINE NAMETHYLTRANSPERASE	┪		130.154						
PARLSS ENTRA RRNA ABENINE NA-METIIVLTRANSFERASIE	7								
	7		126.154		-				
COLI TRANA ADENINE NA-METHYLTRANSPERASE	7		2						
IRNA ADENINE N.	STREPTOCOCCUS PREUNIONIAE								
RUNA ADENINE N-4	STREPTOCOCCUS SANGUIS		3						
RAWA ADENINE N-6	DACTERODES FRAGILIS				T	1			
METHANE MONOO	METHYLOCOCCUS CAPSULATUS						+	-	
•	ESCHERICHTA COLI	67-70			1				
-	THIOBACILLUS FEARDOXIDAMS	2	200			1			
+-	THOBACILLUS FEAROOXIDANS	70-67					1	-	
1-	THIOBACILLUS FERROOXIDANS	93-132				1	$\frac{1}{1}$	\downarrow	
MOB PROTEIN		45-73					+		
	Г	243-370				-			
i tai	Г	26-53							
MOLYBDENDA-PTE	CLOSTRIDIUM PASTEURIANUM	19-92							
JETHANOL LITTLE C	PARACOCCUS DENITURICANS	300-334	101.134					-	+
STATE OF THE ON MICHARDES PROTEIN MOEU	SYNECHOCOCCUS SP	3.36	10-103	{{₹₹-116					-
IN MICHAEL	SYMECHOCOCCUS SP	2.31	912-541	;			-		-
THE PROTEIN	ESCHEDICHIA COLI	136-163							
ALC: DENTABLE TRANSFERASE	BACILLUS SUBTILIS	106-133	147.311		_				
PARE BACCE ROD SHAPE-DETERMINING PROTEIN MIEB	BACELUS CEREUS	116-213							
NOD SHAPE DETER	BACELUS SUBTRUS	85-112				+	1		
CHAPERONE PROT	KLEBSTELLA PNEUMONIAE	198-232	- 1						
	TANCOL STATE OF THE PARTY OF TH	(4.4)	413.416		_				

PCGENE 107117814	Proheryalic Sequences			П		_	П	_	_	
FULL MANE PROJEIN	ORGANISM FILE EBSIELL A BINETACONIAE	188.5	A REAL	7777	1	2		3	1030	A SEA
PARKE LITER FINESTA ADJESTA FROIEST FECTORSON	IN EDUCE I A DATE MANAGE	191.220					T			
PARKE KLEPN MUKE PROJEIN	T	T	99-310	Ī			T			Ī
	Т	2	L	261.791	421-448	507.534	518-622	773-400	1058-1085	
PROB ATP-BINDING	T		413-449							
PNISTA STAEP ERYTHROMYCIN RESISTANCE PROTEIN	T	134-223	233.150							
ACIDIC PROTEIN MS		73-100								
PNITST ECOLI MODIFICATION METHYLASE ECOSTI	ESCHENICHIA COLI	250-284	474.544							
MODIFICATION METI	П	503.540								
MODIFICATION MET	Н	976								
MODIFICATION METH	7	92-39	309.336						1	
<i>FODIFICATION MET</i>	HERPETOSIPHON AURANTIACUS	281-308								
PWTB1_BACAM MODIFICATION METHYLASE BAMMII	BACILLUS AMMIOLIQUEFACIENS	15-62								
CODIFICATION MET	BACILLUS ANEURINOLYTICUS	184-211								
PMIBA BACAR MODIFICATION METHYLASE BANI	BACILLUS ANEURINOLYTICUS	П	382-409							
CODIFICATION METH	BACILLUS SUBTILIS		467-496							
CODIFICATION METH	BACILLUS SUBTILIS	208-235								
PMTCI_CITER MODIFICATION NETHYLASE CFRBI	CITROBACTER FREUNDII	1.16	55-82	151.179						
PMTCI PERAU MODIFICATION METHYLASE HGICI	HERPETOSIPHON AUTANTIACUS	130-147								
PATCZ HERAU MODIFICATION METHYLASE HGICII	HERPETOSIPHON AURANTIACUS	11:31								
PATIEL ECOLI MODIFICATION METHYLASE ECON	ESCHENCHIA COLI	76-110	145-172							
PMTEI_HERAU MODIFICATION METHYLASE HGLEI	HEMPETOSIPHON AURANTIACUS	281.308								
	ESCHENCHIA COLI	9								
PRITES ECOLI MODIFICATION METHYLASE ECO RV	ESCHENICHIA COLI	8								
PMTEC ENTCL MODIFICATION METHYLASE ECAL	ENTEROBACTER CLOACAE	57-01			П					
PMTFI FLAOK MODIFICATION METHYLASE FOKI	FLAVOBACTERIUM OXEANOKOITES	114-21	239.38	35.78	22.5	333-646				
MODIFICATION METH	FUSOBACTERIUM NUCLEATUM	2		Ī		1	1			
	HAEMOTHILUS GALLIPATUM	33:10	700						1	
PATRY ARTTE MODIFICATION METRICASE RINCII	METHANORACTER! IN THE MOSORMICICIAL	7	204-171				1			
MODIFICATION METH	KI FRSTEI A PAFFAGANIAE	Т		T			T		Ī	
AANNITOL I PHOSPH		Т	224.258	349-376			T			
MODIFICATION METH	Γ	Τ	101-04						Ī	I
PMTN1_MEILA MODIFICATION METHYLASE MLAIII	NEISSERIA LACTAMICA	124-158	183-210							
PATES_PROVU MODIFICATION METHYLASE PVU II	PROTEUS VULGARUS	104.335								
PMTPG_SULAC MEMBRANE-ASSOCIATED ATPASE	SULFOLOBUS ACIDOCALDARIUS	19-6								
MODIFICATION METH	1	126-264								
TAYPTOPHAN-SPECIF	1	П	П							
PAITS! STASA MODIFICATION METHYLASE STS!	STREPTOCOCCUS SANGUIS	_	14-461	600-645	Ì					
-	STANDARD STANDARD	3			1					
MODIFICATION MET	I ACTOCOCIIE I ACTIE	T			Ī			T		
MODIFICATION MET	LACTOCOCUSTACTIS	T		Ī	Ī			Ī		T
PO DNA METHYLAS	SPIROPLASMA SP	9	256-290		T		Ì	T	T	
MODIFICATION METH	SERRATIA MARCESCENS	Т				Ī	Ī		Ī	Ī
CODIFICATION METH	THERMUS AQUATICUS	130-157					Ī			
PMTVI_VIBSI MODIFICATION METHYLASE VSPI	VIBRO SP	2.66								
PMUKO ECOLI MUKB PROTEIN		120-311	1014-1048	1216-1252						
PMULI ERWAM MAJOR OUTER MEMBRANE LIPOPROTEIN PREC		74.54								-
PMUL! MOLMO MAJOR OUTER MEMBRANE LIPOPROTEIN P	٦	27.54		F					Ī	F
PARKLI PROMI MAJOR OUTER MEMBRANE LIPOPROTEIN PREC	1	11-63								-
PAGESU UDP-LIGASE	Ī	П	399-326							
CASE STATE		107-134								
PAILINE ECOLI IUDI-MUNAC-PENTAFETTURE STATHETASE	ESCHENICIA COLI	407-437								
THURL ELLE ENDING THE INVESTOR OF	ENTERICHIA CULI	2								
PRUME ENICE ENOTEPTION OF TO A MITAGE BETA GUEINIT	Ŧ	200	1	1	1	1	1			
PMUIA SIRLM IMEINTLMALUNIL-LUA MUIASE BEIA-30	7		1	1	1	1		1		

4.95.					•					
NI TANGE			4	1						
DIALOGUE METHY MALONYL COA MUTASE ALPHA-SUBUMI		11.100		T						
C. CPFCIFIC ADENINE										
ELECTI INC. TICH MAI ONYL. COA MUTASE AL PHA-SUBUNIT	ı	2	Ī							
THOUSE STATE THE MICHARD REPAIR PROTEIN MUTL	_	2	Ī							
THE PROTEIN NUTL.	SALMONELLA TYPHIAIURIUM	• 1		1						
THE MISTRALL OF THE	VIBRIO CHOLERAE	134-169	1	Ī	Ī					
PAIUTL VIBER PROTEIN MOTE	ESCHENCHIA COLI	18-13								
JAA MISMATCH MET	STREPTOMYCES ANGIOFACIENS	60.87								
AUTT-LIKE PROTEIN	PEE: MOMONA CARVALON!	341-368								
OENZYME A REDUC	CHEEPLOCOCIIC DY OCENES	5:139	148-182	190-217	240-301					
	SIRETION CONTROL	100-152								
AYCOLYSIN PRECUI	STRETUMTES CACAGO	616 016								
ANTIC PROTEIN PRECI		T	366 380							
ACOTON ATE MINE	_	٦								
TO THE PROPERTY OF	SAL MONELLA TYPHINIUM	233-260								
PHADE SALTY INCASCRICTIONAL ACCOUNTS	ESCHEDICHIA COLI									
ECOLI MACU PROTEIN	CI DETRIBUTE PERFRINGENS	1.3	990-1017							
HYALUKOMOCLOCOS	RECUEBICHIA COLI	119.153								
PNAGR ECOLI NAGR PROTEIN	C. Arrainina (Caricina)	7	289-330	922.988						
PHANH CLOSE SIALIDASE PRECURSOR	CLOST RUDIUM SET TIL OF	١,	Т							
	CLUSTRUDIUM SURUELLIII									
SALTY STALIDASE										ļ
ENTIRE MAINWHAM ANTIPORTER		9								
POOL I DESDIE A TORY NITRATE REDUCTASE ALPHA CHAIN		186-420								L
TOTAL AND SECTION WASI	ESCHENICHIA COLI	76-103								
RECOLATOR FROITER	ESCHERICHIA COLI	155-189								\downarrow
T		120-247	351-345	111-121	505-538					
NITRATEMINITESE		212.239				L				
	KNIZ UBIUMI MICLILLU II	361							L	L
MEDMYCIN RESISTAN	٦		.00							
7			*******					L		
NA ADCORPTION PRO	Γ	48.513						1	\downarrow	ļ
1	ESCHENCHIA COLI	2	186.220							1
т	ESCHERICHIA COLI	115-342								ļ
PAPEL ELULI	ENTEROBACTER CLOACAF.	9.36								\downarrow
TALL MALLEN ALTERNATION IS	ESCHERICINA COL!	106-233								1
PINIAA ECOLI MAI PINI JAMINOMICE	ESCHENCINA COLI	171-305								
MA(*)M(*)	PSELIDOMONAS CITLORORAPHIS	101-12								
PINIAB PSECL NITULE HYDRATASE SUBURIL DELA	PATRICULAR PROPOCULARITY	16:19			L					
NITRULE HYDRATAS	MODULOCCO MODOCATIONOS	77.							L	
PHIFA AZOBR NIF-SPECIFIC REGULATORY PROTEIN	AZOSPINILLUM BRASILLENSE	200						L		L
	BRADYRUIZOBIUNI JAPONICUNI								L	
BASIE A LIEBAGE NIF.SPECIFIC REGULATORY PROTEIN	HERDASPINILLUM SEROIF DICAL	5	162.203						ļ	-
MIS. COSCIONOR DE CAIR	RHIZOBIUM LEGUMINOSARUNI	20-13				 -				
ELUS OFFICE OF STREET	RHIZOBIUM MELILOTI	171-198								
WILL WILL AND STECKING ALCOHOLOGICAL	RIIODOBACTER CAPSULATUS	200-283								
NIP-STICK IC NICON	A POTOBACTER VINES ANDII	342.369								
	V. EBEIEL A BARTHADAIAE	134.181						L		
NIFB PROTEIN	ALEBSIELLA TREUMOITALE	134.401								
NITROG MOLYBO-IR	ANABAENA SF					-				L
NITROG MOLYBD-IR	AZOSPIRULUM BRASILENSE	100			\downarrow			-	1	1
BUTTO NO VAD. ST	PLECTONEMA BORYANUM	387.414								4
MILLOW NOW NOW NOW THE WAY	THIODACILLUS FERROOXIDANS	33)-410								
7	CLOSTRIDIAM PASTEURIANUM	159-366						_		4
_	SPANCIA CP	\$6-83	L			L				1
PHITH FRATE MITROGENASE INCH PROTEIN	DI ECTONEMA BOBYANIM	267.294			L	L	Ĺ			
NITROGENASE INCH	TOECH CALLED A COM	10.45						L	L	L
NITROG MOLYBD-IR	AZOSPULLUM BICASILENSE	917		\downarrow		ļ				
NITIROG MOLYBD-IR	BIADYRHIZUBIUM JATURICUM				_	1	-	-	ŀ	L
PHIFK BRASP NITROG MOLYBD-IRON PROTEIN	BRADYWIIZOBRUM SP	478-303					1	\downarrow	1	ļ
NITROG MOLYBD-18	CLOSTADBUM PASTEURIANUM	22.72						\downarrow	1	\downarrow
NITROG MOLYBD-IR	I THIOBACILLUS FERROOXIDANS	679.508						-		\downarrow

PCCLNE	1107517654	Proharyotic Sequences	П	П		ĮΠ	П			П	П
FILE MANIE	FROIEIR		П	142	7	1	ANEAL	AREA	ARCAI	ABEAL	AREA
PHIFN BRUA	BIOSYNTHESIS PROTEIN NIFW	BRADYRHIZOBIUM JAPONICUM	130.166			Ī	1				
PNIFS ANASP	NIFS PROTEIN		2				1	1		1	
PMIS LACDE	MIFS PROTEIN HONIOLING	CKII	20.00	1			1			1	1
FNIFT AZOVI	NIFT PROTEIN	K VIMECANDII					1			1	Ī
PNIFU ANASL	NIFU PROTEIN	ANADAENA SF					Ī	T	1	1	Ī
PNIEU ANASP		ANABAENAST				Ī	Ī	1	T	T	T
PNIS O KLEPN	MIFU PROTEIN	HOWINE .	ŀ	287.109	456.411		T			T	
PAIR ECOL	MICHEL HAMSPORT PROTEIN NIKE	SCHEDICHIA COM	Т						T	Ī	
PAINE ECOL	MITELL HANDEN TO THE THE PRINCIPACE		Т	345.372				Ī		T	
NING COL									T		
PHIRC POET	PSETTENMENAS CYTOCHROME OXIDASE PRECURSO	UTZEN	103.333					T	Ī		
A DA L ASING	117 KD MEMBRANE ASSOCIATED PROTEIN	LACTOCOCCUS LACTIS	Τ	107-332	663.697	026-918					
A LUC I ACI A	NICH BIOCYNTHECIS PROTEIN NISC	LACTOCOCCUS LACTIS	T	140-188							
A DA LANK	MISON TRANSPORT PROTECN MIST		2	278.305	426.470						
	HASE ALPHA SUBURNT		T	134.268							
	HOMOCITATE SYNTHASE, ONEGA SUBUNIT		Г	103-132	213.240	283-310					
PIOCE ECOL	POAIN PROTEIN NAME PRECURSOR		22.49	26.63	335-362						
	NODUL ATION PROTEIN C	BRADYRUIIZOBIUM SP	ĕ								
PHODE RUILO	NODULATION PROTEIN C		216-313								
PNODC_NIILT	MODULATION PROTEIN C	NIIZOBIUM LEGUMINOSARUMI	10.01								
PHODE MILLY	NODULATION PROTEIN F	NIIZOBIUM LEGUMINOSARUM	31.50								
PNODE RHIDAS	NODULATION PROTEIN F		39.66					Ī			
PNODG RUBAR	NODULATION PROTEIN G		5								
PNODG RHIMS	NODULATION PROTEIN G		Š								
PHODE, RHILV	NODULATION PROTEIN L	ĭ	26.53								
PNODQ_AZOBA	NODULATION PROTEIN Q		П								
PNODT RHILT	NODURATION PROTEIN T		Т	155.312	420-454						
PRODT PHILY	NODULATION PROTEIN T	AINOSARUM	Т	416-44)						1	
THOOD KHILL	NODULATION PROTEIN U	AMIZOBIOM PREDI	300-310	376.344			1		1		
A IIII A AUGNO	NORTH ATTOM SECTED Y		Т						Ī	T	T
PNO! R RHIFE	NODEL ATION PROTEIN NO. B.	KHIZORUM FREDI	91:11						Ī	T	T
PNOC R RICE	NODVILATION PROTEIN WOLR	KHIZOBIUM MELILOTI									
PHOSD PSEST	NOSD PROTEIN PRECURSOR	PSEUDONIONAS STUTZERI	19.740				Ī			T	T
PNOSA PSEST	REGULATORY PROTEIN HOSR	PSEUDOMONAS STUTZERI	127.154				T			T	T
PNOSZ PSEAE	HICTASE PRECIRSOR	UKA	767.77								
PNOSZ PSEST	MINGASSOXING MEINA TANG PRECORSOR		П			:		:			
PNPRE BACAN	BACILLOL YSIM PRECURSOR	BACILLUS ANYLOLIQUEFACIENS	-	217-244							
PNYKE BACKO	PACILLOLYSIN PRECURSOR	BACILLUS FOLYMYXA	7								
PNINE BACSU	BACILLOL YSIN PRECURSOR	BACILLUS SUBTILIS	9	307.334							
	MADH-UBIQUINORE UNIMAREDUCIANE ZI NO CITAL	TAKACACOS DI MINISTERNA		İ	:	i	j	i		Ì	
PARTITION COLUMN	AMAKE BEHAVET TREBUNG BENKET AKE	:		!	!	i					İ
PARTY FOOL	CYTOCHROME CSS2 PRECURSOR		10.144							1	
PNREG ECOLI	NEG PROTEIN							T			I
PARLI RHORY	ALIPHATIC MITULASE	RHODOCOCCUS RHODOCHROUS	90.136				T	T	Ī		Ī
PNSA LACLA	IISIN-RESISTANCE PROTEIN	LACTOCOCCUS LACTIS	57.79	134-162			T			Ī	
PNTCA ANASF	INA-HINCHING PROTEIN VFI		65.92					Ī	Ī	Ī	Γ
PMICA SY/P7	HOBAL MIROGEM REGULATOR		14:41		Ī						F
PHICA SYNY)	LOBAL MITROGEN REGULATOR		67.94								
PNTRB VIBIL	NTROGEN REGULATION PROTEIN MTRB	VIBNO ALGINOLYTICUS	194-223								
PMING PREMI	ITADGEN REGULATION PROTEIN NA	PROTEUS VOLGARIS	185-413								
PNTRC RUINE	ITROGEN ASSIMILATION REGULATORY PROTEIN	RHIZOBIUM MELILOTI	17								
PAUZC SYMP	NADH-PLASTOQUINONE OXIDOXEDUCTASE CHAIN		6.0								
PINCAC SYNY)	NADHI PLASTOQUIN		7.5								
THUN. STATE	PALMI-TLAS I CONTINUE UNIDUALIDUE I MAIO (STAELHUCUCLUS SI		3]				1	7	1	7

PCCENE 1107117814	130	Probaryoile Sequences	ARFAI	AREA?	AREA AREA 4		AREAS IAB	AREA!		1	3
ME PROJEIN	ORC	ORGANISM SECRETARION OF THE CO	Т					1	+	+	
	TASE SUBUL STR	ECHOCKSTIS SP	160-199					1	1	+	
PROB NADH-UBIQUING	I ASE SUBU SIN	SINECIMONALIS SP	46-80			1		+		+	1
		STATEMENT COLI	368-402				1	1	1	+	
PINTOG ECOLI NADH DEHYDROGENASE I CITAIN	200	F CONTROLLE	10.57	496-513		1	1	+		$\frac{1}{1}$	1
		ESCUEDICHIA COLL	619-261					+		$\frac{1}{1}$	
NADH DEHYDROGENA		Conception CO !	19:11	136.164	156-193					+	1
		CONTRACTOR COLL	29-1;				1	1	1	+	
PHUSA ECOLI MUSA PROTEIN		TENCHA COL	13.65	10.01						1	1
WITH LATION SUBST	_	ESCHERICHIACIALI	141.163							-	
TRANSCRIPTION ANTI		ESCHENCHIA COLI	91,					-		_	
TRANSFEIPTION ANT		THERMOTOGA MARITIMA	200					\mid		┝	
A ANTINOME Y AND A TE	-	FLAVOBACTERIUM SP	23.230			Ī		l		┞	
PAYLE FLAST PANINGHEAMONIE DINER HYDROLASE		FLAVORACTERIUM SP	123-150			1	1	\dagger		\dagger	
ANIMOIIE XANDA IE		MACH 115 CFREUS	301-338					+		+	
_		ACRONACTERINAL TITALS ACTION	137.303					1		+	1
POCCT AGATE OCTOPICE BINDING PROTEIN I PRECURSOR		ACACACACACACACACACACACACACACACACACACAC	123.156								
:-		HOUSE IER VINIERASINI	107.134	800.850							
PODO! BACSU 1: OXOCLUTARATE DEHYDROGENASE EI COMPONE		BACILLUS SCHIILIS									
Т		ESCHERICHIA COLI	1				-	-			
Τ.		BACILLUS SUBTILIS	20:01					-		H	
т		PSEUDOMONAS PUTIDA				Ī		ŀ		\vdash	١
		ESCHERICHIA COLI	674-631				\dagger	-		-	
7	Γ	AZOTOBACTER VINELANDII	\$18-345				1			+	ł
1	Γ	ESCHERICHIA COLI	14-41	<u>=</u>				\dagger		\dagger	١
POUP ELOCI DIATORCHI CAMBO ELOCATOR EL CONTONENT	Γ	BACILLUS STEAROTHERMOPHILUS	249-333				1	1	1	\dagger	١
	Ī	Tutus subtitus	105-332				1	1		1	1
POOPA BACSU PYTUVATE DENTUMBERASE EL COMPONENT	T	MACILLI IS STEAROTHERNIOMILUS	8:0							+	١
BACST PYRUVATE DERYDRODENASE ET COMO	T	BACH LIK SUNTELIS	8.91							+	
POOPB BACSU PYRUVATE DEHYDROGENASE EI COMPONERI	T	CIR ANYDA TRACIONATIS	31.65						1	+	1
S KD CYSTEINE IUC		MEIR CONDRAINGE AE	8.6					1		\dagger	
WITER MEDICINARIE	Ī	METAGERIA MENINCITIDIS	139.186							+	1
COTER MEMBRANE	T	NEISSERIA AMENINGITIDIS	153.380						1	\dagger	
_	Ī	NEISSERIA GONORUNOEAE	61.90					+		+	
OUTER PIEMBANIE		NEISSENIA MENINGITIDIS	63.90				1			\dagger	١
PONIBL RELIME COLLEGE AREAGE AND PROTEIN PIR PRECURSOR	Ī	MEISSERIA COMORAHOEAE	63.90						1	\dagger	١
CHEE WENTENED	Γ	ISSEMA MENINGITIDIS	63.80						+	\dagger	1
CALTER LICENTISTANE P	Γ	NEISSERIA MENINGITIDIS	63.90					+	1	\dagger	
COTTER MEMBANIE		MEISSERIA MENINGITIDIS	24-51	63.90			1	1	1	+	1
OUTER MEMPRANE	Ī	NEISSENIA LACTAMICA	116-143						1	†	
	Γ	MEISSEMJA SICCA	24-51	6).80						+	ļ
DITTE LICELIAND	Γ	TINOBACILLUS PLEUROPHEUNIONIAE	114-131					1	1	\dagger	
CHIER MEMBRANE		HAEMOPHILUS INFLUENZAE	134-184	30.30	341-368				+	\dagger	
DITTER MEMBRANE		IAEMOPIILUS INFLUENZAE	16-31	200	2			1		\dagger	1
OUT TO MENTINE AND	Γ	NEISSERIA GONORRINOEAE	14-41					1		†	١
WAY OUTER MEMBE		STAPHYLOCOCCUS AUREUS	53-40	18-115			Т			\dagger	1
	Т	THERWOTOGA MARUTIMA	100-138	131.170	113.249	255-292	301-328	131-313	1	†	1
OUTER MENDEANE	Т	ESCHENCINA COLI	30-47	64.94					1	†	١
	Γ	NEISSENIA CONORUHOEAE	189-133							†	
CATE MENTINAME	Γ	SALMONELLA TYPH	(61-99)							†	1
CHILL MINITANI		ESCHERICHIA COLI	31.55	231-258					1	†	1
• 1		PHOTOBACTERUDA SP	\$16-262		-				1	1	
FCALL PROTECTS VI PRECURSOR	53	ESCHENICHIA COLI	17-64					1		†	1
	2	WEISSENIA CONONALIOEAE	71-111					1		+	l
	2	NEISSENIA CONORNIOEAE	72.109					1	+	\dagger	
L	2	NEISSERÍA GONORRHOEAE	6	9				1	+	\dagger	
_	Ž	NEISSERJA GONORAJIOGAE	10-10)	140-167				T	1	t	
_	-	NEISSEALA GONORAHOEAE	0					t	+	t	l
1	-		171-171								

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FILE MANIE	PROTEIN		7	3	1	1	7		Т	┰	9
POPAK NEIGO	OPACITY PROTEIN OPASS	MOEAE	62:1				Ì	t	\dagger	T	
POPDA ECOLI	OLICOPEPTIDASE A					I	1	T	t	T	
MOPDA SALTY	OLIGOPEPTIDASE A		7			1	1	T	\dagger	1	
POPDE PSEAE	TRANSCLUPTION FACT	AUGINOSA					1	T		T	
POPPA ECOLI	OLICOPEPTIDE BINDR		402412	1		1	1	1		†	
POPPB SALTY	OLIGOPEPTIDE PERMIE	JUN	103-27			1	Ì	T	+	1	
POPRI NEINE	OPACITY-RELATED PROTEIN POPMI		101-13	1	1	1	1	1	+	1	
POPIU NEIME	OPACITY-RELATED PR	MEISSERIA MENINGITIDIS	2.5					1	1	1	
POSMC ECOLI	OSMOTICALLY INDUC		<u> </u>		П			1	1	1	
POSPA BORBU	OUTER SURFACE PROT		٦	£	27.70		1	1	1	1	
POSPB BORBU	OUTER SUNFACE PRO			262-296		1			1	1	
POTC BACK	CANADAM CARBAMO		188-215						-		
POTCE PERAL	DENITHING CARRAMOYL TRANSFERASE	UGINOSA	17.44								
		PSEUDOMONAS PUTIDA	6:								
	PECES OFFICE CONTRACTOR IN		225-252								
2010	STORE OF THE SECOND SEC	DRA	119-216								
ממוס באאנץ	LEADER FOR HUMBS	ANCIBE	115.149						\mid		
PILK STRPA	IN KO PROTEIN IN PLA	STATE OF THE SAMPLES	10	114.148				Ī			
PPISK STRSA		SINETIUCUCUS SANCOIS	Ī.	900	0011	0361.1661	1444. 1494	1425.1455	l	T	
PPIP LACLC	PI-TYPE PROTEINASE PRECURSOR		2	2			-		İ	Ī	
PP.79 MYCHOL		NIS .	2.30	Т			-	9070 3670	Ì	Ī	
PP2P LACLA			86.133	. T	3	000	_			Ī	
PPIP LACPA	PII. TYPE PROTEINASE PRECURSOR	ARACASEI	3.13	86.94	10.7	0621-152	Ro.	679-100		Ī	
7730 ECOL	PJO PROTEIN		22:52					1	1		
PP34 RICE	PROTEIN P34		9-47	135-173					-		
	PROTEIN PLY PRECURSOR		36-38				_				
		LACTOCOCCUS LACTIS	107.155	904-950	1073-1100	023)-(251	1446-1496	1628-1655	-		
200	AS UND DECITED.	PSEUDOMONAS CHR.ORORAPHIS	216.315								
3100	ECUR		28.03	141-209							
100	PROTEIN PAG PRECITESOR		19-16	101-143	300-334	85-164					
7031	PROTEIN PAR PRICINGOS	CUA	93.69	103-143					_		
VI21 1 0444	PROTEIN PIO PRECURSOR	LISTERIA IVANOVII	101-140	115.359							
L	PROTEIN PSG PRECURSOR	LISTERIA MONOCYTOGENES	103-144								
1	PROTEIN P60 PRECURSOR	LISTERIA SEELIGERI	091-101	170-208	311-368	305-111					
L.	PROTEIN P40 PRECURSOR	LISTERIA WELSHIMERI	113:140	317.361	106-423						
L	PROTEIN P66	MYCOPLASMA HYORHINIS	264-295	431-464	487-917	344-575					
PPABA BACSU		BACILLUS SUBTILIS	17-61								
PPARC BACK	4-AMINO 4-DEOXYCHORISMATE LYASE	BACILLUS SUBTILIS	110-217								
PARC ECOL	4.AMINO 4.DEOXYCH	ESCHENICHIA COLI	140-167								
PPARI STRUE		STREPTOMYCES GRISEUS	11.79					_	-		
PPAC ARTY		ARTHAOBACTER YISCOSUS	130-197	133.363	\$71.606	640.674					
PPAC BACSH	PENICELLIN ACYLASE	BACILLUS SPHAERICUS	333-359								
PPAC STRMU	7	STREPTOCOCCUS MUTANS	146-276	281-465	\$96.968	176-610	1011-5101	1139-1186	PC71-1861		
INVA IIVA	т	BACILLUS SUBTILIS	103-137								
PPAIS BACKU	REGIT ATORY PROTEIN PAI 2	BACILLUS SUBTILIS	145-172								
PPAPE ECOLL	+	ESCHERICHIA COLI	69-20	16-123							
PPAPE ECOLI	MINOR FINERIAL PRO	ESCHELICHIA COLI	===								
1003 00466	+	ESCHENICHIA COLI	262-316								
PPARA AGRTU	PARA PROTEIN	ACROBACTERIUM TUMEFACIENS	60-67								
PPARB ECOLI		ESCHENCHIA COLJ	117-134	249-203							1
PPARE ECOLI	TOPOISOMERASE IV	ESCHENCHIA COLI	44471	\$36-553							_
PPARE SALTY		SALMONELLA TYPHIMURIUM	44471	\$36-553	-						•
BACA		BACILLUS ANTIURACIS	25.5	135.153	296-315	\$19.581	650-684				
PPBP2 ECULI		ESCHENCINA COLI	17.136	178-205	207-241						
PPBP2 NEICO	PENICILLIN-BINDING PROTEIN 2	NEISSERIA GONORRHOEAE	193.220								
PPBP2 NEIME	PENICILLIN-BINDING PROTEIN 3		103-220								
PPBP2 STRUN	PENICILLIN-BINDING	NEUMONIAE	144-18)	216-243	259.286	105-633			1	\int	
PPBP) ECOLI	PENICIL IN BINDING PROTEIN I PRECURSOR	ESCHERICHIA COLI	124-251	334.368					1		

COLAL	107s170s	Sequences	AREAL	AREA! AP	AREAL AR	ARKA 4 ARI	AREAS AREAS	1 ARIA1	DREA	2010
3878 3713	PROTEIN				1	+		-		
PPBP4 BACSU	PENICULIN-BINDING PROTEIN 4	EXCIPEITHIA COLI	136-363					-		
PPBP4 ECOU!			145-172							
PPBPA ECOLI			63.06	363.290						
PPBPB ECOLI	PENICILLIN BINDING	MEIGINAE		304-733						
PPBPX STRPN	PENICILLIN-BINDING		70.108	176-203 26	263.324 502	\$02-529				
PPBP STAAU			L	136-353	-	-				
PPCAB PSEPU	_		16:13		-	H				
PPELI ERWCA	PECTATE LYASE III PI		110-117		-	H				
PPELA ERWCA	FECTATE LYASE A PRECURSOR		130-137			-				
PPELB ERWCA	PECTATE LYASE B PRECURSOR	EAWINIA CAROTOVORA				-	_		L	
PPELC ERWCA	PECTATE LYASE C PRECURSOR		Ţ	146.341	-	l	-			
PPELF ERWCH	PECTATE LYASE E PR	ERWINIA CHRYSANTHENII	Ť			+		-	-	
PPEI P ENVCA			433-482		1	$\frac{1}{1}$				l
	REDIGIO A SAVICE DE CTAT	RCULOSIS	459-489		-				1	
ייברי ובאים	CANTON STATE OF STATE	ERWINIA CAROTOVORA	198-318	_						
FFELX ERWCA	CONTROL OF THE CASE AND THE CONTROL OF THE CONTROL	=	164-493			-		$\frac{1}{1}$		
PPELX ENWCH			364-314							
PPEPD ECOLI	AMINOACYL-HISTIDI		251-278			_	_			
PPEPQ ECOLI	X.PRO DIPEPTIDASE	ESCRETATION				ŀ		-		
PPERT BORBA						+			-	L
PPERT BORDA	PERTACTIN PRECURS	USSIS	660-070	\dagger	+		+	+	-	L
PPERT NORPE	PERTACTOR PRECURS	BONDETELLA PERTUSSIS	(200					 	-	
שניג נטונים		CORYMEBACTERUM GLUTNIICUM						1	+	1
200		ESCHERICHIA COLI	912-911		-	$\frac{1}{1}$				
LCA ELCO	THOUSENED THE A PARKET	METHANOBACTERIUM BRYANTII	16-61							
PLA MEIOR	THOST TOTAL CENT OF THE PRINCE	THERMUS AGUATICUS	333-349							
PKK NEIN	rmosrnove i ceso i	FRWDAL CAROTOVORA	111.111							
PPGLI ERWCA		CALLANDELLA TVPMING BILDS	66.93		L		_			
PPGTE SALTY	OUTER MENBILANE P	FRENCE I A DIPLOSIPHON	2		-		F			Ц
PPHAI FREDI	C-PHYCOCYAMIN-I ALTHA CHAIN	Cherry I A Die Octobal	1.4				-		-	_
PPHAJ FREDI	C-PHYCOCYANIN-3 A	PACH TELLA DIFLOSIFICATION	266.201	T		-				L
PPIAN PSEOL	POLY(1.HYDROXYAL	ANABARNA POT INDRICA	7	-						L
PPHAB ANACY	ALLOPHYCOCTAMIN BEIN CHAIN	ANABAGNA VARIABII IS	17	-		-	L			L
PPHAB ANAVA	LI OPHYCOCYANIN	FREMVELLA DIPLOSIPHON	67-8							
PPHAB PREDI	LLOTING TAPIN	MARTICOCI ADDIS LAMINOSLIS	17.7			-				
PPHAB MASLA	ALLOPHYCOCYANIN	EVAFORCED CONTRACTOR C	1			-	-	_	L	Ц
PPHAB SYNP6	ALLOPHYCOCYANIN	SOURCE CONTRACTOR CO	8	-		-	-	-	-	L
PPIIAC SYNP6	ALLOPHYCOCYANIN	STATE OF THE PROPERTY.	07.61		ŀ	-	-	-	-	L
PPILAG FREDI	ALLOPHYCOCYANIN	TREM TELLA DIPLOSITACIO		\dagger	\dagger	\dagger			-	L
PPHB) FREDI		FACE FLAT DISCOSITION		t	$\frac{1}{1}$	\mid			-	L
PPHED ALCEU	ACETOACETYL-COA	ALCALIGENES ECINOMICS							ļ	
PPIKCA SYNYI	C.PHYCOCYANIN AL	SYNECHOCYSTIS SP	3	T	\dagger	\mid			-	
PPHCB_SYNP6	C.PHYCOCYANIN BE	STRECHOCCUS SP			\mid	$\frac{1}{1}$	-		-	L
PPHICE SYND?	C.PHYCOCYANIN BE	STNECHOCOCCOS ST		1	\dagger	\dagger	+		-	-
PPHCB_SYNY!		STMECHOCTS113 SP		1	+	\dagger			-	ļ
PPHEA ECOLI	CHORUSMATE MUTAS	ESCHENICHIA COLI	1	т			+		+	
PPHEA ERWIE	CHONISMATE MUTA	ERWINIA HERBICOLA	16-01	╗	937.70	+	+			1
PPICEA PSESP	PHENOL 1-MONDO)	PSEUDOMONAS SP	171-201	202-310	437.464	+			+	1
PPITE MASLA	PHYCOERYTHOLOCY	MASTIGOCLADUS LAMINOSUS	35.		1	1	1	1	1	-
PPIER PSESP	T	PSEUDOMONAS SP	24-51			1				-
PRICE SYNC	LINKER POLYPEPTI	SYNECHOCOCCUS SP	158-115		_				$\frac{1}{1}$	4
DUI BELLE	PHENYLALANINE-S	ESCHENICHIA COLI	284-311			1			-	٠
POLICE CLOSE		CLOSTRUDIUM PASTEURIANUM	434-471		-			1	4	4
PPIN BACT	SPHINGOMYELINA	BACILLUS CEREUS	2.36							_
Prid 3 BACE	SPHINGOMYELINA	BACILLUS CEREUS	2.36				-			4
PPIG 3 BACCE	SPHINGOMYELINAS	BACILLUS CEREUS	3.36				1		-	4
PPIAC BACCE	_	BACILLUS CEXEUS		179.206	+		+		1	4
PPIEC CLOBI	I PHOSPHOLIPASE C PRECURSOR	CLOSTRIDIUM BIFERMENTANS	I	335-365	1	\dagger	1	+	\downarrow	\downarrow
PPHIC CLOPE	_	CLOSTRIDIUM PERFRINGENS	10.00	104.348	1	1	$\frac{1}{1}$	$\left \right $		$\left \cdot \right $

The Children Digitalization Digita	INJULA	107-178-4	Prehargette Sequences	П	\Box		п		H	П	П	П
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1.00 10.10	Т	CITTER MEAGRANE PORE PRUTEIN E PRECURSOR		Г	Γ		26-253					
The Beach of the Perconsol All Control of the Beach Street Stre	т	THITE MEMBRANE PORE PROTEIN E PRECURSOR		Г	26.93			-	_	_	L	
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ATT ATT ATT ATT ATT	PPHIRA SYNRY	I-PHYCOCYANIN II A		ì	1		1	1	1			1
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	╗			20.0		1	1	\dagger	1		+	Т
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INTERIOR FOLKER	_			П	639.666					_		٦
ILLINGGENE PROFESSION 150-101	1	SENSOR PROTEIN PILS		0.46						_	_	
ILLUS CRIEGATE PODITION 1 MODALELLA LACUNATA 191-112 191-1	Г	PLPROTEIN		130-181								
19.11 19.1	Γ	PILIN GENE INVERTING PROTEIN		42.69	152-162				\mid		-	
HOSPHODISTIEAASE PRECUSOR BACILLUS GENEUS 117-141 HOSPHODISTIEAASE PRECUSOR BACILLUS TOWNOGENESS 116-151 HOSPHODISTIEAASE PRECUSOR BACILLUS TOWNOGENESS 116-151 HOSPHODISTIEAASE PRECUSOR BACILLUS TOWNOGENESS 116-151 HOSPHODISTIEAASE PRECUSOR BEGENERAL COLL 176-170 HOSPHODISTIEAASE PRECUSOR BEGENERAL COLL 176-170 HOSPHODISTIEAASE PRECUSOR BEGENERAL CANOTOVORA 176-170 HOSPHODISTIEAASE PRECUSOR BEGENERAL COLL 176-170 HOSPHODISTIEAASE PRECUSOR BEGENERAL CANOTOVORA 176-170 HOSPHODISTIEAASE PRECUSOR BEGENERAL CANOTOVORA A STANDORA 176-170 HOSPHODISTIEAASE PRECUSOR SECIENACINA COLL 176-170 176-170 HOSPHODISTIEAASE PRECUSOR SECIENACINA COLL 176-170 HOSPHODISTIEAASE PRECUSOR SECIENACINA COLL 176-170 HOSPHODISTIEAASE PRECUSOR SECIENACINA COLL 176-170 HOSPHODISTI	Т	PILIN GENE INVERTING PROTEIN		15.112						_	_	Г
	Г	PHOSPHODIESTERASE PRECURSOR		217-245						-		Г
VALING PRECURSOR LISTERAL MONGOCYTOGENES 111-185	T			216-245	Ī	ĺ			-	-		Τ
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PTRILET FROM STAMMELLA TYTHIMARIUM 171-70		FOTION TRANSF		200.234			-	;		_		
PYRUVATE ORTIOPHOSPHAISE BACTEROIDES SYBDIOSUS 17-18		PRINCIPAL PROPERTY	JA!	174-205								_
OUTER A REGREAME PORINF PRECURSOR PSEUDOMONAS SYRINGLE 111-131		PYRUVATE, ORTHOPHOSPHATE DIKINASE		11-11			-		-		L	Г
PORTION OF PECCUS OR PSEUDOMONAS ARRUCINOS 190-424		OUTER MEMBRANE PORIN F PRECURSOR		# P							L	Γ
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PPT11 I ACCA	PHOSPHOTRANSFERASE FACTOR III	LACTOBACILLUS CASE!	40-67	_			1	1			
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PPURI BACSU	AMIDOPHOSPHONBOSYLTRANSF PREC	SACILLUS SUBTILIS	194-421		1	1		1			
PPL/NJ BACSU	PHOSPHORUBOSYLAMINE GLYCINE LIGASE	BACILLUS SUBTILIS	349-376		1		1				
PPLAN BACSU	FORMYLTRANSFERASE	BACILLUS SUBTILIS	149-176		j		1	1			
PHATE ECOLI	FORMYLTRANSFERASE :	ESCHENICHIA COLI	17-54				1	1			
PPUR BACSU	SYNTHASE	BACILLUS SUBTILIS	18-45					1			
PPIRS BACSU	_	BACILLUS SUBTILIS	183-184								
PPING FOOL	-	ESCHENICHIA COLI	131.158								
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PPI DE ECON	ADENYI OSLICCINATE	ESCHEATCHIA COLI	Γ	276-166							
PPLM BACK		BACILLUS SUBTILIS	19-53	348-313							
PPI III	ANCAR TRANSFORMYLASE	ESCHERICHIA COLI	339.300								
١.	AICAR TRANSFORMYLASE	SALMONELLA TYPHIMURIUM	218-247	-							
	SYNTHASE II	BACILLUS SUBTILIS	9(9-609								
PPYG! ANASP	_	ANABAENA SP	111:00								
PYG! MASLA	LINKER POLYPEPTIDE CPCGI	MASTIGOCLADUS LAMINOSUS	911-61								
PRVC3 ANASP	LINKER POLYPEPTIDE CPCG2	ANABAENA SP	\$11.88								
PPVG2 MASLA	LINKER POLYPEPTIDE CPCG2	MASTIGOCLADUS LAMINOSUS	911.68								
PPYG1 MASLA	LINKER POLYPEPTIDE CPCG3	MASTIGOCLADUS LANINOSUS	2(1-16								
POVCA ANASP	LINKER POLYPEPTIDE CPCC4	ANABAENA SP	161.00								
PPYR! ANASP	32 I KD LINKER POLYPEPTIDE	ANABAENA SP	13-61		1						-
PYTU FREDI	_	FREMYELLA DIPLOSIPHON	761-501								
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PYRE FREDI	10.8 KD LINKER POLYPEPTIDE	FREMYELLA DIPLOSIPHON	43.70	113-140							
PPYRB BACSU	•	BACTLUS SUBTILIS	25					1			
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PAGE BACSO ALPHAGASAL AND THE STANDARD A	SSIDASE REASE DET SYSTEM COMPONENT PERON REPLESSOR CEIVATION PROTEIN A CEIVATION PROTEIN A		132-162			+	1			
PAGA ECCL ALTRACAGE TO THE STATE OF THE STAT	SREASE TRASE		89.116			1	1			
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PRCSA ENUS BIOSTNINESSS PRCSA ELECAL INCAPARESS NOTH PRCSE ECOLI CAPSULE SYNTH PRCSE PROTEIN			174-201			1	+			
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			7	Т		1				
TO THE POST OF THE PROPERTY OF THE PARTY OF		FACIENS		22-136	5		1			
MELA AURIO MECATAGOLES			112-349				-			
PRECA AMAYA RELA FRUIEIN			1 06-19	136-153	_					
PRECA AQUPY MECA PROTEIN			104-135							
PRECA BACFR RECAPROTEIN			261.704				-	L		
PRECA BACSU RECEPROTEIN	q	BACILLOS SUBSILIOS	Ť	91.11	101.101					L
PRECA BRUAB RECAPROTEIN		BRUCELLA ABORTUS	,	T				-		
PRECA BURCE RECAPROTEIN		BUTCH OLDENA CEPACIA		T		T				
PRECA FAWCA RECAPROTEIN		ERWINIA CAROTOVORA		1	1	Ì	l			
PRECA LACDE INECA PROTEIN		LACTOBACILLUS DELBRUECKII	2	1		T	+			L
		LACTOBACILLUS MELVETICUS	Т			1	+		1	
PRECA LACIA RECAPROTEIN	,	LACTOCOCCUS LACTIS	Т	Т	+	†		 		
PRECA LICTOR RECAPROTEIN		METHYLOMONAS CLARA	266-303	1	1	†	$\frac{1}{1}$			
METER RECAPACITION		METHYLOBACILLUS FLAGELLATUM	276-303	1	1	1	+			
AND AND DECA PROTEIN		MYCOPLASMA PULMONIS	30-53				\dagger		1	
PRECA MICAO NECA MOTERA		MYCOBACTERUM TUBERCULOSIS	349-376							
		NEISSERIA COMORDIOEAE	261-310							
PRECA METOD MECAPROLEIM		PROTEIN MIRABILIS	213.310							
PRECA PROMI MELA PROIEIN	<u> </u>	BESTEWANDERS AFRICANOSA	212.309		H					
		BUILDORN DE LEGISTINGS ARTIN	Т	=======================================	280.307		-	_		
7	-	A HITCORY I ECITATION AND IN	3	Т		T	ŀ			L
		Military and in Oth	Т	264.204	Ì	T	-			L
_		MILLORIUM MELILOVII	Т		T					L
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PRECA STRPN RECAPROTEIN		STREPTOCOCCUS PREUNOPIAE	7		t	1				
PRECA SYND? RECAPROTEIN		SYNECHOCOCCUS SP	124-121		1	Ì	1	1		
1	,	VIBRIO CHOLERAE			1	1	1		+	\downarrow
-		BACILLUS SUBTILIS	4.31	178.205						
+		ESCHERICHIA COLI	83.109	147.174						
		PROTEIS MIRABILIS	86-113					L		1
-		PEET INDIANA CHITIDA	1111		F		-		L	-
PRECE PSETU NECT PROTEIN		SALMONELLA TYPHINGRUMS	147.174		-					
_		SOUTH TOTAL STATE OF THE STATE	9, 5		1	T		-		L
PRECI ECOCI EXONUCLEASE REC	NEC)	BACH LIFE COMPLETE		14.124	193.347	300.116	144.171			L
	N FRUIEIN	ECCUENCIA COLI	468.405		T	Т			-	L
Т	MECQ	ESCUEDICHIA COLI	680.707	T	T	T			-	
PRELA ECOLI GIP PTRUPHOSPHURINASE	THURSDAY TENANCE PROTEIN	BACILLIS SUBTILIS	Т	81-18		Ī				
PREMA BACSU REPLICATION AND		STAPHYLOCOCCUS AUREUS	Γ	81:	Ī			_		
PREMA SIAAU METLICATION										

COLME		140.2	5	O VOICE	45.42	OKIA I				
FILEMANE	PROTEIN	STABING OCCCUS EPIDERNIDIS	Т							1
LENLY STAEP	REPLICATION AND MA	FCKERICHIA COLL	30-77	20:13		1	1			1
LEPS ECOLI	REPLICATION PROTEIN	BACILLUS SUBTILIS				1		1	1	1
PREPA BACSU	NEPA PROTEIN	ESCHERICITA COLI	91118	228-255		1	1		\downarrow	1
THEFA ECOL	BEEN FROIDING	NEISSERJA GONORAJIOEAE	┪	2		+	1	+	-	1
CALLED IATE	MENICATION PROTEIN REFO	LACTOBACILLUS MANTARUM	2		1	\dagger		1	1	1
PREBLY CTAAL	BEPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS		1	†	+			-	-
PREPA STARU		STAPHYLOCOCCUS AUREUS	10.00		1		<u> </u>	-	-	ļ
PREPR STRAG	REPR PROTEIN	STREPTOCOCCUS AGALACTIAE	930-46)		†	+		+	1	ļ
PREPS STRPY	REPS PROTEIN	STREPTOCOCCUS PYOGENES	433-467		1	\dagger			+	ļ
PREPY STANII	NULL CEA 438	STAPHYLOCOCCUS AUREUS		017:21	1	+	$\frac{1}{1}$			1
SERV ECO I		ESCHENICHIA COLI	T	┑		+			1	1
200	BEN ICATION PROTEIN	CLOSTRIDIUM PENFRINGENS	╗	٦	20:02		1	1		1
		ESCHENCHIA COLI	119-146	205-243		1	+	1		1
2000	PET THE PROVERY	LACTOBACILLUS PLANTARUM		260-287		-	-	-		1
TALE LALE	20171000	CLOSTRIDIUM PENFRINGENS	701-99	151-185		1	-	1		4
אביי כרתב	SECOLARSE PERSONE CUATA BELEACE FACTOR 2	BACILLUS SUBTILIS	36-68				-			1
PICE BALSO		ESCHENCHIA COLI	(11-98	163-204			-	+		4
TELOPE SEE SECOL		SALMONELLA TYPHINURUM	16-113	163.204			1	1		1
200		ESCHENCHIA COLI	180-210	123	1	1		+	+	4
2000		ESCHENICHIA COLI	199-326				$\frac{1}{1}$	1	1	1
2000	PIOCONTURES CONTRIBUTED READ	ESCHENICHIA COLI	185-212				1		1	1
1000	1 3 CHILDRY TRANSFERASE	ESCHENCIUA COLI	39-66	╗		-				1
AL 173	1 2 CT DECKYT TRANSFERASE	SALMONELLA TYPHINIUM	68.95	14.13 14.13	136-261			1		-
DECAP CALTY	1 2.N. ACETYLCL UCOSAMINETRANSFERASE	SALMONELLA TYPHIMURUM	335.369		1	1	1		1	\downarrow
	O ANTHER I KASE	ESCHENICHIA COU	366-393							4
V 142 141	O. ANTROFAL IGASE	SALMONELLA TYPHINURIUM	326-360		1		+		1	1
LEAP ECOLI	120	ESCHENICHIA COLI	=			+	+	1	+	1
PRFAS ECOL!	BIOSYNTHESIS PROTEIN RFAS	ESCITERICITIA COLI		2		\dagger		-	-	ļ
PRYAY ECOL!		ESCHERICHIA COLI	T	13	1		-	L	L	L
PIUAZ ECOLI			2					-		
N'BB SALTY	DIDP-CLUCUSE 4.9-DEHTDRATASE		113.361							
THE SALL	PARATORE SYNTHASE		22.56	105-111					4	4
ALES VIBAN	PRECINCOL FOR FERE	VIBRIO ANGUILLARUM	149.176						-	\downarrow
Serie Foot	PEPTIDE CHAIN RELE	ESCHENCHIA COLI	13.110	П					-	4
PRCES BACTU		BACILLUS THUMNGIENSIS	15-68	29-762	10.00		1	+	+	+
PRHAB ECOLI		ESCHENICHIA COLI	175-203				1		1	\downarrow
PRIMB SALTY	NUMBER OKINASE	SALMÖNELLA TYPHINGRIUNI	13:303		1	1	1	1	$\frac{1}{1}$	+
MAAR ECOLI	L-NUKALINOSE OPERO!	ESCHE NICHIA COLI	5		1		+			\downarrow
PRUIAS ECOLU	L.RHAMMOSE OPERO	ESCHERICHIA COLI	152-179		1	1	+	+	+	+
PRJIIR RHILV	-	RHIZOBIUM LEGUMINOSARUM				†		 	+	+
PRIMAL B. ECOLL	RNA HELICASE RHLB	ESCIENCINA COLI		97, 11,	1	1		1	\mid	ļ
PRING BORBU	TRANS TERM FACTOR	BORNELIA BURGON ERI	797.617	100.00	1			+	+	ļ
PRIOR BACSU	PROTEASE PRODINEG	BACILLUS SUBTILIS	5		1	†		+	-	\mid
MHSA ECOLI	RHSA PROTEDY PREC	ESCHEMICHIA COLI	8 1			1	$\frac{1}{1}$		+	ł
PAHSB ECOLI	MASS PROTEIN PRECI	ESCHENCIA COL		707.77	1014-1011	\dagger	$\frac{1}{1}$	+		╀
THISC ECOCI	MASC PROTEIN PREC	ESCHEDIST COL	100	1011.1008		\dagger				Ľ
PRUISD ECOL	_	ESCHEDICHIA COLI	26:300		T	l				-
	ACTION TO ANGEROACE	ESCHERICHIA COLI	93.127				_		F	L
	ALEI TLI MONSTENS	ESCHENICHIA COLI	167.194				-		L	L
Pulle Eller	BIRDEL AVIN SYNTHU	PHOTOBACTERIUM LEIOGNATIII	5	31.15						
USDAM MAUST	т	BACILLUS SUBTILIS	1.35						$\frac{1}{1}$	4
PRISB PHOLE	Т	PHOTOBACTERUM LEIOGNATH	14.4						1	+
PALIO STRAT	Г	STREPTOMIYCES ANTINIOTICUS	≈	106-133						_
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ij		ORGANISM	1	٩						
L	SOS RIBOSOWAL PROTEIN LIS	IOPHILUS	5			+	$\frac{1}{1}$			
	SOS RIBOSOMAL PROTEIN LIA		11-45			1	1			
PILLIA MOCLU	SOS RIBOSOMAL PROTEIN LIA	LUN	16-15		1	+	1	1		
اما	SOS AUBUSONIAL PROTEIN LIG		21-48		+	\dagger	-			
13 BACLI	SOS RIBOSONIAL PROTEIN LTD	HILUS	05.134	1	+	+			1	
PRL15 BACST	SOS MBOSOMAL PROTEIN LES		2 2	\dagger	+	+				
-	SOS MIBOSOMAL PROTEIN CO.	ONIATIS	10-144		+	\dagger				
J١.	SOS ECHOSOMIAL PROTEIN LIS			T	-	\dagger		-		
PRE ECOLI	NO PUBLISHED FOR THE TOTAL TOT	118	1	1		+		 		
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PRL 13 METVA	NO KIROSCHIAL PROTEIN 115			İ	+	t		-		
PRE 13 MYCCA	NO MUNICIPAL PROTEIN 13	THE CS		t	†	t		-		
PRE IN BACST	NO REPOSONIAL PROTECT IN		3.86	Ť	\dagger	+	-			
PRE 18 CHEVIA	NO MINOSONIAL PROTECTION	-	è			t	+			
HALLA	NO PERCENTAL PROTEIN III		- N		+	T	1		-	L
	SO MINISTER PROPERTY 19	F.SCHENICHIA COLI	2		1	†				
	SO KIMISOCALLI PROTEILI IS	HALOARCULA MARISMORTI'I	2	1	İ	+	+		-	L
PEL IN HALMA	PRODUCE ON RIBOSONIAL PROTEIN	AIE THANOCOCCUS VANNIELII	~	İ		t			-	L
т	AND STATE OF	PROTEUS VUI GARIS	7		1			 -		L
Т	SOC BIBOSONIAL PROTEIN LA	SULFOLORUS SOLFATARICUS	1		1		+	-		L
1	SOC REDISSONAL PROTEIN L'70	ESCHERICHIA COLI		Ť	+	T		-	L	
١	SOC RIBOSONIAL PROTEIN LTD	G'NT ANS		Ť			-			
	SOS RIBOSONIAL PROFEIN LZI									
	SOS AUBOSONAL PROTEIN L'33	ESCHENCHIA COLI	5.0							
1<	SOS RUDOSONIAL PROTEIN L2)	MEINANG OCCUS AND SECTION	8.2							
PRL23 MYCCA		MATCHENSIA CAMERICANI	2:3							4
PRL34 HALMA	SOS NIBOSONIAL PROTEIN L'24	WETHANDCOCCUS VANNIELII	8.9						1	\downarrow
	SOS MBOSONIAL PROTEIN LA	MICROCOCCUS LUTEUS	16.63		İ	1		1	+	-
	NO MUBOSCHIAL PROTEIN (19	CHLAMYDIA TRACHOMATIS	8	Ì		1	1		-	
PAL 79 CRUTA	SOS RIBOSOMIAL PRO	ESCHENCHIA COLI	9			1			L	
PRL 79 MYCCA	SOS RUBOSOMAL PROTEIN L29	MYCOPLASMA CAPATCOLUM	1	Ī	T					Ц
PAL BACST	SOS RIBOSOMAL PROTEIN L4	BACILLUS STEAROTHERANDITION	198	Ī						
ادا	SOS RIBOSOMAL PROTEIN LA	THERMIN ACHATICUS	20.00						-	1
PRL S THETH	SOS RUBOSOMAL PROTEIN L.S	BACKLUS STEAROTHERMOPHILUS	79.106					+	+	\downarrow
PILL BACST	SOS REBOSCIMAL PROTEIN LA	ESCHERICHIA COLI	19.46			1	+		1	-
אוני בינהי	SOC REDISCOLAL PROTEIN LA	AIETHANOCOCCUS VANNIEL!!	5			1	+		-	-
THE ME I ST	SOC BIBOSOMAL PROTEIN L9	BACILLUS STEAROTHERMOPHILUS			Ī	1	-		-	
PAL O ECOL!	SOS RINGSOMAL PROTEIN LO	ESCHERICHIA COLI		İ	•		<u> </u>	1		-
FRI AD HALCU	ACTINE RINOSOMAL	HALODACTERIUM CUIRURUM		Ī		T	+			
PRLAG HALHA	ACIDIC MBOSOMAL	HALOBACTERUM MALUBIUM	10,79	153.184		Ī	-			
PILAO HALMA	ACIDIC RIBOSOMAL	HALDARCOLA MADOSHIORIO	164.221							
PALAO METVA	ACIDIC NIBOSOMAL	WE INVICED TO STRACTS BEING NECC 41227	20.05							
PILA HALEU	RIBOSOMAL PROTEIN'A	LIAT ONACTERITM HALOMINA	2.39							1
FRLA HALIIA		IIAI DARCIH A MARISMOR TUI	2.2	İ	•					
FREA HALMA	SOS RINOSOMAL PRO	METHANOCOCCUS VANNIELII	3.70							+
PALA METVA	RIBOSOMAL PROTEIN A	MICROCOCCUS LUTEUS	\$5.02	90-117				-	$\frac{1}{1}$	-
PRLA MICEO		SALMONELLA TYPHIANIZIUM	126-260		╗		+		$\frac{1}{1}$	1
X SALIY	A) NO RELAXATION	STAPHYLOCOCCUS AUREUS	5.30	103-133	177.218	86.38	+	+	+	1
A CONTRACTOR	33 ED BELAXATION PROTEIN	SALMONELLA TYPHINURIUM	19-53			1	+	1	1	1
PRI X2 STANU	ALX PROTEIN	STAPHYLOCOCCUS AUREUS	2	103-133	201.793		1	1	+	ļ
PRLXU STANU	LX PROTEIN	STAPHYLOCOCCUS AUMEUS	2	917-00			1		-	
S OS US X THE	DS RUBOSOMAL PRO	SULFOCOBUS SOLFATANCUS		130,146				-		L
	County lead to the state of the	IDACILLIS AMTLUCARANTALINA								

PCCENE	107:171:4		AREAI	AREA?	AREAL	AREA 4	ARCAS (AMEAL IS		1000	9
LTANE	PROTEIN	PECHENICHIA COLI	Г	_							
PRIC ECOLI	MIBONUCLEASE III		113-440	628-662							
1000		OLA	15-114								
NEWS DACKE	BIRONICI FASE PK		28-186					1			
PONC ECO!			991-91			1		1	1		
PRN BACCI	NBONUCL EASE		6 2		1		1				
PRN BACIN	RIBONUCLEASE PRECURSOR		~		1		T	1			
PRP28 BACTK	ANA POLYMERASE SIGMA-21 FACTOR PRECURSOR	IS					Ì	1	Ī	Ţ	
PRESS CITER	RNA POLYNERASE SIGMA-32 FACTOR		I		1			T			
PRP35 BACTK	ANA POLYMERASE SIGMA-15 FACTOR PRECURSOR		Т	8.60				Ť			
PRPS4 ALCEU	RNA POLYMERASE SIGMA-34 FACTOR		239.266		1						
PRPS4 AZOCA	RNA POLYMERASE SIGMA-SA FACTOR	AZORHIZOBIUM CAULINODANS	اء	T	7			Ì			
PRPS4 BACSU	RNA POLYMERASE SIGMA-34 FACTOR		Т	27.124	274-308	780-423		1	T		
PRPS4 BRAJA	RNA POLYMERASE SIGMA-54 FACTOR I	- CNI	97.124								
PRPS4 KLEPN	RNA POLYMERASE SIGMA-34 FACTOR		14 E2					1			
PRUSA RHOCA	ANA POLYNERASE SIGNA-S4 FACTOR		23.153						T		
PRUSS BRAJA	RNA POLYNGRASE SIGNIA-54 FACTOR 2	Š	22		1						
SM ALCEU	PROBABLE SIGMA(S4)	ROPHUS	2								
SM ECOLI	PROBABLE SIGMA(54)		21.67								
PRPSH SALTY	PROBABLE SIGMA(54) MODULATION PROTEIN	MON	9 5	71.00	11.211	338.366	101.111	T			
70 BUCAP	ANA POLYMERASE SIC		200	Т	Т						
PRP TO CHELTR	RNA FOLYNERASE SIGMA-10 FACTOR	CHLANTUIA I MACHUMIA IIS	137.161								
PR 70 ECOLI	ANA POLYNERASE SIGMA-70 FACTOR	PERCINOSA	134.368								
PRP70 PSEAE	TANA POLYMERASE SIGMA-10 PACION		244-321	148.382							
TAP TO MICH	ENA POLTNIERASE SIL		208-335	118.343	359.316						
ALTER MATERIA	_	SYNECHOCOCCUS SP	180-207								
DA BACSU	DNA-DIRECTED MA		13-10)					Ì			
PRPOA ECOLI	A-DIRECTED RNA POL		2.50								
		SALAIONELLA TYPHIMORIUM	141.004								
PRPOA HALHA	DNA.DIRECTED RNA		330.370								L
PRPOA HALMO		FRATOAUTOTROFILICU		486.513	643.669						
PAFOA MELLIN	DAY DIRECTED BY			125-005	693.720						
PREDA THECE	DNA-DIRECTED RNA POLYMERASE SUBUNIT A		128-161								
PRECIOE ECOL	DNA.DIRECTED RNA POLYNERASE BETA CHAIN		929-665	1011-101							
OO MYCLE	DNA.DIRECTED RNA	MYCOBACTERIUM LEPRAE	123.760	1084-1111							
OB SALTY	A-DIRECTED ANA POLYMERASE BETA CITAIN	SALAKONELLA TYPHIMURIUM	300-626	958-985	101 1101						
PROB SULAC	A-DIRECTED RIVA POLYMERASE SUBUNIT B	SULFOLOBUS ACIDOCALDARIUS	200	787-667	310.30	98-77					
OB THEMA	A-DIRECTED RIVA POLYMERASE BETA CHAIN	THERMOTOGA MARITIMA	10.194								
PILPOC ANASP	DNA-DIRECTED RNA POLYMERANE GAMMA CHAIN	ECHERICHIA CON I	716-813	948.934	1223-1257						L
PRPOC ECOLI	WAS DIRECTED BY POLYMERASE BETT CHANGE		13.303								
	TAROC HALIN DAY THE CITED BIA POLYMERASE SUBUNIT C	HAL OCOCCUS MORNHUAE	2.54	13.14	207.234						
THE PERSON NAMED IN	DNA-DIRECTED RNA POLYMERASE SUBUNIT C	METHANOBACTERIUM THERMOAUTOTROPHICU	38.83	173-301	327-354						
PRPOC MYCLE	A-DIRECTED RNA POL	-		188-098	911-938	1131-1158					
PRPOC NOSCO	DNA-DIRECTED RNA		150.93								
PRIOC SULAC	DNA-DIRECTED RNA	SULFOLOBUS ACIDOCALDANUS	3	13.24	24-251						
PRIVOC THECE	DNA-DIRECTED RNA	THERMOCOCCUS CELER	S:-2								1
OD MOCCO	DNA-DIRECTED RNA	NOSTOC CONDAINE	3.E8	\$ 7 40 0 7 40	30.00						1
PRINCE ECOL!	WA POLYMERASE SI	ESCHENCHOA COCI	5.39		-						
PRIVOS ECOLI	INA POLYNŒRASE SI	ESCHENCHA COLI	100								\downarrow
NO HALLIN	DINA DIRECTED RNA POLYMERASE SUBUNIT B	ACADOMAC I ENDING MALOBIONI	110.143	107.437							
PRPSA AGRTU	THA POLYMERASE S	ANABARNA SP	10.15								L
PRESA AMASE	ANA POLIMENASE S	ACETOBUTYLICUM	5.				L				
2											

47.49.14	100000000000000000000000000000000000000	Proharyeist Segurners	7	1	1 1 10 1	4004	ABFAG	ARFA 4 ARFA 7	A 7 AREA 6	6 AREA	3
FILL HANIE	PROTEIN			7		т			1		
PRPSB ANASP	RNA POLYMERASE SIGNIA-B FACTOR			169.196	300.230	-					
_	RNA POLYMERASE SIGNIA-B FACTOR		1	Т		l	-			L	
Т	RNA POLYMERASE SIGNIA-B FACTOR		+	İ							
	BNA POLYMERASE SIGNIA-B FACTOR	AUKANTIACA		T				-	-	-	
PARC ANACP	BWA POLYMERASE SIGNIA-C FACTOR		10.00	1	\dagger	t				-	Ī
	BNA POLYNGRASE SIGNIA-D FACTOR		107-761	1	+	\mid	T			╀	
	BAN BOI VAICHAGE SIGNIA E FACTOR PRECURSOR		7			\dagger	T	-		ł	Ī
THE SECOND	BUY BOL VALEBACE CICHA F FACTOR	LICUNI	1	8		1	1		-	ł	Ī
	ANA COLINERASE SICHA E BATTOR		╗	191-248		1	1			+	Ī
\neg	ANA POLYPIERASE SIGNIA E SACTOR		191.225		1	1	1		+	+	T
	KINA FULTALE SIGNATION CONTRACTOR		11.31	101.248					1	+	
	RNA POLYMERASE SIGMA P PALION	Seven Contract Contra	191-218					_		+	
_	RNA POLYMERASE SIGMA-H FACTOR		116.311	T	-	-					
PRPSH BACSU	RNA POLYMERASE SIGNIA-H FACTOR		Т	100.314		t		-		\vdash	
DEPCK RACK!	RNA POLYMERASE SIGMA-K FACTOR	BACILLUS SUBTILIS	٦			l	t			ŀ	Ī
200	BAY BOI VAIR BAKE SIGNA FACTOR PLAC		976			1	1	1		+	Ī
200	THE POST INCH A SEC SIL	STREPTONIYCES COELICOLOR	112.271			1	1		1	+	Ī
NOW SHEED	MAN FOLIMENASE SI		3-60							+	T
-	POSSIBLE BUA FOLT		00			_			-	-	1
PRS10 ECOLI	SOS AUBOSOMAL PRUIEIN SIO		278						-	$\frac{1}{1}$	Ţ
PASH BACSU	30S RUBOSOMAL PROTEIN 311		14.13			ŀ		_		_	
PRS13 BACSU	JOS NIBOSOMÁL PROTEIN \$13		15.51		l			-	-	-	
PRS17 METVA	105 NIBOSOMAL PROTEIN SI?	VANALELII	T.	161.77				_	-	\vdash	
שנו בנטי	105 RIBOSOMAL PROTEIN SI		7	†			İ			┞	T
П	THE BROKENAL PROTEIN SI		٦	1		1	1	$\frac{1}{1}$		╁	I
1	SAS BISOCOMA! PROTEIN SI)TI	91-125	711.111		1		1	1	+	T
Į,	103 ADDOOMNE THOUSAND THE	BACTILUS STEAROTHERAIOPHILUS	1.26							+	Ī
اء	JOS FUBICIONAL PROTEIN SE	COLDUDI ACLEA CITAL)	521-16							1	1
PRS2 SPICE	305 IUBOSOMAL PROTEIN 34	ACTION THE ACTION AND AND	91.10			_					
PRS3 ACHEA	30S PUBOSOMAL PROTEIN ST	ACROCETASMA LATOLINA	Τ	136-163							
PRS) MYCCA	305 NIBOSOMAL PROTEIN S3	MILUTURAIN CAPACIONI	Τ			Ī				ŀ	
PRS4 ECOLI	105 NIBOSONIAL PROTEIN S4	ESCHEMURIA COLI		Ī		ľ	T			\vdash	
PRSS HALMA	JUS AUBOSOMAL PROTEIN SS	HALOARCULA MAUSRICKTU	T		1	Ī	T	L	_	┞	
PRSS MYCCA	105 RIBOSOMAL PROTEIN SS	MYCOPLASMA CAPRICOCOM	Ī		Ì	Ì		-	_	-	
PRS6 THETH	JOS NUBOSONIAL PROTEIN S6	THEIMUS AQUATICUS			T	Ì			-		
PRS7 METVA	105 RIBOSOMAL PROTEIN S7	METHANGCUCCUS VANNELII	97		1	T				\vdash	
PRS7 MYCLE	JOS NIBOSOMAL PROTEIN \$7	MYCOBACTERUM LEPRAE		Ī	Ì	Ì			 	┞	
PRSB MICLU	305 RUBOSOMAL PROTEIN SE	MICROCOCCUS LUTEUS			1	T	T			-	
PRS8 MYCCA	105 RUBOSOMAL PROTEIN SB	MYCOPLASMA CAPIULOLUM			T		Ī	-		\mid	
PRSCA ECOLI	ENUTIN LIKE PROTE	ESCHENCHIA COLI	2		Ī	1				\dagger	
PRT67 ECOL	UNA-DIRECTED DHA	ESCHERICHIA COLI	Т		1	T	T	-		t	
PRACE BACAM	EVANSUCAASE PRE	BACILLUS AMYLOLIQUEI ACIENS	Т	197-667		1	1			ł	Ī
PSACB BACSU	LEVANSUCRASE PRECURSOR	BACILLUS SUBTILIS	_	7		1		1		t	T
PSACE STRUKU	LEVANSUCRASE PRE	STREPTOCOCCUS MUTANS		2	A0(-)			1		\dagger	T
PKACO BACLI		BACILLUS LICHENIFORMIS	┪			1		1	1	\dagger	T
PCACT BACK		BACILLUS SUBTILIS	╗	97.49						\dagger	Ī
AGELS GOVE	REPERTOCOCCAL ACID GLYCOPROTEIN	STREPTOCOCCUS PYOGENES		362-319						\dagger	
NO.		BACELUS SP	150-177						1	+	Ī
TOWN AND A	_	CLOSTRUDIUM BIFERMENTANS	1743							+	
באלו הרחם	_	RACH LUS CEREUS	31-58							4	
PSASG BACCE	_	BACH 115 CTEARCTHEBANCHILL 115	17.64							-	
PSASG BACST	_	Secretary Of the Secret	218.360	117.14	\$18.505	89779	776-812	831-165 913	915-942	├	
PSBCC ECOLI		ESCREMINIA COLI	3		Ŧ	Т	Т	Т		-	Į
PSBCD ECOLI	_	ESCHERICHIA COLI						l		\dagger	ŀ
PSBM ECOLI	_	ESCHENICHIA COLI	2	20.4.00	331-380	1	T	+	+	\dagger	Ī
PSRP BACSU	SBP PROTEIN	BACILLUS SUBTILIS	28.55							+	
VOTS ATON	CSA PEPTIDASE PREC	STREPTOCOCCUS PYOGENES	126-160	784-811	8				+	+	Ī
PKCEB KLEPN	1	KLEBSIELLA PNEUNIONIAE	╗						1	†	
PSCRB LACLA	SUCROSE 4-PIIOSPIL	LACTOCOCCUS LACTIS	П	34.15	≈ ₹		1	1	$\frac{1}{1}$	\dagger	
PSCRD STRUMU	-	STREPTOCOCCUS MUTANS	115-362			1	1	+	+	\dagger	Ī
TI IV	FRIKTOKINASE	SALMONELLA THONIPSON	97.124						-	+	
1	7							!			

PCCFNF	107417844	Probaryotic Sequences	П		г	П	_		_		
FILEMANE		700000	4	3	TARE	1	1	<u>व</u> र	NO TOTAL	4	1
PSCRK SALTY			Т	240-267					-		
PSCRY KLEPN	SUCROSE PORIN PREC	4	Γ	Г	340.267			H		H	
PEFF BACK	PREPARTEN TAANSL	BACILLUS SUBTILIS	12.39	236-260							
PSECA ECOLI	PREPROTEIN TRANSL	ESCHENICHIA COLI	2	- - -	1	1	1	+	+	1	
PSECB ECOLI	PROTEIN-EXPORT PRO		7			1	1	†	+	†	Ī
PSECD ECUL!	PROTEIN EXPORT MENIBRANE PROTEIN SECO		1		·	1	1	†	$\frac{1}{1}$	†	T
PSECF ECOLI	ROTEIN-EXPORT ME		2	1	1		1	+	$\frac{1}{1}$	\dagger	T
PSECY ECOL!	REPROTEIN TRANS					1	1	+		\dagger	T
PSECY LACLA	PREPROTEIN TRANSLOCASE SECY SUBUNIT		T		1	1	+	\dagger	1	+	
PSECY ACETVA	MEPROTEIN TRANS		Ī	196-421					1	1	
PSECY STACA	REPROTEIN TRANS	žuš	╗		1	1	1		1	+	
PSEFC SALEN	LEFC PROTEIN PRECU	LIDIS	3	25.50		1			1	1	
PSERA BACSU	3.3.PHOSPHIOGL YCER	BACILLUS SUBTILIS	16.43	147.374				1			
PSFAA ECOLI	S-FINDRIAL PROTEIN	ESCHENCHIA COLI	11:30							1	
PSFSA ECOLI	SUGAR FERMENTATIO	ESCHERICHIA COLI	\$11.118					1		7	
PSFUA SERMA	ROW TRANSPORT SFL	SERRATIA MARCESCENS	19.41							1	
PSIGN ECOLI	SHUTFLOW PROTEIN A		234.362	_							
PSOUN ECOLI	SINGILON PROTEIN A		234-362								
PSHUD ECOLI	SIRIFICON PROTEIN B		234.262								
PSHIM FCOLU	SINDELON PROTEIN B	ESCHERICHIA COLI	294-362					_			
PSHEIS FCOLI	SPAREL ON PROTEIN C		234-762	402-429							
PSIGIN ECOLI	SUBSTITUTE OF PROTEIN C		234-362								
PEND FOR I	CLARGE ON PROTEIN DY		234.262								
TOTAL BALL	Zaloga Exp	IP OR NIS	9.10	43.80						r	
Person Paris	SING PROTEIN		9.16	5.70					-		
PSI AP ACERI	CELL SIMEACE PROTEIN PRECINSOR	6	3	182-100	113-433	458-489	\$17.544	563-593	641-685 726	126-753	
PSLPA FCOLI	11=		91:19								
PS/D COL	SACT PROTECN	ESCITERICIIIA COLI	15.42								
PSVEPB FCOA.		ESCHERICIIIA COLI	1	8-11							
PSNP ECOLI	SAP PROTEIN PACCURSOR	ESCHERICIIIA COLI	1.98								
PSMTB SYNP!	TRANSCRIPTIONAL REPRESSOR SAITB		63.96								
PSODF COXBU	SUPEROXIDE DISKIUT		16.16							1	
PSOOF ECOL!	SUPEROXIDE DISMUT		115-142							1	
PSODF METTH	SUPEROXIDE DISKUT	DAUTOTROFILICU	22						1		
PSODE MIDLE			22-63				1			1	
PSUDM PROFIE	SUPEROXIDE DISMUTASE	PROPIONIBACTERIUM FREUDENMITCIIII	3		1	1	1	\dagger	+	1	
PSOID ECOL	SOME PROTEIN PRECUASOR		1	T	3	1	+	\dagger	+	†	Ī
SONG ECOCI	SOUR PROTEIN				1		1	+	+	t	Ī
PERSONAL PACELL	STACE O SPORTA ATION PROTEIN J		35.15					T		\dagger	
PSPIA BACKE		HUM	19.53	T							
PSPZA BACSU		BACILLUS SUBTILIS	21.55								
PSP2B BACLI	-	115	43-69						H	H	
PSP2B_BACME	STAGE II SPORULATION PROTEIN AB	BACILLUS MEGATERIUM	16.73								
PSP1D_BACSU			134-161								
PSP1G BACTK	POSSIBLE ASPARTYL PROTEASE	IENSIS		13.144							
PSP D DACSU	STAGE II SPORULATION PROTEIN I			65.500							
PSP1D BACSU			35	25.E6				1			
PSP31 MACGU	STAGE III SPORULAT				7			+		1	
PSP4A BACSU	STAGE IV SPORULAT		29.10		-			+	1		·
PSP4D BACSU	STAGE IV SPORULAT		90.0		1					1	
PSP4G BACSU		BACILLUS SUBTILIS			1	1	1	1	1	1	
PSP3A BACSU	STAGE V SPORULATION PROTEIN AF	NANEI	184.218		T	T	1	1	1	†	
PER BACK	SUBTIL IN BIOSYNTH	BACILLUS SUBTILIS	107-101			T	1		\dagger	t	T
PAPAT BACKU	SUBTILIN BIOSYNTHESIS PROTEIN SPAC		311.338		T			 		t	Ī
										1	

	107817014		A SEA		_	7		2			
1 1		ORGANISM	Т	18:32	Г						
PSPAK BACSU	SENSOR PROTEIN SPAK		Ī,	Г	Г	576-630	1071-1098	1155-1182	1377-1430		
	CELL SURFACE ANTIGEN IN PRECURSOR		Т	Т	Т						
INDEASON AND AND AND AND AND AND AND AND AND AN	REGUL A TORY PROTEIN		T						Ī		
	COUNTY IN TRANSPORT PROTEIN SPAT		1	107-077		J		T		I	
2	EVATOWIN TWEE C PRECURSOR	STREPTOCOCCUS PYOCENES	1			T			T		
2000	7		1	20.66				1	T		
STILL STILL	N. A.	SPIROPLASNIA MELLIFERUNI	195-322	1							
THE STIME	A JOSOF LOS V. P. BORNOSPILOSPINOSPILA		637-664								
SPOT ECOL	The state of the s		138-305						7		
PSPPA ECOLI		116	190.617								
OHC ZYPORO	SQUALENE-HOPENE CYCLASE		159-166	244.271							
PSNEA BACSU	ASE SUBUNIT A		+								
PCPS ECOS	CICHAL BECOGNITION PARTICLE PROTEIN			Т							
200	SIGNAL BECOGNITION PARTICLE PROTEIN		┪	٦	194-478						
	SCHOOL STREET, STREET, SECOND	IICA	131-13	358-389	465-518	\$29.570	160.904				
PSSAI PASHA	MINGEN I PRECONSOR	1	37.59								
SSAB STRPA	*		Ī	101.128							
SSAR STRSA	€	ANGUIS	1								
Section 1	ING PROTEIN		2								
232	PAINT C STRAND BRUTHS PROTEIN	PROTEUS MIRABILIS	53.104								
SB PROPE	SINCE OF THE PROPERTY OF THE P	ENS	63-104								
PSSB SERVA	SINGLE-STRAND BINDING THOLES	2	131-133	178-287	295-483	565-593	676-710	1011-1101			
PSSPS STRSA	ACCLUTININ RECEPTOR PRECURSOR		28:185								
PSTAV STRAV	STREPTAVION PRECURSOR		6								
PSTA ECOLI	STREPTOTHINGIN ACETYLTRANSFERASE		Τ.	т	111 000						L
PETER STABIL	STAMINI OCOAGULASE PRECURSOR		7	4	1100						
			,	264-791							
יייייייייייייייייייייייייייייייייייייי	TOWNER VENTOR		47.74								
ור ררופני	The state of the s		16-63								
PSTPA ECOLI		USEUS	183.210								
PSTRI STRGR	INOSANINE-PIOSPIA	411.15	209.336	281-308							
IN STREO			209-236								
PSIRP SIRPY	STREPTOKINASEAP		Т	101.185							
PSTRU STRSP	STREFIORINASEUF		435-462	\$32.563	603-639	L					
USE BACSO			40-67	911-60	121-148	554-597					
PSUBP BALSU	DACILLOCET HUNSCH	SALMONELLA TYPHINIURIUNI	17.74								
100			63.94								
CON STREET			16-75								
PSUBIL SYNT	SOLIA TE-BIACHIO PROTEIN TRACKING	RACH LIST ICHENIFORMIS	111-161								
PSUBT BACLI			911.16			L					
PSUBT BACMS	-	BACH 1.16 CD	16-63	20.00		L					
PSUBT BACS9	SUBTILISIN PRECURSOR	A . C	197.224								
UBT BACSA	SUBTRLISOR ANTLOS	0ACHELO 2000 1000	111.76								L
PSUBT BACSD	SUBTRLISM	BACILLUS SUBTILLS									L
PSUBT BACST	SUBTILISIN I PRECUI	BACILLUS STEAROTHERAIOFIILUS		1	-						ļ
PSUMT DACSU	SIMTH ISIN F. PRICLE	AACILLUS SUMTILUS	27.75								1
PETRIN DACE	MINUR EXTRACELL	DACILLUS SUBTILIS	× 100	2	141.708						
POLICE SCOLI	SUCCINAL COA SYN	ESCHEMICHIA COLI	65.E9								
May a Julia	STICKED SPHOSPHOR	AGROBACTERIUM VITIS	449-476								1
	Т.,	ENTEROBACTER AEROGENES	113-139								
1	AT ANY TENA SYN	ESCHENCHIA COLI	187-783	125-752	70.82	_					
STA CLOSS	ACCESSION TOWN CV	ESCRIENCINA COL!	330-357								
310 55	AMAT. IVA PLAT	BACILLUS STEAROTHERAIOPHILUS	49.76								
OVE OVE	OCCUPANT TOTAL	BACKLUS SUBTILIS	49.36	31.38							
SYE BAGE	CLUTANOT TRNA	THERMUS AQUATICUS	405-432		-						1
SYE INCIN	MIENY ALANYI .TR	BACILLUS SUBTILIS	=								_
VI VIII		_	140-367	407-441							
SALE BACS	SHENY AT ANY . TR	_	246-573	607.634	144-771						
200	Т	_	354-383	417.514							4
2010	Т	STREPTOCOCCUS EQUISIMILIS 176-401	376-403			L	_				
200											ĺ

PCGENE	107117814	Sequences	7		A B CA 3	AREAL	AREAS	AREAG	ARCA! AP	AREAI	AREAS
THEMARE	LEGITOR	DECINENTIAL COLL	Т	Т		П		_			
PSYKI ECOLI	LYSYLTRNA SYNTHETASE		45.72	283-310					1		
PSYK2 ECOLI	LYSYL-INCA STRINGIASE, REAL PROCESS.		120-247				1	1	1		
PSYL ECOLI	LEUCTIONAL TONA SYNTIETASE	THEMNOFISHUS	69.69		1	1	1	1	1	1	
1000	ARE THIONYL. TANA SYNTHETASE		21.134			1	1	1	\dagger	1	
PSVP ECOL	PROLYL-TRUM SYMTHETASE		200		1	†		Ť		T	
PSYO ECOLI	GLUTANINYL-TINA SYNTHETASE		7			1	T	T	1		
PSYRD PSESY		KINGAI.		1	1	T		T		T	
PSYR ECOLI	ARGINYL-TRNA SYNTHETASE		T	017.79				T			
PSYTI BACSU	THREONYL-TRNA SYNTHETASE		T	176 00	T						
PSYV BACST	VALYL-TRNA SYNTHETASE	THERMORISTUS	7	Т	014.011	T	1	T	\mid		
PSYV ECOU	VALYL-TRINA SYNTHETASE		T	T		T				Ī	
PSYW BACST	TRYPTOPHANYL-TRNA SYNTHETASE	HERNOPHII.US	Τ	87.467	1			T	T	T	
PSYYI BACSU	TYROSYL-TRNA SYNT				1		1				
PSYY3 BACSU	TYROSYL-TRNA SYNT		T		1		T				
PSYY BACCA	IYROSYL-FRWA SYNT		277		1	T			l		
PSYY BACST		THE KATOPHICOS	Т	Т	(1)					Ī	
PTIMI ECOU	ENZYME ECORITY IN PROTEIN		Т	T	Т	168.703	143.870	966-1000			
PTIRI ECOLI	ENZYME ECORISUS R PROTEIN		Ţ,	Т	Т	Т	T		İ		
PTIR ECOLI					Ī		Ī		İ		
PTISI ECOLI	ENZYME ECORIZAM I SPECIFICITY PROTEIN			T						Ī	
PTISA ECOLI	ENZYNIE ECOA I SPECIFICITY PROTEIN		3							Ī	
PTISB ECOLI	ENZYME ECOB I SPECIFICITY PROTEIN		716-9/7								
PTISD ECOLI									l	Ī	
PTISE ECOL!	ENZYME ECOE I SPECIFICITY PROTEIN		3								
PTIS SALPO	ENZYNE SPECIFICITY PROTEIN		Т	72.	91.7						
PILS SALTY	ENZYNŒ SPECIFICITY PROTEIN	HINDROW	Т	Т	Т	410.617	447.736	026-054		Ī	
FESS ECOLI		ESCHENCHIA COLI	Т	Т	т	Т	Τ				
PIZAL ACICA				116.2311	234.210						
PT2BF BACSU				Т	Т	555.215			-		
PT2BR BACSU	TYPE II RESTRUCTION ENZYME BOUND		13.63		Т						
PTZCI CITER	_	TIACUS	176.215								
PTIC IERAD	TYPE II KESTRUCTION		203-273								
PT2CI HE LAC	TYPE II RESTRUCTION	DESTRIPOVIBRIO DESULFUNCANS	15-122								
100		STREPTOCOCCUS PNEUMONIAE	313-240								
1012	TOTAL INC. INC. INC. INC. INC. INC. INC. INC.	ESCHENCHIA COLI	8.2								
175	TYPE II BESTRICTION ENZYME ECORII	ESCHENCILIA COLI	133.360								
PT7ES ECOLI	TYPE II RESTRICTION ENZYME ECORY	ESCHENICHIA COLI	П	214-241							
PT2F1 FLAOK	TYPE IIS RESTRICTION ENZYNE FOX!	FLAVOBACTERUM OKEANOKOITES	302-336								
PT2HI HAEIN	TYPE II RESTRICTION	IIAEMOPIILUS INFLUENZAE		8	1						
PEZIU HAFFA	I YET: II RESTRICTION	HAEMONIII US PARAINI LUENZAI	2							Ī	
FT2113 IIÀEIIA	TYPE II RESTRICTION	IIAEMOPIILUS IIAEMOLYTICUS	8							T	
PT2112 HAEIN		HAEMOPHILUS INFLUENZAE	20.00	304						Ī	
PTZKI KLEPN	TYPE II RESTRICTION	ALEBSELLA PACINE		Т	336,363				İ		
PT2MI MORBO	TYPE II RESTRICTION ENCYME MOON	MONOTON DO 13	1.10	Т	117.164						
PT2M2 MOXBO	TAPE IIS NEST MOCI ION ENGINE MEDII	METHANOBACTERITM THERMOFORMICICUM	105-151								
1 2 M 2 M 2 M 2 M 2 M 2 M 2 M 2 M 2 M 2	Var II BECTBICTION	NEISSERIA GONDRANDEAE	117-144	221-230							
2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TYPE II RESTRICTION	STREPTOCOCCUS SANGUIS	2.53	1.61	395-446						,
5000	TYPE II RESTRICTION	SHIGELLA SONNE!	206-243	258-288	ŀ						
71636 3103C	TYPE (1 RESTRICTION	STAPHYLOCOCCUS AUREUS	70-102								
A SYLVE	TYPE II MESTRUCTION	SALMONELLA INFANTIS	144-181								
PT2SM SELMA	TYPE II NESTRUCTION	SENATIA MARCESCENS	10-19								
PT2TA THEAQ	TYPE II RESTRICTION ENZYNG TACH	THERMUS AQUATICUS	- C	20).237							
PTJMO ECOL	SYSTEM ECOPIS ENZYNE MOD	ESCHENICHIA COLI	2	75-102	20-78	9					
PTINE BACCE S	SYSTEM ENZYME RES	BACILLUS CENEUS	\$7.70	34.20							

	10/11/01				1		Ì				
П	PROJEIN.		П			1	1	1		1	l
<			П	298-329		1	1	1	\dagger		
				134.40			1	1	1	Ī	
PTACY BACAL	ALVEOLYSIN PRECURSOR	SKEDKIEKS	270-311								
PTACY CLOPE	PERFRINGOLYSIN O PRECURSOR		93-120		╗		1	1	1		
PTACY LISIV	IVANOLYSIN PRECURSOR	TOGENES	821-86	168.196	╗	20.75	1	1	1		
PTACY LISMO	LISTENOLYSIN O PRECURSOR		П	294-323	349-336	24.6		1	1	Ī	
PTACY LISSE	SEELIGERIOL YSIN PRECURSOR	ELMONIAE	134-272					1			
PTACY STRUM	PHELIMOLYSIN		\$6-133	155-382	440-470		1		1		
ACY STRPY	STREPTOLYSIN O PREC		42.69					1		1	
PTAGB BACSU	TECHOIC ACID BIOSYN PROTEIN B PREC	5ACIL 103 300 11213	346-375								
PTAGE BACSU		BACILLUS SUBSILIS	Τ	2.5	185.243	265-595	600-627				
PTAGE NACSU	TECHOIC ACID BIOSYNTHESIS PROTEIN E	BACILLUS SUBTILIS	,		Т						
INJUNE STATE		BACILLUS SUBTILIS	Т	117.164	101.425	110-018					
2012		MEISSERUA CONORTHOEAE	T	Т	Т						
ופרו אבונט		PSEUDOMONAS PICKETTII	0	Т							
FIBUD PSET	_	SALMONELLA TYPHIMUMUM	103-132			9.	11. 77.	717 037			
PICOT SALTY	IKANSCHOT HOME IN	VIBRIO CHOL ERAE	Ş		12.61						
CINC VIBOR		VIBRIO CHOLERAE	24-59	77-111							
ICPE VIBOR		VIRKIO CHOL ERAE	32.66	211.238					T		
ICPF VIBCH	TCP PILUS SECRETION PROTEIN ICE	VIBRIO CHOLERAE	95-122						1		
PICPH VIBCH	- 1	VIREIO CHOLERAE	25-52	134-261	× 108	146.37			1		
ICM VIBOR	TCP PILUS BIOSYNIN	VIEW CHOIFEAE	48.75								
ICPN VIBCH	TCP PILUS VIRULENCE REGULATORY PROTE	VIDEIO CHOI FRAE	130-257								
ICPO_VIBCH		Wight Cuoi FRAS	131.148								
PTCPY VIBCH	TCP PILUS BIOSYNTHESIS PROTEIN ICFT	STATE OF THE PERSON	44.85								
PTCPZ VIBCH		BACH IN CIDATI IS	404.434								1
PICIU BACSU	TETRACYCLINE RESISTANCE PROTEIN	DACH LING STEADOTHERNIOPHILUS	422-453								
PTCR BACST	TETRACYCLINE MESISTANCE PROTEIN	STAPHYL OCOCCUS AUREUS	404.431								
PICE STAND	TETRACYCLINE MESIS I AMERICANICAL	STREPTOCOCCUS AGALACTIAE	422-453								1
PTCR STRAC	TELEGICAL TOTAL PROTEIN	STREPTOCOCCUS PNEUMONIAF.	433.453								ļ
PICK SIRON	-	ESCHENCIUA COLI	210.239								ŀ
TOTAL ECOL	VACC BEOTEON	ESCHERICIUA COLI	374.36								L
200	-	STREPTOCOCCUS PYOGENES									
PTELL FCOLL	TETRACYCLINE REP	ESCHERICHIA COLI									
PTER ECOL	TETRACYCLINE REPRESSOR PROTEIN CLASS D	ESCHENCHIA COLI									L
PTERA ALCSP	PELLURIUM RESISTA	ALCALIGENES SP									Ľ
PTESB ECOLI	ACYL-COA THIOESTE	ESCHENCIA COLI	9	130-130	179.206	217.344					
PIETS ENTEA	TETRACYCLINE RESI	ENTEROCOCCUS PARCALLIS	1	10.130	217.244	260-287				L	
PIETO ENTEA	TETRACYCLINE RESI	ENTEROCOCCUS PARCALIS	30,104	1 2						L	
PTETC ECOLI	TRANSPOSON THIS T	ESCHEUCHIA COLI									L
THE STREET	TETRACYCLINE RESI	STREPTOMYCES LIVIDANS	5	97,00	313.344	340.783					L
PTETM UNEUR	TETRACYCLINE RES	UNEAPLASMA UNEALTICOM	2 2					L			L
TETO CAMCO		CALT TUBACTER COLI	97.5								
PTETO CAMPE	TETRACYCLINE RES	CANITIONACIENTONI	2						L		
TETO STRUCT	U TETRACYCLINE RESISTANCE PROTEIN TETO	SIME TOUCKUS MOINIS	3					_		L	
PTETX BACFR	TETRACYCLINE RES	BACTEROIDES FRAULIS	27.75	3 65	615.66	693.310	2101.510	1240-1277			L
PTETX CLOTE	TETANUS TOXIN PRE	CLOSTRIDUM TETANI									L
PTE2B PYRWO	TRANS INITIATION F.	PYROCOCCUS WOESE									L
PIFDC ALCEL	CHLOROCATECHOL	ALCALIGENES EUTROPHUS				-					
PICT ECOLI	QUEUTINE TRUMA-RUBO	ESCHENCHIA COLI	161.10								
PTION LACLA	THOLEONINE DELIYED	CACIOCOCOS LACIOS	301.100			Ļ			L		Н
Prilips ecqui	THOLEONINE DEHYDI	ESCHERCIA COCI	2	192-226	302:316	191418					
saye agua	U FURAN OXIDATION PROTEIN THUS	PYCHERICHIA COLI	326-260	4043							4
PTHOF ECOLI	FURAN OXIDATION	PSELIDOMONAS PUTIDA	126-360								4
Photo Psero	PURANCAUALION	BACELUS CEREUS	4.38	240-267	L	_	_				4

	107817304	44000					7				
EILE MAME	CROIGIN	RACH LUS THERMOPROTEOLYTICUS						1	1	1	
PINER BACTH	THE MOULT SIN	THERMOACTINOMYCES VULGARUS					1	1	1		
THE THEY	THE MAIN TO SEE	ESCHENCHIA COUI	╗	20:32	1	1	1	\dagger	†		
בוווים בנסו		ESCHENCHIA COLI	7		1	†	Ì	T	T	T	
PTIOS SULAC		SULFOLOBUS ACIDOCAL DARIUS		10.00	+		Ī	T	T		١
PTICE BRELA		BRE VIBACTERIUM LACTOFERATEM UM	10.00	Ì	1	T	T	T	T		
PTHTR SACER		SACCHAROPOL TSPORA ERT I INACA									
PTIG ECOLI	TRICCER FACTOR	ESCHENCHIA COLI	236-266	Ì	Ì						
PTAUA TREPA	TREPONEALAL NOENGR	I ALTUMENA I ALLUCATI	44.71								
PTACH TREPA	TREPONEMAL MENDR	TREFUNEMA FALLIDORI	41-64								
PTACE TREPH	TREPONENTAL MEMBR	INEPONEMA PRACEDENIS	74.100								
PTNAB ECOLI	LOW AFFINITY TRYPTOPHAN PERMEASE	ESCHENICHIA COLI	8.5	117.140					Ī		
PTNP4 STAAU	TRANSPOSASE	STATHYLOCOCCUS AUREUS	Τ					ĺ	Ī		
PINP! ENTRA	THAMSPOSON THRIT RESOLVASE	ENTEROCOCCUS FAECALIS	Т					T	Ī		
PINPA STANU	TRANSPOSASE A	STAPHYLOCOCCUS AUREUS			1		T	T			
PTINPB STAAU	TRANSPOSASE B	STAPHYLOCOCCUS AUREUS	٩	1	, ,		T	T	T		
PTNP BACTU		BACILLUS THUNUNGIENSIS	T	T		T		T	T		
PTNSB ECOLI		ESCHENICHIA COLI	Ţ	10.00	1						١
PTNSC ECOL!		ESCHENCHIA COLI	Т		1			Ī			
PINSD ECOL!	TRANSPOSON TNY TIL	ESCHERICHA COLI		T			Ī	T			
PINSE ECOLI	TRANSPOSON TNT TR	ESCHENICHIA COLL		Ī							
PTODI PSEPU	TOLUENE 1,3-DIOXYG	PSEUDOMONAS PUTIDA	10-01	Ī				Ī			
PTOD2 PSEPU	TOLUENE 1,2-DIOXYG	PSEUDOMONAS PUTIDA					Ī	T			
PTODA PSEPU	TOLUENE 1,3-DIOXYG	PSEUDOMONAS PUTIDA	1/2-713					T	Ī	Ī	
PTODJ PSEPU		PSEUDOMONAS PUTIDA	201.00					T	Ī		
PTOLA ECOLI	TOLA PROTEIN	ESCHENCHIA COLI			336. 916	111	111.41				
PTOLC ECOLI	_	ESCHENICHIA COLI	919.100	Т	Т						
PTOPI SYNP?	DNA TOPOISOMERAS	STRECHOCOCCUS ST	707.874								
PTORA ECOLI	TRING THYLAMINE.N.	EXCHENCIAL COLO	179.206								
PTOXI BORPE	PERTUSSIS TOXIN SUBUNIT I (SI) PRECUESOR	BOADE IELLA FERTUSSIS	2								
PTOX2 BONDE	PERTUSSIS TOXIN SUL	CI OSTRIBALDA DEFICILE	20.88	99.159	204-231	142-369	373-414	847-962	966-996	997-1024	1344-140
FTOX CLOD	TOWN A PRECITE OF	PSEUDOMONAS AERUGINOSA	470-497								
FIOXA PSEA	TOWN O LANGUE	CLOSTIUDIUM DIFFICILE	38.72	133-163	196-241	125-869	933-950	24.03	1403-1433	1506-1565	1716-174
TOY BY		VIBRIO CHOLERAE	13.40								
PTOC TREPA	ANTICEN TPFI	TREPONEMA PALLIDUM	106-143					1	1		
A PLANT	TRIOSEPHOSPHATE ISOMERASE	ESCHERICHIA COLI	83-110								
PTPIS MORSP	TRUOSEPHOSPHATE IS	MORAXELLA SP	39-166								
DEC MALE	THIOL PROTEASE PR	POILPHYROMONAS GINGIVALIS	117.144								
PTRUM AGREE	TRYPTOPHAN 2-MON	AGROBACTERIUM TUNEFACIENS	239-266	501-529							
PTROM AGRT4	TRYPTOPHAN 3-MONC	AGROBACTERIUM TUMEFACIENS	239-200	201-329					T		
PTRIM PSESS	TRYPTOPHAN 2-MONOOXYGENASE	PSEUDOMONAS SYLINGAE									
PTRAI STANU		STATISTICATION AUTORITIES		1							
PTRAZ STANU		STATE COLOR COLI	31.38								
PIRAS ECOLI	_	BINZORUM MEL BOTI	79.20			L					
PTA INDM	Т	STAPHYLOCOCCUS AUREUS	97.5	56-99							
PITAN STAND	I KANSPOSASE	ESCHERICHIA COLI	181.308	104-340	720-754						
TIMA ECOL	-+	ESCHERICHIA COLI	\$1.31								
PTIME ECOLI	TICASTOSASE	SHIGELLA SONNEL	2:3	200.227	131.25						
CONS ONLY		ESCHENICHIA COLI	321-255		-						
אונא ברסרו	I PATATIVE TRANSPOSASE	MYCOBACTEMUM TUBERCULOSIS	159-186								
BY BY	S231B PROBABLE TR	BACQLUS THURINGENSIS	181-308	419-446							
PTRAC BACTB	IS331C PROBABLE TI	BACELUS TRUMMGENSIS	281-308	419446							
PTIME STAM	TILANSPOSASE	STAPHYLOCOCCUS AUREUS	- P	22.3							
PTRAX BACTB	B IS231 PROBABLE TRANSPOSASE	BACELLUS THUMINGENSIS									
TAN ANTO	THANSPOSASE										

		Probaryate Sequences	П	Т		0.140.	7 7 1 2 0 7	48647	ABFAT	ABFAS
FILE NAME PROTE			7		-	┰	Т	Т	7	
PTRA PSEAE TRANSPOSASE		RUGINOSA	Т				T			
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NISTON TOUR PROPERTY			٥٠.١					T	Ī	
+			20.07						Ī	
THE PROPERTY OF THE PARTY OF TH	7.		006-1058	1					Ť	
7			102.1149					T	T	
T			16-931					1		
•		ESCHERICHIA COLI	Т					1		
THE PARTY OF THE P	BELLAS AST PRECUASOR		162-403 417-508	2				1		
_			240-307					1		
-	NATURE SCORE BEOTERN	E SCHEBICHIA COLI	\$-13 105-	٦						
-	INTIONAL REPRESSOR PROTES		61.86 630.657	657 (1) 1.858	865-895					
_			196-333							
PIRCS ECOLI TRACP		ESCRENICIA COLI	104.223 \$18.545	\$5						
PING ECOLI INCO			Т	Т	1140.11					
STRIL GOOD TRAINBROIEN			Т							
L			٦	Т	200			Ī		
T		ESCHERUCHIA COLI	47.74 328.371	E.				1		
Т			16-63							
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			107.137							
	ETHYLTRANSFERASE		Т	136-253						
	METHYL THANSPENASE		Т							
	ASE ALPITA CHAIN				-					
	LASE ALPHA CHAIN									
т	ASE ALPHA CHAIN		10-70)		1					
	LASE DETA CHAIN	ACINETOBACTER CALCOACETICUS								
THE PARTY OF THE P	ACE META CHAIN 6.			316-345						
	200000000000000000000000000000000000000	PREVIOACTERIUM LACTOFERMENTUM	173.199							
			111.6							
PIRPB LACCA TRYPTO			17.104 164.19	161	L					
	TRYPTOPHAN SYNTHASE BETA CHAIN	41000	T							
PIRFO VIOFA TRYPT	ASE BETA CHAIN	A PENTINA	230.34		L					
PIRE DRELA INDOCI	INDOLE . J. GLYCEROL PHOSPHATE SYNTHASE				-					
PTRIPC ECOLI (INDOL	INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE	ESCHEDICHIA CULI	1							
	E.J.GLYCEROL MIOSPHATE SYNTHASE		74. 77.							
PINC VIBPA INDOL	E.J.GLYCEROL MIOSPHATE SYNTHASE	VIBIUO PAILAHAEMOL YTICUS	T	100						
1	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE	ACINETOBACTER CALCOACETICUS	T		-					
-	ANTIGAMILATE FIOSPHIORIDOSYLTRANSFERASE	PSEUDOMONAS AERUGINOSA	707:07	<u> </u>						
	ANTHRANILATE PHUSHIORIUOSYLTRANYFERASE	PSEUDOMONAS PUTIDA	205-202							
PERPONIENT ANTI-	ANTIBANILATE PHOSPHORIBOSYLTRANSMERASE	VIBRIO PARAHAEMOLYTICUS	2.2							
	ANTHONILATE SYNTHASE COMPONENT (,	DACILLUS PUMILUS	99							
THE CLOSE ANTHE	ANTHRANII ATE SYNTHASE COMPONENT I	CLOSTRIDRUM THERMOCELLUM	165-326							
NA A SA L SALE	ANTHER MILE SYNTHASE COMPONENT IS	LACTOCOCCUS LACTIS	143-191							
No.	ANTIBANII ATE SYNTHANE CONTONUNT I	LUTTOSPIRA DIFLEXA	145-179							
1.	ANTOINE AND A THE CONTINUES.	RIIZOBIUM MELILOTI	139.166							
+	ANTIBOTE AND ATE CONTINACE COMPONENT I	SALMONELLA TYPHOAURUM	161-218		L					
-	A THE SALE ATE CALLED A COMPONENT I	SULFOLOBUS SOLFATANICUS	143-163 296	196-328						
VIEW SUCSO	ANTIBANI ATE CAMILLAGE COMPONENT IL	VIBRIO PARAIIAEMOLYTICUS	9.36 34.81	=	_					
	THE PROPERTY OF THE PROPERTY O	ACIMITODACTICA CALCOACIETICITS	13.39	<u> </u> -						
	A COMPANY AND A SECOND CONTINUE OF THE PARTY	AZOSFIRIL UM BRASILENSE	1	_						
ΞT	ARTHRANGALIC STATISTICS COMPONENT II	FCMFRICHIA COLI	5.33							, ' <u>'</u>
┪	ANTIIKANICATE STATINGSE COMPONENT II	II ACTOCOCCUS I ACTUS	5				L			1
PING LACE ANTH	ANTRICALLA IE STRUMASE COMPONENT II	PSEUDOMONAS AERUGINOSA	12.39							
-	ANTIGARIENTE STRUMPER COMPONENT II	CAL MONELL A TYPITIMITALISM	13	-	-					Ŀ
_	ANTIMAMILATE STATINGS COMPONENT II	SERBATIA MARCESCENS	7		L					
_	ANTIBORILATE STRUTTASE COMPONENT II	SHIGEL LA DYSENTERIAE	5.32		-					
ALL SALES	PITATIVE TRANSCRIPTIONAL REGULATOR!	PSEUDOMONAS AERUGINOSA	147.174							
-		ESCHENICIDA COLI	611-51							
7	RESISTANCE PROTEIN PRECURSOR :	ESCHENCHIA COL!	184-331							
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PCGENE	1107117814	Preharyotic Sequences	П	1.1		П	П		П	П	П
FILERAME	regien	ORGANISM	AREA SEA	ANEAL	7	1	7 7 7 7	ARIA ARIA	AZ AKTAL	AREA.	J
PTRY1 SALTY	TRAY PROTEIN		100		Ī		\dagger	+		+	T
PTRYP STACK	TRYPSIN PRECURSO					1	1	1	1	+	T
PISR STRAZ	RENA METHYLTRAN		_			1	1		1	+	1
PTSST_STAAU	TOXIC SHOCK SYND	AUREUS	7	27.70			+			$\frac{1}{1}$	1
PTSX ECOLI	CHANNEL-FORMING PROTEIN 15X PRECURSOR		70-67			1	1	+		+	T
TIK ECOLI	HYPOTIE FICAL 243					1	†	$\frac{1}{1}$		+	T
PTUS ECOLI	SITE-BINDING PROTEIN	1	٦.			1	1	1	1	1	T
PIYCA BACBA	TYROCIDINE SYNTHETASE I		7	374.30	1017-1031	1				$\frac{1}{1}$	Ī
PIYFI TREPE	ANTIGEN TYF!	MUE	T				+	+	1	+	T
PTYRA BACSU	POSSIBLE PREPIENATE DEHYDROGENASE	2	╗	112-342						1	٦
PIYMA ECOLI	CHORUSMATE MUTAS		22.78					1		+	
PTYNK ECOLI	TRANSCRIPTIONAL R		€ 5:3							-	Ī
PTYSY LACCA	THYMIDY ATE SYN		139-173								
ATYKY I ACTA	THYMIDM ATE SYN	LACTOCOCCUS LACTIS	25-109							L	
PTYSY STAND	THYMIDYLATE SYNTHASE	ŒUS	8.8					-			
PIDIN KCOIL	FINCE PROTEIN LA		276.303	316.303			-	-		L	
PINCOR SALTY	ENSOR PROTEIN UP	HINGTON	Т	316.343				-		L	
AL IVE CALLY	DAME PROTEIN		Ţ					-	_	-	Γ
	PRACH BUCCELORIBORY TRANSFERACE		10.53			T	-	-			ĺ
	THACK PROJECT		150-184							+	T
100 V	LINE A CE A I BALA CERTANIT	OBI	2		I					\mid	Τ
TORE OF THE	UNE ALTHA SUG		8					-		1	Ī
TOPE TROPE	UNEXASE ALTHA SOBURIT		8			ľ				+	T
TOKE THONG	UKEASE ALFRIA SUB	i valetima	Τ	(1)	T	Ī		+		+	Ī
PURE UREUR	UNEASE ALPHA SUB		Τ						1	+	T
MEZ MELPY	UREASE BEIA SUBURII					1			1	1	T
PURED HELPY	UNEASE OFEROM UN	2		Ī	Ī	1	l	1		\downarrow	T
PURE PROM	UNEASE ACCESSORY PROTEIN UNE					1	†	$\frac{1}{1}$	$\frac{1}{1}$	+	T
ACKEN KIEW	UKEASE ALCESSURT	NACOSTAN ACADOMICS	T	146.333	126-101					+	T
יייייייייייייייייייייייייייייייייייייי			T							+	T
PUSHA CALTV	CHEM PROTECULARACO PRECINICIONAL	HACURITAL	3				+	-		+	T
TOUR A COLLEGE	ı		Į,	171.191				-		ļ	T
PUVEA MICLU	EXCONCLEASE ADC	MICROCOCCUS LUTEUS	Т	619.646	614.718	973.949		\mid		\mid	Τ
PUVILA PARDE	EXCINICLEASE ABO	ICANS	Г							ŀ	Γ
PUVRC BACSU	EXCINICLEASE ABC SUBUNIT C	BACILLUS SUBTILIS	142.372	511.518						L	
PUVAC ECOLI	EXCINUCLEASE ARC SUBUNIT C		П	332-362				<u> </u>		_	
PUVRD ECOLI	IELICASE II		280-307					L	L	-	
PVANA ENTEC	VANCOMYCIN RESISTANCE PROTEIN VARA		187-309								
PVANC ENTGA	VANCOMYCIN RES	ENTEROCOCCUS GALLINARUM	≡.: :::								
PVID4 ACRTS	VIRD4 PROTEIN PR		2				1	1	1	+	Ī
PVIDS ACRTS	VIRDS PROTEIN	ACROUACTERIUM I UNIERACTENS	127-08-1				1	1		4	1
LAIR ACK	VIRIO FROIEIN	ACROSACTERISM TIMERACIENS	2 8	T		1	1	$\frac{1}{1}$	1	$\frac{1}{1}$	T
100 VOV	VIALUE AND LEIN		Т			1	1	$\frac{1}{1}$	$\frac{1}{1}$	+	T
FVIBX ACRES	VIABIOTACIEN	ACROBACTERIOR TOPERACIENS	T				1		+	+	Ī
PVIBX ACRIE	7	ACROSACTERION TONERACIENS		11.			+	1		+	Ī
VIBA ACKIV	_	A PAGE A CIENO	Ţ			1	†			+	T
TAIC ACARA	7		3 2			1				+	
FVICE ACKES	VIACITACIEN	ACROINCIERION I CPIET ACIONS	5					1		4	٦
PVIC. ACRIB		AUROBACIENUM IUMERALIENS	╗							-	J
LAND) ACION	VIKU) FROIEIN	ACROBAC I ENOM ANACOCENES		262-60			1	+		7	
A VOV	WIDE HOST RANGE		T	I						4	Ì
PVIIIA ACILIE	WIDE HOST RANCE	ACROBACTERIUM TUNER ACTENS	T		633.680		1	+		+	-
VIIIA ACH	WIDE HOST KANGE	AUKUBAC I ENDUM TUMEP ACIEMS	T	2	633-660		1			-	Ī
TVING SHIPE	_	VERENTA ENTEROCOUTICA		107-134	72.71		1	+	+	$\frac{1}{1}$	T
Z CALVA		ACROBACTERISARNIZOGENES				1	\dagger	$\frac{1}{1}$	+	+	T
PVIRI AGR 16	LIMITED HOST RANG	AGRODACTERIUM TUMEFACIENS	106-157	Ī	Ī	Ī	\dagger	+	+	$\frac{1}{2}$	T
]				1	$\frac{1}{1}$	$\frac{1}{2}$	7

		103117814	Sequences	1000	ARFAI	ARFAS	AREA	AREAS	AREA	AREA!	AREAI	AREA?
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VALUE REGIONAL STATEMENTS 199411 19941	SC ECOL!			24:112								
Value Valu	PA MYCHIR V			11.65								
10 10 10 10 10 10 10 10	101 BONNE O	- 1 -		333-359								
The OFFICE PROPERTY AND STATE AND				136.33				1	1	1		
TO OVILLE FROME NOTES 111-111		1=		2			1				Ī	Ì
		LITER MEMBRANE LIPOPROTEIN 25 PRECURSOR		25.5%			1		Ī		T	
TRANSCRIPTION ALTO DATE OF THE PROCESSORY 1949 191-40 19	TA AZOVI N	ITROGEN FIXATION PROTEIN VNFA			200		1	1	1			
THE PROPERTY CONTRIVERS 11-131 11	K AZOCH N	ITROCENASE VANADIUM IRON PROTEIN		61.93			1			1		
11 DATABLEGE PROTEIN ALLAMORELLA DURLN 19.93 111.318 11.318 1		TROCENASE VANADIUM IRON PROTEIN		ŝ	272-403	1		Ī	1	T		
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TOP TIME STREET OF THE PRECURED 19-11 11-116		BELLE ENCE PROTEIN VSDE		3.36								
The Particle The	LIVEN BY	VITEN VIEW SECRETION PROTEIN	VIBRIO VULNIFICUS	36-75		1			1			
FORTINGENERAL STATE 194-111 194-114 19		ALL ASSOCIATED PROTEIN PRECURSOR		17	313-316		1					
FOUNDEFFINE SCHEMULA COLI 104-111 104-	AA FCOLL	REPRESSOR BINDING PROTEIN	ESCHENICHIA COLI	9.19			1					
STOCK TOTAL POPETING STOCK TOTAL POPET	X 11023 1		ESCHENICHIA COL!	2.5					1			
TATIONE FILE 194111 1941	ECO11	POLYPEPTIDE	ESCHENCHIA COLI	<u>8</u> .								
STORTINGE A STORTINGE A STORTINGE A STORTINGE A	Т	POLYPEPTIDE		104-131				1				
STORE PRICE STATE CONCEINAGE PRICE STATE	Ī			-	20.00	797-167	T		T			
TOTATION TOTATION	AB ECOLI P	2	ESCHENCHIA COLI	268-295					1			
TOTAL DOSE KRANSE	LA STAXY X	YLOSE ISOMERASE	STAPHYLOCOCCUS XYLOSUS						T			
VICTOR REPRESSOR VICTOR REPROSUS VICTOR REPROSUS VICTOR REPRESSOR VICTOR REPRES	LK KLEAE X	YLULOSE KINASE	KLEBSIELLA AEROGENES	3								
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VECTOR V	LK STAXY X	YLULOSE KINASE			26. 26.	7		T				
TAPHTOSE EFFESSOR	LR BACSU X	YLOSE REPRESSOR	2000	343.380								
VICTIVE EPOD-1 & BETA-XYLANASE PLECINSOR 15-73 104-131 104	LA LACPE X	YLOSE REPRESSOR	CACHUBACHEEUS PENTOSUS	300	101-158	Т	т	274-301				
VITATIVE ENDO.1.4 BETA.XYLANASE PRECURSOR 19.235 13.200 13	LK STANT IN	- 1-	PSEUDOMONAS PUTIDA	51.78	26-53							
STATESTANTA NAME PRECURSOR 1 BACILLUS CURCULANS 17.74	23.22	ITATIVE ENDOLIA-BETA-XYLANASE	CALDOCELLUM SACCHAROLYTICUM	191-225								
17.200 1.8 17.200 17.2	NA BACCI O	1 4-BETA-XYLANASE PRECURSOR	BACILLUS CIRCULANS	47.74								
STATE STAT	NA BACSS E	NDO-1,4-BETA-XYLANASE PRECURSOR;	BACILLUS SP	22.00		1						
STATE STAT	NA BACSU E	NDO-1,4-BETA-XYLAMASE PRECURSOR ,1	BACILLUS SUBTILIS	***	776			T				
The Dot 1, and	NA CALSA E	NDO-1,4-BETA-XYLANASE A PRECURSOR	CALDOCELLUM SALCHANOLT IICUM	20.0	200							
International Caldocellum saccinatury Ticum 11-13 11-134	NA PSEFL E	NDO:14-BETA-XYLAMASE PRECURSOR	BACILLUS PUMILUS	459.486								
STATE ALCOHOLOGISTICAL STATE S	S S S S S S S S S S S S S S S S S S S	TO AN OSIDANE	CALDOCELLUM SACCITAROLYTICUM	440-474								
ALTERACTION ALTERACTION	_	13	PSEUDOMONAS FLUORESCENS	11.18	151.178		475-502					
INTEGRAL INTEGRAL	т-	13	PSEUDOMONAS FLUORESCENS	21.78	241-278							
INTEGRICETICAL 149 KD PROTEIN 1	N STREET	1	STREPTOMYCES LIVIDANS	9								
INFOPINETICAL 21 KD PROTEIN STREPTOCOCCUS GAALIS 21-105 172-218	K HALMO	IYPOTHETICAL 14.9 KD PROTEIN ;	HALOCOCCUS MORINHUAE	× 0								
	K STROR	IYPOTITETICAL 23.1 KD PROTEIN	STREPTOCOCCUS ORALIS	26.103								
	K METSM	IMPOSITIETICAL 36 7 KD PROTEIN	METHANOBRE VIDACTER SKITTIII	730-102								
VYPOTITETICAL 39 & COPROTEIN VERTICAL COLI 15-10	_	IYPOTHETICAL 34 6 KD PROTEIN	ESCHENCHIA COLI	100								
		TYPOTHETICAL 31 9 KD PROTEIN	PSEUDOMONAS PLUORESCENS	0.0								
		IYPOTHETICAL SP I KD PROTEIN	ESCHENICHIA COLI									1
INTEGRATE INTE		AYPOTRIETICAL SE 6 KD PROTEIN	ESCHENCHIA COLI									
VERTILE CALL AT SECULO 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15.15 13.15	AQ_ECOL!		ESCHENCHIA COLI									
	BC ECOL!		ESCHEMICHIA COLI		17,51,							-
ATTOPHETICAL 13 F AD PROTEIN PASTED AND A ACTION 15.10 114.14	BG ECOLI	4YPOTHETICAL 89 7 KD PROTEIN	ESCHENICHIA COLI		,(0./70	1						
THE PRESENCE THE PROPERTY THE	BN ECCLI	AYPOTHETICAL 6) 9 KD PROTEIN	ESCHEDUCHIA COCI									
HYOTIE HIGH. 21 B KD FROTEIN CLOST KIDUM ACETORUTY LICUNI 113-159 163-196 HYOTIE HIGH. LAND FROTEIN CLOST KIDUM ACETORUTY LICUNI 11-15 HYOTIE HEALTH (CLOST KIDUM ACETORUTY LICUNI 11-15 HYOTIE HEALTH FROTEIN 11-15 HYOTI FRANCH PRECURSOR 150-130 HYERSTRIA FREUTENCOLITICA 150-130 HYERTRIA FREUTENCOLITICA 150-130 HYERSTRIA FREUTENCOLITICA 150-130 H	S PSEAR	AYPOTHETICAL 15 9 KD PROTEIN	PSEUDOMONAS AERUGINOSA									
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INVASIN PRECINSOR NAVASIN PRECINSOR YERSINIA PREUMOTUMENCUL DALS 135-202 100-200	03 CLOND		CLOSTRIDIUM ACETORUTY L'ECUM	1								
YERSINA PSEUDOTUMERCULOSIS 135: 242			YERSINIA ENTEROCOLITICA	196-230	347.374	118-311						
	1	NAVA COL PRECINCIA	YERSINIA PSEUDOTUNERCUI OSIS	135.203	297.340							

PCGENE	1107x118x4	Prohamade Sequences	П	П		П		П	- 1	П	\prod
FILE MAME		DRGANISM	4	7	TEA	ARA	2474	7 7 7 7 7	1	1	AREA
PYADC ECOLI	HYPOTHETICAL PROTEIN	ESCHERICHIA COLI	9	9							
PYAEA RICRI	17 KD PROTEIN	RICKETTSIA RICKETTSII									
PYALIS ECOLI	HYPOTHETICAL 29 4 K	ESCHERICHIA COLI	231-248		Ì						
PYAFD ECOLI	HYPOTHETICAL 29 I K	ESCHENCHIA COLI	14-71			Ì					
PYAFE ECOLI	HYPOTHETICAL 23 0 K	ESCHENCHIA COLI	22-150		1						
PYAIB ESCFE		ESCHENCHIA FERGUSONII	<u>~</u>								
PYAMI SALTY	PUTATIVE AMIDASE	SALMONELLA TYPIIMURIIIM	33.180				1	Ì			
FYASI SYNY)		SYNECHOCYSTIS SP	1	٦		٦	Ì				
PYATP MYCLE	HYPO PROTEIN PUTATIVE ATP OFERON	MYCOBACTERUM LEPRAE	T	25.	<u> </u>	1		1			Ī
PYATA BACFI	PYATH BACKI HYPOL ATP-BINDING TRANSPORT PROTEIN	BACILLUS FIRMUS									
PYATS MYCGA	HYPOTHETICAL PROTEIN	MYCOPLASMA GALLISEPTICUM									
PYATU MYCGA	PYATU MYCGAIHYPOTIGITCAL PROTEIN	MYCOPLASMA GALLISEPTICUM	95-62	18.09							
VALUE VALUE	HAPOTHETICAL SO KD AVIRID ENCE PROTEIN		Γ	199.126							
	THE CONTRACTOR OF THE PROPERTY.		49.79								
יייייייייייייייייייייייייייייייייייייי	ATTOLICAL MARKETIN		94.6					Ī			
PYBBA ECOLI	MTPUTHETHEAL ABL TRANSPORTER				Ī	Ī		T			T
PYBED ECOLI	HYPOTHETICAL FORD PROTEIN				1			1		I	
PYBID ECOL!	HYPOTHETICAL 14 I KD PROTEIN		27.174		1						
PYCAE ECOLI	HYPOTHETICAL 24 S KD PROTEIN	1	14-61								
PYCBA ECOLI	HYPOTIETICAL PROTEIN		38-93								
PYCBL BACCA	HYPOTHETICAL 17 3 KD PROTEIN	BACTEROIDES UNIFORNIS	99.100								
PYCEA BACLA	HYPOTHE TICAL PROTEIN	BACILLUS LAUTUS	10:111								
PACE ECOIL	HYPOTHETICAL 22 9 KD PROTEIN	ESCHENICHIA COLI	61-18								
113	UNDOTHER AL PROTEIN	ROPHUS	31-48								
200			3								
PYCIB ECOLI	HYPOTHETICAL 20 B	ESCALABORIST COLI		777 761	Ī	T	I				
PYCIF ECOLI			,	8	Ī		I				
PYCIK ECOLI	HYPOTIETICAL PROTEIN		79.67								
PYCLI ECOLI	HYPOTHETICAL 43 3 KD PROTEIN 5	ESCIENCHIA COLI	2.5								İ
PYCPI SYMPY	HYPOTIGETICAL 29 3 KD PROTEIN		154-221								
PYCP3 SYNY3	HYPOTHETICAL 28 0 KD PROTEIN	SYNECHOCYSTIS SP	7.34	120.154							
PYCPS SYNY)	HYPOTHETICAL 19 5 KD PROTEIN (277.308								
PYCPG MASLA	HYPOTHETICAL PROT	MINDSUS	2.29								
PYCPY PSEA	HYPO PHYCOCYANIN		310.407								
PYCEL BACTX	HYPOTHETICAL 29 I K	GIENSIS	43.74	133-150							
PYCSS ECOU	HYPOTHETICAL PROTEIN PRECURSOR	ESCHENCHIA COLI	12-59								
PYCWS BACSU	HYPOTHETICAL PROTEIN	BACILLUS SUBTILIS		59.86							
PYDIM HERAU	HYPOTHETICAL 68 4 KD PROTEIN	HERPETOSIPHON AURANTIACUS	12.19	131-171	319.090						
PYDBA ECOLI	HYPOTIETICAL PROTEIN	ESCHENCHIA COLI	12.66	113.144	163.216	131.267	95.129	458-415	676-717	1136-1163	1499.1530
PYDDD ECOLI	HYPOTHETICAL PROTEIN	ESCHENCHIA COLI	10.107								
PYDDB ECOL!	HYPOTHETICAL 86 7 KD PROTEIN	ESCIENCITIA COLI	606-641	613.714	126.753						
PYDDC ECOLI	HYPOTHETICAL 80 8 KD PROTEIN	ESCHENICHIA COLI	333-400	431-452	631.648						Ī
PYDDD FCOLI	INPOTIETICAL 24 I KD PROTEIN	ESCHENCIHA COLI	133-174								
PYDEH ECOLI	HYPOTHETICAL 30 S KD PROTEIN	ESCHERUCHIA COLI	96-130								
PYDEL ECOLI	HYPOTHETICAL 18) KD PROTEIN	ESCIENCHIA COLI	11:3								
PYDEK ECOLI	HYPOTHETICAL 65 S KD PROTEIN	ESCHENCILIA COLI	33.360	324-551	565.592						
PYDNN BORBU	PYDNN BORBU HYPOTHETICAL II 2 KD PROTEIN	ONFEN	95.36								
PYDOI SULSO	PYPOTHETICAL 147		5.2	1-101							
PYD01 SULSO	HYPOTIETICAL 16 9 KD PROTEIN	SULFOLOBUS SOLFATANCUS	<u> </u>						Ī		
PYERA ECOLI	HYPOTHETICAL PRO		91-130	Γ		Γ	Γ				
LUC ECO.	-	ESCHERICHIA COLI	\$0.33		Ī						
PYEEF ECOLI	HYPOTHETICAL 38 5		97.50		F					Ī	-
PYEEF ECOL	HYPO 49 8 KD TILANS		147.174	T	Ē	Ī	Γ	Ī	Ī	Ī	T
PYFGA ECOL		ESCHENICHIA COLI	145-172		-		Ī				F
22 1	HYPOTHETICAL 36 9		69.106	213.310		Ī			T		
PYEND ECOLI	HYPOTHETICAL 92 3		L	301-545		Γ					
PYEIR ECOLI	HYPOTHETICAL 19 1	ESCHENCHIA COLI	Т				Ī				T
PYEHF ECOU	HYPOTHETICAL 141.0 KD PROTEIN	ESCIIEMCIIIA COLI	24)-570								
PYEHI ECOLI			Т	102-179			ĺ				
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107:178:4	Prohaty self Sequences	AREAL	AREA?	ARCAL	AREAS	ARCA!	ABCAS	AREA? A	AREAL	AREAS
PROTEIN	ESCUEDICUIA COST	326-351	Г							
	F C T F B C W A C O L	46-80								
	E CHERTHIA COLI	91-19						_		
HYPOTHETICAL PROFEIN	ESCUEDICHIA COLI	13-23								
	TOUR LOUIS COLUMN	9)-110								
HYPOTHE HICAL ABC HANSTONIEN	ECCIENTALION COLI	453-480								
HTFOLKELICAL FACILIA	FSCIIERICIIIA COLI	199.433								
	F CCIFFEE COLI	175-202								
	BACH LUS STEAROTHERMOPHILUS	133.160								
ILICAL VOR NUTROLLING	BRADYRHIZOBIUM JAPONICUM	109-150								
EliCAL PROTEIN	BACH LIS MEGATERIUM	40-67								
GTICAL 17 7 KD PROTEIN	SCHEDICHA COLI	214-241								
HAPOTHETICAL 29 4 KD PROTEIN	E CLEBICITA COL	225-252								
ETICAL JOY AD PROJEIN	E COMPONION CON	209.236								
HYPOTIETICAL JI EKO PROTEIN	BACK THE THIRD SERVICE	26.61								
ETICAL 12 I KD PROTEIN	PECITIONAL PITTIDA	145.172								
HYPOTHETICAL 32 4 KD PROTEIN	FECURE ICHA COLL	223.264								
ETICAL 41 4 KD PROJEIN	A CHILL OTE ABOTHER MOPHILLIS	5						-		
HYPOTHETICAL IS S KU PROTEIN	STOREST STEWART THE PROPERTY OF THE PROPERTY O	183.209								
HYPOTIŒTICAL PROTEIN	BACILLUS SIEAKUTEKKIOTALUS	10, 13,					T			
HYPOTHETICAL 15 KD PROTEIN	DACILLUS CEREUS	30.47					T		Ī	
IETICAL PROTEIN	BACILLUS SUBTILIS					Ī		l	Ī	
IETICAL 17 I KD PROTEIN	BACILLUS SUBILLIS	00 136					İ	l	Ī	١
HETICAL 190 KD PROTEIN	BACILLUS SUBTILLIS						l	\dagger	T	
	CLOSTNDRUM ACETOBUT YLICUM	166-210				Ī			Ī	l
HYPOTHETICAL PROTEIN 2	STREPTOCOCCUS MUTANS		200	707-67		T		t	Ť	
RETICAL 20 6 KD PROTEIN	ESCHERICHIA COLI	8 2					Ì	t	T	
HYPOTHETICAL 45 2 KD PROTEIN	ESCHENCHIA COLI	9	177				T	T	T	
TETICAL PROTEIN	ESCHENICHIA COLI	136.301			Ī				Ī	
SLE ABC TRANSPORTER	ESCHEMICALIA COLI	101.76	104.13	143.174			Ī		Ī	
PROBABLE ABC TRANSPORTER	TUIDBACHTIK FERROOXIDANS	113:140						İ		
BLE ABC INAMSTORIER	FCHERCHA COLL	267.297								
HATOILIE II CAL 33 CAUTAOLEIN	BACIL LUS SUBTIL IS	333.33								
METICAL MOTEON	ANABAENA SP	13.99								
HEILCAL TRUITIN	ESCHERICHIA COLI	\$9.9¢								
THE STREET AT 14 I ROTEIN	ESCHERICHIA COLI	43.77								
THE PROPERTY OF THE PROPERTY O	ESCHEDICHIA COLI	6.6	-							
	I ACTOCOCCIUS I ACTUS	167.194	-					-		
HYPOTHETICAL TROICIN	I ACTOCOCCIIS I ACTIS	80.134	132.150							
HYDOTACTICAL TO TAD PROTEIN	LACTOCOCCUS LACTIS	93.148	L							
HYPOTHETICAL 30 7 KD PROTEIN .	LACTOCOCCUS LACTIS	2.10	180-181							.]
IIVMIIII IICAL PROTEIN	STAMINIOCKEUS AURIEUS	1								
	VIDIO CHOLERAE	96-136								
HYPOTHETICAL 32 ND PROTEIN	METHANOTHERMUS FERVIDUS	106-133								
HYPOTHETICAL II O KD PROTEIN	CLOSTUDIUM ACETOBUTYLICUM	41-65								
HYPOTHETICAL 30 6 KD PROTEIN	CLOSTADIUM ACETOBUTYLICUM	98-125						İ		
INVENTIBILITY AT A KID PROTEIN	AILDAIN ACITOROTIVA	23-32	£	274.10						
IIYETIIIIIIIEMEAL PROTEIN	LACTONACILLUS III:I.VETICUS	93-130	ž.							
IIYPOTILETICAL PROTEIN	PSEUDOMONAS SP	213.266							1	+
HYPOTHETICAL 38 0 KD PROTEIN	HALOBACTERUM HALOBIUM	245-272						1		-
YPOTHETICAL 4 6 KD PROTEIN	MYCOBACTERUM TUBERCULOSIS	19-46					1		1	1
ILYPOTHETICAL 42 6 KD PROTEIN	PSEUDOMONAS AMYLODERAMOSA	9.76								
ISMI HYPOTHETICAL 48.3 KD PROTEIN	METHANOBREVIBACTER SMITHIL	33.18	32.52	136.365				1		
HYPOTHETICAL 31 KD PROTEDM IL	HALOBACTERIUM HALOBIUM	86.113						1	-	
HYPOTHETICAL 340 KD PROTEIN	ESCHENCHIA COLI	202-219	1					1		
HETICAL PROTEIN	ESCHENCIA COLI	1		1						
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PCCENE	107217864	Prokaryotic Sequences	Π.	гт	П	П	П				1
FILEMANE	1	ORGANISM	10,000	1	3	4	1000	100	Т	Т	Ţ
TYBO ECOL		ESCHERICHIA COLI	143.170	Ī		T		-		-	Τ
PYCC ECOLI		ECCHERICKIA COLI	133-139			Ī	-	ŀ	-		
PYICE ECOLI	HYPOTHETICAL JI I ND TROTHER	ESCUEDICUIA COL 1	401-435			Ī		_	_	-	Γ
LACE ECOL	HIPOTORIUS IN TO PROTEIN	ECONEDICHIA COLI	133.149			Ī				F	
מאנים ברסבו	LICENTIFICATION OF DEPOTED	F SCHERICHIA COLI	76-103					L			
	STATE TICK! AS A KD PROTECT	ESCIENCHIA COLI	330-347								
NIDS ECIN	SIVEOTHETICAL IS B KD PROTEIN	ESCHENCHIA COLI									
PYIDE ECOLI	HYPOTHETICAL 38 9 KD PROTEIN	ESCHENCHIA COLI	11 (11-91	113-209	177.104						٦
PYID! ECO!	HYPOTHETICAL 15 7 KD PROTEIN	ESCHENCHIA COLI	(1.96							-	٦
PVIDK FCOL		ESCHENCHIA COLI	3.39	Ī							٦
PVIDE ECOL	HYPOTHETICAL 27 3 KD PROTEIN	ESCHENCINA COLI	63.97								
PYIEA FOOL	HYPOTHETICAL 49 2 KD PROTEIN	ESCHE ACHIA COLI	221.248								
Ner Front	SEYPOTHETICAL 40 6 KD PROTEIN	ESCHENCIIIA COLI	20.58	270-297							
HUMBU DENG	HYPOTHETICAL PRO	ERWINIA CHRYSANTHENI	13-67	Ī			_	-	_	\vdash	
PVIED ECOLI	HYPOTHETICAL 14 8 KD PROTEIN	ESCHERICHIA COLI	971-98								
VIEG ECO.	HYPOTHETICAL 46 9	ESCHENICHIA COLI	155.591							_	
PYIEII ECOLI	HYPOTHETICAL 24 7	ESCIENCINA COLI	81.18								
PYIEM ECOL	HYPOTHETICAL 13 0 KD PROTEIN	ESCHERICHIA COLI	13-105								
PYIED ECOL		ESCHERICHIA COLI	101-343	180-407							
PYISC ECOLI		ESCIENCHIA COLI	175-202			Ĭ					
PYIGI ECOLI		ESCHENICHIA COLI	11.92								П
PYICH ECOLI		ESCHENCHIA COLI	120-154								П
PYIGN ECOL		ESCHENICHIA COLI	207-234								
PYICO ECOLI	HYPOTHETICAL 28 I KD PROTEIN	ESCHERICHIA COLI	96-69								
PYIGF ECOLI	HYPOTIETICAL 22.3 KD PROTEIN P	ESCHENICHIA COLI	001-11								
PYIGT ECOLI	HYPOTHETICAL 27.8 KD PROTEIN	ESCHŒRICHIA COLI	133-159						-		
PYING ECOLI	HYPOTHETICAL 21.3	ESCHENCHIA COLI	2-40					1		4	1
PYND ECOL		ESCHENICHIA COLI	20.55					1	+	+	
PYHE ECOL	HYPOTHETICAL S4	ESCIERICHIA COLI	272.306				1	$\frac{1}{1}$	1	+	T
PYNG ECOLI	HYPOTIETICAL 19	ESO-EXICHIA COLI	60.2					+	+	+	T
LYBK ECOLI		ESCHENICALA COLI		3	41, 101	Ī	+	+	+	+	T
PYRON ECOL.	HAFOINE INCAL 18 VALUE AND BEOTEIN	BECLEBICAL COLI	1.	K 13		1		$\frac{1}{1}$	+		T
PYING ECOL	HATOIREIKAL II. BAD PROLEIM	ESCHEDITA COLI	157.184	Ī		T	Ť	+	+	+	T
NIN ECOL	HVPOTHETICAL 31	ESCHERICHIA COLI	2.8	Ī	Ī	Ī	t	-		ł	Τ
NINK ECOL	HYPOTHETICAL 23 S KD PROTEIN .	ESCIENCINA COLI	97.6			T		-	-	-	Γ
PYTHZ ECOLI	HYPOTHETICAL 15	ESCIENCHIA COLI	Ç						_		Γ
PYIIF ECOLI	HYPOTHETICAL 32.9	ESCITERICISIA COLI	13-63					Н		Н	П
PYIN ECOLI	HYPOTHETICAL 96	ESCHENICHIA COLI	18-71				+				
PYIJC ECOLI	HYPOTHETICAL 26 6 KD PROTEIN '	ESCHERICHIA COLI	36-163					-			٦
PYIM ECOLI	HYPOTHETICAL 18 3 KD PROTEIN	ESCHENCHIA COLI	225.263					1		+	7
PYIIK ECOLI	HYPOTHETICAL II 2 KD PROTEIN	ESCHENCHIA COLI	2			1		1	+	$\frac{1}{1}$	T
PYIJO ECOLI	HYPOTHETICAL 12 I KD PROTEIN	FISCHERICIIA COLI	7	,		1		+	1	$\frac{1}{1}$	T
PYIJP ECOLI		LICENSIA MONOCINE	T	9-440		1	+	+	+	+	T
N I I	HIPOTREIICAL IN TAUTANTEIN	CHICKLY MOTOCI LOGGES				1	+	1	+	1	T
PYISI SHISO	INSERTION ELEMENT 13000	STRUCTURA SOUNCE	40.70				1	\dagger	$\frac{1}{1}$	+	T
2000	PARENTAL ELECTRICAL	CHICELL A CONTROL			I	Ì		+		+	T
	LIVEOTUETICAL AT	BACH LIE CP	911.11		Ī		\dagger	\dagger		+	T
	AND THE HEAL STA	ECCLEBICATA COLI					1	+		1	T
A PLACE CONTRACTOR	HYPOTHETICAL 41 VOA	ESCHERICHA COLL		I			t	\dagger	1	1	Ŧ
NAME OF THE PARTY	HYPOTIETICAL 71 S	ESCHENICHIA COLI	021.6				+	+	-	+	Τ
PYIBL ECOLI	HYPOTHETICAL 9.7 N	ESCIENCIUA COLI	30.57					-	-		Τ
PYBM ECOL	HYPOTHETICAL 26.7	ESCHENICHIA COLI	113-149							-	Τ
PY/30 ECOLI	П	ESCHENICHIA COLI	П	łI							
PYICC ECOLI	HYPOTHETICAL 60 8 KD PROTEIN	ESCHENCHIA COU	38-65	414-441	451-492				\exists	Н	П
				ĺ			ĺ		1		ĺ

FULL MANIE PROTEIN PYICE ECOL! HYPOTHETICAL 60 1 KD PROTEIN	ORGANISM		V V V V V	ABFA 3 A	ARFAILA	AREA 9 A	AREAG	AREA?	AREA	AREA
HYPOTHETICAL 60 5 KI	Commission Coll	11777	Γ		1	1	1	П	Г	
	ESCHENCIA COLI	194-421								
HYPOTHETICAL 59 2 K	ESCHENICATA COLI	911:16								
-	ESCHERICHIA COLI	242.269								
HYPOTHETICAL 31 4 AUTHORISM	ESCHENICHIA COLI	366-396								
HITCHICAL IN AD TO A DECEMBER	ESCHERICHIA COLI	20-05								
PATCH ELOCI METOTING AND ENDERNIES	ESCHENCHIA COLI	3-29	451-485					1		
INVESTIGATION OF THE PROPERTY	ESCHENICHTA COLI	103-134				1	1			
INVESTIGATION IN SIND PROTEIN PRECURSOR	ESCHENCHIA COLI	Ħ	11.129		1	1				
SONOTHETICAL ALEKD PROTEIN	BACILLUS FIRMUS	321-355			1	1	1	1		ĺ
SA ALL ACAD SECTION SECTION	LACTOBACTION ACIDOPHILUS	47-74			1	1	1		Ī	
	LACTOBACILLUS ACIDOPHILUS	15-43				1	1			ĺ
THE LACK AND THE PARTY OF THE PROTEIN	LACTOBACELLUS ACEDOPHILUS	47-74								
CONTRACTOR SAMED BOTTON	SULFOLOBUS SOLFATANCUS	23.50								
TILAC SULSO INTO INC. INC. INC. INC. INC. INC. INC. INC.	PSEUDOMONAS PUTIDA	Г	314.341							
STATE OF THE STATE	YERSINIA ENTEROCOLITICA	184-221								
LEAST LEAST AND PROTECT	ANABAENA VANABILIS	173-199								
PYLIJ AKAYA HITOIREIKALAIANO FROIEN	I ACTOCOCCUS LACTIS	15.70								
PYLUD LALLA MITOLIE IIIAA 27. NOTAO EIII	BACULUS SUBTILIS	53.79								
PYMES BALSO HITOINEIGAL SOUND BEOTEN PRECINCOR	MYCOPLASMA GENITALIUM	\$6.83	189.193	420-445	1001-186					
TYPOTHETICAL INC.	CLOSTRIDIUM PERFUNCENS	139.166								
STATES OF DATE INVESTIGATION AND PROTEIN	CLOSTRUDIUM PERFICINCENS	13.49	63.63	1187-311						
TATOLINE HEALT ALL BROTH	METHANOCOCCUS THERATOLITHOTADPHICUS	55.89								
_	PARACOCCUS DENITRIFICANS	52:86								
TANGI FALLE MITOLINE MACANIEM	SV VIGTORIA	171-198								
PYNT3 ANASP HYPOTHETICAL 28 1 ROTROTEIN	ALABATINA CO	87.165								
HYPOTHE HEAL PRO	TOO THOUSAND	5								
PYOND ECOLI HYPOTHETICAL 21 4 KD PROTEIN T	ESCHEROLINA COL	Ē	210.316			Ī				
HYPOTHETICAL 43 J	ESCHEROLIS COL.	T								
HYPOTHETICAL 13.0 KD PROTEIN	ESCHEDIA COL	301.100					Ī			
HYPOTHETICAL 93.3 KD PROTEIN	ESCHERICALA COLI	7			Ī	T				
ILLIAN METICAL TO THE PROTEIN	E CONTRACTOR COLI	145.193			Ī					
HYPOTAL DATA NOT ROTEIN	S CHERICHIA COLI	12.50								
HINDING III AL JOSENIA MONDE INCOME	PANTONACTERINACSP	33.50								
SOTE IN THE PROPERTY	VERSINIA ENTEROCOLÍTICA	63.103								
ROIEIR-I TROSINE P	VERCENTA PSEUDOTUBERCIA OSIS	69.105								
KUIEIM-ITAUSINE F	VER COM ENTREDCO ITICA	Τ	3	235.262			Ī			
GUTER MEMBICANE PROTEIN TOTAL	VERSION POERTION OF THE POERTING	T	Γ	315.365						
COTTER MEMBRANE PROTEIN TOTAL	CERSINA ENTRECOMO ITICA	T	Τ					ĺ		
PYONG VEREN YONG PROTEIN PRECURSOR	WANTED	147.174					Ī			
HITCHIRE IN ALL STANDS IN THE SECOND STANDS IN THE	I ICTERIA MONOCYTOGENES	13.77								
PIORA LISMO MITOINEILAL MANDITOLINA	PVINCOCCIIS WORKEI	101.210					Ī			L
UNITEDITAL AND PROTEIN	LA ENCOCOCIO TO TOTAL PER MANAGEMENTA PER	19.66					Ī			
MYPOTHETICAL 19 8 KD PROTEIN	TACABOTHE OF THE TACABOTHE	40.70					Ī			
PTORC MARIN INTRODUCED IN THE PARTY OF THE P	LIAR BACKELL IN TAFF. UF NZ AF	Τ	05:100							
Store of the store	HAEMOPHILUS INFLUENZAE	2								L
Management 11 1 to 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	HAFACOPITIE US INFLUENZAE	1.5								
PTOCH HACIN ALLAND BEOTERN	HAFMORNILLIS INFLITENZAE	2	611.722							
VI THOUSEN	DACH LINE CIRTH IS	Т								
PYCHO BACSO HYPOTHEIRAL JAKOTACHA	PVROCOCCIIS WORKEI	10.64			-		Ī			<u> </u>
CHINGS THE TANK THE PROPERTY OF THE PROPERTY O	I ICTEDIA MONOCYTOGENES	23.54								
MITOTOR INC. 18 TAN PROPERTY	KYABUM APAPPIK ALMERIK	11.01	110.119							L
PYPIS STAKE MYPOINGINGINGAL 13.5 KD PROTEIN	BACTLUS SUBTRUS	57.04								
HANDINETICAL 22 2	STAPHYLOCOCCUS AUREUS	19-70								
HYPOTHETICAL 26 9	STAPHYLOCOCCUS AUREUS	¥:19								
1	STAPHYLOCOCCUS AUREUS	23-40	61-89	179-206						
HYPOTHETICAL 27.7 I	STAPHYLOCOCCUS AUREUS		129-176							

г	107417814	Preharyeie Seascaces		1				ľ			
ELLCHAME	ROUFIN	ORGAMISM	AREAL	AREA?	AREAL	AREA!	AREAS /	AREAS	AREA?	AREAI	AREAS
	YPOTHETICAL PROTEIN ?	AGROBACTERUM TUMEFACIENS	29.56							Г	
PYPA1 LEGPN H	HYPOTHETICAL PROTEIN	LEGIONELLA PNEUMOPHILA	94-135								
		ENTEROCOCCUS FAECALIS	901-62				Ī				
П	HYPOTHETICAL 21 6 KD PROTEIN	BACILLUS ANTHUACIS	13-47	115-162							
PYPCI ECOLI H		ESCHENCHIA COLI	2.								
PYPDA BACSU H	HYPOTITETICAL 27 3 KD PROTEIN	BACILLUS SUBTILIS	184-232								
PYPT ECOLI III	VPOTHETICAL 12 6 KD PROTEIN	ESCHERICHIA COLI	16-43								
		SYNECHOCOCCUS SP									
		CLOSTIUDIUM PENFRINGENS		4).11	471-61						
	HYPOTHETICAL 14 S KD PROTEIN	CLOSTAIDIUM PEAFAINGENS	3.59								Ī
Г	HYPOTHETICAL 38 4 KD PROTEIN	CLOSTRIDIUM PERFRINGENS	100	263.290	303.340		Ī			Ì	
7	HYPOTHETICAL 18 5 KD PROTEIN	PSEUDOMONAS AERUGINOSA	23.53	┰			Ī	T		Ī	I
	PPOTITETICAL PROCESSING PROTEASE	BACILLUS SUBTILIS	329.356								
Ţ.,	HYPOTHETICAL PROTEIN	KLEBSTELLA PNEUMONIAE	243.270	Ī				T		T	T
	HYPOTHETICAL 13.1 KD PROTEIN		23.54				Ī	T	T	Ī	
Т	HYPOTHETICAL 40.7 KD PROTEIN	INIOFORMICICUM		56.59	T		T	T	T		
PYPV3 METTE HY	POTHETICAL 22.5 KD PROTEIN	Т	T	Ī	Ì		T	Ì	T	Ť	
PYPV7 METTE HY		Т	69.117			T	T			Ť	Ī
PYPVB METTE IN		Т	Γ.	110.430		Ī	T	T	Ī	T	T
PYPYB BACSU HY	HYPOTHETICAL 72 4 KD PROTEIN	Т	Т				T	1		T	
PYPZI METTF HY	POTIETICAL 40 6 KD PROTEIN	IN THERMOFORMICICUM	T	308-335		T	T	1	1		
PYPZ3_METTF HY	POTHETICAL 11 1 KD PROTEIN	T	Γ	154-188	l		T	T	Ī	Ì	
PYP2S METTE HY	POTHETICAL S4.1 KD PROTEIN	T	٩	T	391.408		Ī	T	T	T	T
PYP27 METTF HY	POTIETICAL 9.7 KD PROTEIN		П	+		Ī		Ī			T
PYRIS THEPE MY	POTHETICAL 18 7 KD PROTEIN		601-28					l		T	
PYRBI HALCU HY	HYPOTHETICAL 40 KD GTP-BINDING PROTEIN	ТІКОВКОМ	20-51				Ī	T		T	I
PYREC SYNDY HY	POTICETICAL 28.7 KD PROTEIN 15		19.76								
PYILTO SALTY HY	HYPOTICETICAL 40 4 KD PROTEIN		143-190 143-190								
TAKE SALIY	POTHETICAL STORD PROTEIN		\$ \$	Ì							
	NATOTICE HEAL 20 6 KD PROTEIN	SALMONELLA TYPHIMURIUM	200	1							
	UVECTION BECTER			1	1	1	1	1			
	HYPOTHETICAL PROTEIN	NIF: 11	1000	25 1 00	1	1	1	1			
			T		1	T	1	1	1	1	
PYRES SULAC HY	POTHETICAL II.S KD PROTEIN .				1	T	1	1	1		
	HYPOTHETICAL 14 S KD PROTEIN	SULFOLOBUS ACIDOCALDANUS	11.71		T	T	T	T	T	T	T
	HYPOTHETICAL 25.3 KD PROTEIN		39.62					T		T	
PYRTS BACSU IN	POTHETICAL 11.4 KD PROTEIN 1:		П	14-81							
PYSCB YEARN HY	POTENTICAL YSC OPERON PROTEIN BY		8 23 8							Ī	Ī
SVECTO VENERA 13	TISCL TEKEN TO UPERON PROTEIN C PRECURSOR	TERSINIA ENTEROCOCITICA	7	265.38							
PVCCH VERFIN VC	PACCE VERSIA VAC DEBON PROTEIN IN		697.702								
PYSCII YERPS IVS	YSC OPERON PROTEIN H	1 0616			1	1	1				
-			1 2 3	1	1	T		1		1	
PYSCI_YEMPS YS	YSC OPERON PROTEIN I	LOSIS	49.76	T		1	1	†		1	
PYSCI YEREN YS	YSC OPERON LIPOPROTEIN J PRECURSOR		93.126	T	T	1	1		1	1	
PYSCI YELUS YS	C OPERON LIPOPROTEIN I PRECURSOR !		90.136	T	T	T	T	†	Ť	T	
1	YSC OPERON PROTEIN L		20-	T	T	T	T	\dagger	1	1	
PYSCL YEAPS YS	YSC OPERON PROTEIN L		99:19			T	\dagger	T	T	1	T
PYSMA SEDMA HI			11.30		-			l	T	\dagger	L
	POTHETICAL 21.3 KD PROTEIN		601-89		F	T	T	T	Ì	Ť	Ī
ΞĪ	HYPOTHETICAL PROTEIN	LENS	88-138			T		T	T		F
TASKS LEVIL	POINTIEST PROTEIN	2		П							Γ
r IZ	POTRETICAL 10 6 KD PROTEIN	MYCUTLASMA MYCOIDES	T	185-227	300-327						
PYSYN METER HY	HYPOTHETICAL PROTEIN	FERVIDUS	11.10	Ì	\dagger	1	1	1			
PYTJJ STRIFR HY	POTHETICAL 17.1 KD PROTEIN		16.7%	T	†	1	1	1	1	1	1
					1	1	1	1	1	1	7

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	Park americ Comences							
PCCFNE 10311384	The state of the s	TABLE I ABEAT	Г	AREA	ARFAS JAREA JAREAS JAREAS JAREAS	REAS IA	CA1 AREAL	1 ABBA2
2011000	ORGANISM	Т	Τ					
THE DOCK	MACTILIS SUBTOLIS	244-271 1277-300						
HYPOTHETICAL 33 6	I COTOCOUR A RIGI EXA	14-113	_			1		
PYTHE LEPBI HYPOTHETICAL 13 KD PROTEIN		1						
ACT A TACE A MYPOTHETICAL 13) KU PROTEIN	LACTOCOCCUS LACTIS		-			-		
	BACILLUS SUBTILIS	37.64	-			1		
HTPOINE III	COIRDE ASMA CITIL	102-149						$\frac{1}{1}$
HYPOTIGETICAL 1)	\$1 11.6 CI B 111 16	17-64 69.95						
HYPOTIETICAL IT	DACTION SOUTH THE	142.169						
PYXON BACSU (HYPOTHETICAL 11 0 KD PROTEIN	BACILLO3 SOBTILES					-	-	L
0 76 10 20 10 10 10 10 10 10 10 10 10 10 10 10 10	BACILLUS SUBTILIS	17:31				1		
HATOINE IN A 18 O	DACH LIS SUBTRICES	165-207 262-289						+
HYPOTHETICAL OF		1.30	94.143			_	_	_
PYX11 BACSU HYPOTHETICAL 44 B KD PROTEIN	BACILLO3 SOBINCIS	Ī					L	-
STATE BACKET THE TICAL BIT KO PROTEIN	BACILLUS SUBTILIS	20.00	1		1			
TAKE BALLO MINISTER STATE OF THE STATE OF TH	BACILLUS SUBTILIS	24.50						
PYANG BACSU INTRODUCE IN THE PROPERTY.	AZABARA SP	23:194						
PYXIZ ANASP HYPOTIETICAL INVICION	CAL DOCE LINE CACCILARON VIICIDA	9:0	_					-
PYXYB CALSA HIYPOTHETICAL 107 KU PKU EIM	2.1 000 11 10 1 0 1 0 1 0 1 0 1 0 1 0 1 0	2						-
PYXYC CALSA HYPOTHETICAL PROTEIN	CALLOCELEUM SALCHANDE I INC.						_	
ACTOR OF THE PROPERTY OF THE P	ESCHEDICHIA COLI							

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TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

PCGENE	107317816 Mailf Segren on All Homan Protein Seguences	П	AUCA 1 ABVA 1	П	AUTAL	AREAS	AREA	ARLA 7	AREAT	AKEAS
FILENAME		9	Т	Т	т	т	1	,		
PIAJE HUMAN	RAGA(EMT)		1	+	t	T				
PLASS HOMEN		2/-0		+	\dagger	T			I	
PIATE LE MANAN		26-19		$\frac{1}{1}$	†	t				
77.4	_	21-55		\dashv	1	1				Ī
100	THE STATE OF THE PROPERTY AND STATE OF A STA	11.114		_	_					
LAZI HUMAN	PLACLASS I RESIDENCE A VISION A JOAN, 191 A 1990 ALPHA CITAIN	87.114		L						
NA HIBAN	MA CLASS I USI COMPA I MILLION CONTRACTOR OF THE CHAIN	211.4			H					
1802 HOKA	HEA CLASS HUS CLAREN BELLIT ANTICEN STORE ALL CHAIN	Ť	41.10	-	T					
PIBOS HEMAN	HEA CLASS I HOSTOCOMPATIBILITY ANTICEN, B. 11 B. 11 OL ALTHA CLASS	T		-	t	İ				
PIBIO HUMAN	⋍			1	\dagger	1				
PIBIT HOMAN	•	6		+	+	1				
NAMAN SIBIR	+=	76-107		+	1					
	-	84-115		_						
A HOMAN	-	2113		L						
	-	111.78		-	T					
PIB22 HUMAN	IN CLASS INSTOCOMPATIBILITY ANTIGEN, B-13 B-1302 ALTHA CHAIN				t					
PIB23 HUMAN	ILLA CLASS I HISTOCOMPATIBILITY ANTIGEM, B-33 B-3303 ALTHA CHAIM		1	+	1	T			-	
P.B24 HUMAN	_	1014/		+	1	T				
P.B.S HUMAN	•	2		1	1	Ţ				
PIRZE HEIMAN	ILLA CLASS I HISTOCOMPATIBILITY ANTIGEN, 8-35 0-3506 ALPHA CHAIN	=			1	1			+	
PIRT MINAN	IN A CLASS I HISTOCOMPATIBILITY ANTIGEN, 8-35 8-3507 ALPIN CHAIN	84-115		-	7				-	
MANUAL MINISTRA	+	84-113		-	1	1				
200	LA C. ACC. LUCTOCOLORATINI ITY ANTICEN B.37 B.3701 ALPHA CILAIN	11:11	_							
FIBTS HUMAN	-	13:114								
FIBS HUMAN	7	10.09		L						
PIB33 HUMAN				1	T					
PIB34 HUMAN	HOLA CLASS I HISTOCONDATIBILITY ANTIGEN, B-40 B 4001 ALTHA CHAIN			T	+	Ī			-	
PIB35 HUMAN	HE A CLASS I HISTOCOMPATIBILITY ANTIGEN, B-40 B'400) ALTHA CHAIM		1	+	1	Ī	Ī			
PIBLE HUMAN	III.A CLASS I HISTOCOMPATIBILITY ANTIGEN, B 40 B * 4004 ALMIA CHAIN			+	†					
PIRT HIMAN	۲	84-115		1	1				1	
PIRTO HIDAAN	✝	17-114		+	1					
PIRAC SERVIN	7	84-111		-	1					
NAME IN PARTY	_	11.11								
747	+	117.114							7	
NAVA LITERAL	-	811.98								
NAME AND ASSESSED.	+	87-114		L						
MAN STATE	-	811.9								
	-	84-115		_						
7774	7	87-114		-						
	+	84-113		-	T					
	_	87.114	_	-						
Towns real.	7	17.114		-	T					
TIESS HUMAN	-	13:114		-						
TEN HUMAN	-	13.114		-						
TIES HOME	-+-	211.6		-	T			L	L	
LIBS HOLE	۳	17:114		L	Ī					
A LONG	7	87.114		\vdash	T	ſ				
	-	87.114	-	+					L	
A POR		23:14		\vdash	T			L	L	
NOW (CO)		17.114		<u> </u> 						
NOW HOME		11.114		-	Ī					
NAME AND A	-+	13.114		-						
	_	-		-						
STATE OF THE PARTY	-	17:114		-	Г					
THE PROPERTY OF	7	•		-	İ					
בייייייייייייייייייייייייייייייייייייי	_	\$93-620		-	Ī					
24745		67-73	74.81							·
NAAA HANAN		9.36	41-66 79-106	8	П					
PLABA HUMAN		177-218								
PALL MUMAN		33-66								
	1									

PCCENE	107al78ad Mail Search on All Human Protein Sequences	П	┪	7					1	
EILENAME	PROTEIN	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	9 7:10 1:10 1:10 1:10 1:10 1:10 1:10 1:10	70780	1	1	4			
PAS HUMAN	RUM-ENTITION PROTEIN 4 I LEAVE 4. L'ENVIOLE COMP.	8	\$18-545	-						
PG2 HIBAAN	FINC) (LYMPHOCYTE ACTIVATION	201:102							-	
PSHIE HUMAN	S-HYDROXYTRYPTAMME IE RECEPTOR (S-HT-1E) (SEROTOWIN RECEPTOR)	311:336								
PSHIF HUMAN	5-HYDROXYTRYPTALONE IF RECEPTOR (5-HT-1F) (SEROTOMIN RECEPTOR)	132-353		1	1	1			1	
PSH2A_HUBMAN	S-HYDROXYTRYPTAMINE 2A RECEPTOR (3-HT-2A) (SEROTONIN RECEPTOR)	*			1	1	1			
PSH7 HUMAN	S-HYDROXYTRYPTANINE TRECEPTOR (S-HT-3) (S-HT-X) (SEROTONIN RECEPTOR)	1			1	1		T		Ī
PAIAC HEDIAN	ALPHA-I-ANTICHMADTRYPSIN PRECURSOR (ACT)	T	10-131	$\frac{1}{1}$	1	1				Ī
PAINO HUMAN	ALPHA-1-ACID GLYCOPROTEIN I PRECURSOR (OROSOMUCOID) (OAU)			\dagger	T	1		T	1	Ī
LYIVE HIMON		101	Ì	+	T	T			F	
PAIAU HURAN		T	365.395	+		T	Ī		T	
TALK HUMAN		Т		1	T	T				
PACE POPULATION OF THE PACE POPULATION OF THE	AT BUANDA MACROSCO COLOR TA BRICA CALINACA CALINDA CALINACA CALINDA CA	T	19.140	1065-1112	1403-1420					
777.0	ALTERACE MICE ACT ANY OID AS PROTEIN PLECURSOR (PROTE ASE NEXIN-II)	Ţ	1							
PAACT MINAN	AL PHA-ACTININ O'-ACTIN CROSS LINKING PROTEIN	1	130.747	-					-	
	A COAD ATT AND THE ANCIETY ANTICOMORDAL PRECIDENCE (C. 2 6 1 1)	96.136								
NAME OF STREET		Ť	119.10	2604-2633	ľ		Ì			Ī
NAME OF STREET	-	-	Т						-	
PACIS MUNICIPAL		Т	183.209	668-700						
PACTA MARKAN			Т	313.340						
PACET HUMAN		П		676-710						
PACE HUMAN		683-689	100-137	1250-1284						
PACHA MUMAN		8.10								
PACHE HUMAN		П								
PACHO HUMAN	ACETYLCHOLING NECEPTOR PROTEIN, GANDA CHAIN PRECURSOR		104-33					Ì	1	
PACHO HUMAN	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-4 CHAIN (FRAGMENT)	╛	20.02	1	1	1		1	-	
PACED HUMAN	ACROSON PRECURSOR (EC.) 4.31.10).	11:22	1	+	1				Ī	T
PACYA MOAA	ACTUMOSPILATASE, MUSCLE TYPE (SOCYME (EC.) 6.1.7) (ALTLYNOSPILATE	981 691		+		1		Ī	Ī	
PADI2 RUMA		5	†		T	T			-	
PAK'N WALAN	_	Т	11718	+	T					
PALFA HUMAN	-	T								
PALFO HUMAN	-	19:113								
PANDI KUMAN		99-65				Ī				
PAND) HUBLAN		П	П							
PANON HORAN	ALGNOPEPTIDASE N (EC 1.4.11.1) (MICROSOMAL AMINOPEPTIDASE) (GP150)	492.523	879-89	926.964			1	1		
PANDE HUMAN	ANOHOREGULIN PRECURSOR (AR.)	Т	900		1	1	Ĭ			
AND HOLY		Т		\dagger	T	T	Ī		Ī	Ī
A SECTION AND A	AARVED ANKVERS 1 AND 3 SERVINGOCYTE ANKVERN	117.119	1004-1031 11617-1644	617.1644	T	T	Ī			
PANKE HERAN	ANKYRIN BRAIN VARLANT I (ANKYRIN B) (ANKYRIN NONERYTHROLD)	1544-1571			İ					
PANKC HUMAN		=								
PANDA HUMAN	I ATRIAL WATHURETIC PEPTIDE RECEPTOR A PRECURSOR (ANP.A) (AMPAA) (GC.A)	Ħ	125-652							
PANTE HUDGAN	ATRIAL NATURIETIC PEPTIDE RECEPTOR B PRECURSOR (ANP.8) (ANPR8) (GC.8)	iga iga		+	Ì					
PANTI HUMAN		98.18		1	1					
PANCE HEMAN	ANNEXTA II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHOMOBINDIN 8)			†	1	1	Ī	Ī	T	T
PANCE HUMAN	ANNEXE THE CHOCOLLINE HIS CRACKENIAL AND KNOWN CHOCOLOGY I THOUSE HIS	1	626-653	†	T	T				Ī
A NATIONAL PRINCES		T	3		T	Ì	T	Ī		
PACE HERAN	_	T	2.5							
PAOFE HIDAAN	-	T								
PAPAL HUMAN	+-	33.64								
PAPB HUMAN	APOLIPOPROTEIN B-100 PRECURSOR (APO B-100/APO B-41)		1073-1100	1073-1100 1353-1380 1524-1384 2074-2113	24-1384		1132-2159		1240-1271	2360-2369
		3464-3507	1129-1159 2850-1000	150-3000		3480-3570	1620-3654	4040-4074	4090-4120	4135-4167
		47.44.4301	197-4638	4774-4301 4397-4638 4465-4492 4477-4344	77.6366	1	1]	1	7

PCGENE (167,1784 Maid Search on AN Human Protein Sequences		П		•					\Box	
-	40:	\exists	7	7887	V V V	OREA: OFFA	1	78.77	1	N N N
PAPCE HUMAN APOLIPOPROTEIN CII PRECURSOR (APO-CII)	145.1	T _z	117651	134.061	1795-1822	21.72.2212 2572.2609	1372.2609			
PART HERICAL ABOVE INCREMENTED BESTOR (APO. F.)	-	T	Т	Т						
75		3								
	+	=								
	ACK-1) 323	125-553								
HERAN	69	101				ŀ				
PARNT HIBAAN ARYL HYDROCALBOOK RECEPTOR MUCLEAR TRANSLOCATOR (ARNT PROTEIN) (DIO 213-350	(AUNT PROTEIN) (DIO 223	330								
PAINT HIMAN BETA-ARLESTIN 2.	111	-	05-332							
PAULS REMAN AUDESTON (RETONAL S-ANTIGEN) (18 KD PROTEIN) (S-AG).		194-152				Ì				
	1.1.5) (MINAT) 7-34								1	
PARYS HUMAN ARYLANDRE N-ACETYLTRANSFERASE, POLYMORPHIC (EC 2.3 I S) (PNAT)		П			Ì					
PASKIS HIMAN ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (EC 6.3.5.4) (1511 CELL	_		347.374							
PATCO HUMAN CALCIUM-TRANSPORTING ATPASE SARCOPLASMIC RETICULUM	-	8			Ì					
PATCE HUMAN CALCIUM-TRANSPORTING ATPASE ENDOPLASHIC RETICULUM	=+	0.1.0	1							
	307	017-10				T		Ţ	-	
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		10.00	1						-	Ī
PATER HUMAN INCREMENTATION PACTOR ATTENDED ATTENDED TO THE TAIL ATTENDED		130.161	T				Ī			T
		10.0	T							
7=		1	145.372							
	T	1=								
	Т	1	\$25.562	609-636						
ℸ≂	190	H								
	81	F	10-337	173-107						
	178	178-205								
	13-61	2								
	72.	Ť								1
		7			ĺ				1	
PRIOR HUMAN BONE MORPHOGENETIC PROTEIN 2 PRECINSOR (BMP-2) (BMP-2A)	7	216-230	1				1	Ī		
	4	V. 127	1		T	T	T			T
PRIME HUBANA BURE MUNICIPALIZATION OF PECUNOSA (BRIDA)	7	102.210		Ī		Ī				
	+-	116-31	T							
-	Г	261-195								
Ţ	10-33	"								
	21	2	33.383							
-	16-53	2	1							
-	C.ENETETRAKYDROFOJJO	30.363				Ī				
PCJA HORAN MOR CLASS II HANSACHIVA CHITA	92	20-150	Ī		T		Ī			
_	150	341.368			Ī	Ī				T
-	7-	¥.5								
	+	057-557		Ī		Ī				
_	Г	39-56								
	П	F	133.350							
PCADP KIDKAN PLACENTAL CADIERDIN PRECURSOR (P-CADHERIN).		111	100-085							
PCAGA HUMAN CALGRANGEDN A (AGGRATION DROBITORY FACTOR RELATED PROTEIN 8) (AUV-8)		•								
-	9	П								
_	٦	╗	467-494							
PCAPI HIDAAN CALPAIN (LARGE (CATALTTR) SUBURIT (EC.) 4 22 17) (CALCIUM-ACTIVATED	T	361-361	101							T
PCAZ HUMAN CALTAIN & DAGE (CATALYTIC) SUBINIT (C.) 4.22 17/CALCIDA.		7				Ī				1
		8								
		Ţ.,	163-197	331-355			Ī			Γ
		1	1							

П	nn Frutein Sequences	1 7.197	Chera !	ANGAN ANGAN ARKA		NREA'S AREAG		VIII.V	-!YAKY	AREA .
	CAL RETININ (19 KD CALBINDIN)			}						
PCASB HUMAN BETA	BETA CASEIN PRECINSOR.	3								
	CATALASE (EC 1.11 1.6).	422-456								
	CATHEPSIN D PRECURSOR (EC 1 4 2) 5)	233-202								
	CATHEPSIN H PRECURSOR (EC 3 4.12 16)	29 7								
	CATHEPSIN LIPRECURSOR (EC 3.4 22 15) (MAJOR EXCRETED PROTEIN) (MEP)	٦								1
	CATHEPSON S PRECURSOR (EC 3.4.22.27)	Ī	42-169			1	1	1		
PCBFB HEMAN CCA	AT-BINDONG PRANSCRIPTION FACTOR SUBUNIT B (CBF-B) (NF-Y PROTEIN	7		Ī			1	1		
PCBG HUMAN CORT	٦	7	┪				1	1		
PCBPB HUMAN CARE	ī	П	24-303	36.746					-	
	CARBOXYPEPTIDASE H PRECURSOR (EC 1.4.17 10) (CARBOXYPEPTIDASE E) (CPE)	355.382							7	
	I HOMOLOG (PI-CDC1I) (FRAGAENT)	35-62								
	PROTEIN CICCINIS.	109-140								
	TRANSCRIPTION INTIATION FACTOR THID 250 KD SUBUNIT (TBP-ASSOCIATED	1291-1342							1	
	MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR (MYELOID CELL-SPECIF	•					Ì		.]	!
	I-CELL SURFACE GLYCOPROTEIN CDIA PRECURSOR (CDIA ANTIGEN) (T-CIII.	12-63	101-101						-	
	T-CELL SUIL'ACE GL'YCOPROTEIN CDIE PRECURSOR (CDIE ANTIGEN) (RJGI)	17.104								
	B-LYMPHOCYTE ANTIGEN CD20 (B-LYMPHOCYTE SURFACE ANTIGEN BI) (LEU-16)	336-355								
	CDIO RECEPTOR PRECURSOR	336-355								
•	T-CELL SURFACE ANTIGEN CD3 PRECURSOR (T-CELL, SURFACE ANTIGEN	611.81								
-	HEMOPOIETIC PROGENITOR CELL ANTIGEN CD14 PRECURSOR.	34-108								
-	LEUXOCYTE ANTIGEN CD)?	101-128								
-	OTEIN COJ GAMMA CIIAIN PRECURSOR (T-CELL RECEPT	7.34								
PCDJL HUMAN CDJO	CDJ6 LIGAND (CDJ6-L)	0(1-8	187-213						-	
PODAX HUMAN COM	CD44 ANTIGEN, EPITHELIAL FORM PRECURSOR (CD44E) (PHAGOCYTIC								-	
POP HUMAN T-CEI	I-CELL SUNFACE OLYCOPROTEIN CD4 PRECURSOR (T-CELL SUNFACE ANTIGEN	44.71	40.767				Ī			
PCDS3 HUMAN LEUK	LEUKOCYTE SURFACE ANTIGEN CD33	27:110					Ī		Į.	
PCD72 HUMAN B-CEI	B-CELL DIFFERENTIATION ANTICEN CD12 (LYB-2)	111.177								
PCDK3 HUMAN CELL	CELL DIVISION PROTEIN KINASE 3 (EC 2.7.1)	5-32								
	CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1) (KINASE PSSALRE)	5.33								
	CCATIENHANCER BINDING PROTEIN BETA (CEBP BETA) (NUCLEAR FACTOR	296-330							-	
	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENT-B)	268-393							-	
PODIC HUMAN CENT	CENTROMERE MOTEUN C (CENT-C) (CENTROMERE AUTOANTIGEN C)	✝	T	┱		╗	╗	┪		
PCENE HUMAN CENT	ROMENIC PROTEIN E (CENT.E PROTEIN)			200	713-72				80.00	080
		22-1140	179-1239	1250-1277 1340-1367	740-1367	440-1481	1486-1556	-	1684-1724	200
		ΞŤ	1890-1917	1940	2021-204	200	2478	2498-2363		
PLEASE MUNICIPAL CENT	PLEAU KUMAN (LEKULUTLASMAN PRELURSUN (EL T. 10.3.1) (FEMALASE)	2		Ī				1		
MELL RUMAN CHO	CHOLESTER IL ESTER INVINEER PROTEIN TRECORSOR.	Т	9.0		V44. 1781					
	CTSTILL PIEROSIS TRANSMENDIANE CONDUCTION CENTRAL (CTTA)	314.341	Т	7	27:15					
-	CVCTATHOODING GAMAL YASP (F.C. 44.1.1)	81.31			I		1			T
ℸ	CHA DADECONE REDUCTASE (F.C. 1.1. 225) (CDR.)	13.51		T		Ī			Ī	Ī
-	CHORODERAEMIA-LINE PROTEIN.	Ī	30.257	451-478				T		Ī
	CHORODERAEMIA PROTEIN (TCD PROTEIN)	113.139	Т						Ì	
	SODIUM CHANNEL PROTEDI, CARDIAC AND SKELETAL MUSCLE ALPHA-SUBUNIT	313.614	016-190							
PCICA HIMAN CLAT	CLATIOLN LIGHT CHAIN A (BILAIN AND LYNPHOCYTE LCA)	131-141								
PCICE HUMAN CLA	CLATHBUN LIGHT CHAIN B (BILADN AND LYNCHOCYTE LCB)	137-159								
	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH	9.50								
PCLUS HUMAN CLU	CLUSTERIN PRECURSOR (COMPLEMENT-ASSOCIATED PROTEIN SP-40,40)			367-394						
	П		430-457							
	CILIARY NEUROTROPHIC FACTOR (CNTF).	П								
П	TURIOR-ASSOCIATED ANTIGEN CO-019.		95-148							
Ť	COMPLEMENT CLIPRECURSOR.		20.620	137:867						
_	COMPLEMENT CAPRECURSOR	-1	7	╗						
	COMPLEMENT CS PRECIDENCE	291-142	3	970-997	270-1304		1			
PCO HUMAN CON	CONTRIBUTE OF PRECIMENT	196.366	T	T	Ī	Ī	1	1	1	T
			1	1		1	1	1	1	7

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	PROTEIN	13.180	т	Т						
PCOXI HUMAN CY	CYTOCHROME CONIDASE FOLITE (100 CON CON CON CON CONTROL CON CONTROL CON CONTROL CON CONTROL CO	Ī.	146-373							
_	COTOCURORIE PAGE INC. 1 A 14 11 (PASO 254C) (FRAGACINI).	109-136							-	
	CONTINUED A SOUTH OF THE THE PASSON ETHANOL PROUCHE.	221-258						1		
-	CARRAMONT, PHOSPHAYE SYNTHASE (ANMONIA) MITOCHONDRIAL PRECURSOR	771-211	420-447				1			
	ANTIOCHONDRIAL CARNITING PALMITOYL TRANSFERASE II PRECURSOR	410-437	•							
		126-257					1			
	CYTOCHIONG PASO XIXAI (AROMATASE) (EC 1.14 14 1) (ESTROGEN	124-221	,							
STATE OF THE PERSON NAMED IN	MAPHEMENT RECEPTOR TYPE 1 PRECURSOR (CR.) (COMPLEMENT CID RECEPTOR)	101-986								
A TAINING	Γ	-	379-420	633-678	724.754	163.790				
The same of the sa	CAL THE SECONDER OF PLACE THE BEATTERNY A AND B (CREB.A AND CREB.B)	24:125							^	
	Γ	310-414								
	CAMP ALESTON SECTION DESCRIPTION OF THE COMPANY OF	6.63	200							
┪	CALACITY FACTORSOR	116.106	İ	Ī	:		: :	:	: •	
-	CLEAVAGE SIGNAL-1 PROTEIN (C3-1)	9	Ī							
	ACROPHAGE COLONY STRUCTATION PACTORS PRECORSON (1-317) (FILLS)		Ť	Ī					-	
	CLEAVAGE STIMULATION FACTOR, 30 RD SUBORT (LST) 78 RD SUBORT (LST)			I					.	
	ALPHA-CATEMIN (CADILEMIN-ASSOCIATED PROTEIN)									Ī
_	ALPHA-CATENIN KELATED TRUIEIN (LATENIN ALTINA)						Ī			
-	GAP IUNCTION BETA-2 PROTEIN (CONNEXIN 16) (C.XIO)		Ī						Ţ.	
	GAP JUNCTION BETA-I PROTEIN (CONNEXIN 12) (LA11) (UA) JUNCTION (CAN)			Ī						
	GAP RUNCTION ALPHA-4 PROTEIN (CONNEXIN 37) (CX37)		Ì							Ī
	CYTOCHROME BS	,	131.761	149,104						
	GUANYLATE CYCLASE SOLUBLE, BETA-I CHAIN (EL 40 I 3) (10 KD CHAI.1)	T.	T	2						
	JANYLATE CYCLASE SOLUBLE, ALPHA-2 CHAIN (EC 4 6 1 2)	3	1						-	
	RETINAL GUANYLYL CYCLASE PRECURSOR (EC 4 0 1.1)	160.00	1							
	CYTOKINE RECEPTOR COMMON GANDAR CHAIN PRECURSOR (GANDAR-C)	271.62	1							
_	CYSTATIN A (STEFIN A) (CYSTATIN AS)	7	760	107 301	101					
	PROTO-ONCOCENE DBL PRECURSOR (CONTAINS MCP.2)	٠		3						
	DESMIN	•	7				,,,,	937	100	410.474
PDESP, HUMAN DE	DESNIOPLAKIN I AND II (DPI AND DPII) (FRAGAENT)	2		11.740	704-7	т.	/01/10	200	20	200
		<u>.</u> T	+	430-146	130					
PDHAN HUMAN A	DHAP HUNAM ALDEHYDE DEIYDROGENASE, DINEIUC MADY-PREFERUNG (EC. 1.2.1.5)	7			98. 198	1001	0101 1010	8641 1061 0101 1101	1344 1364	1414.1474
ום אאאא שאמא	DYSTROPHEN		1:					1017 101		
ĺ		ê	200	1017-1167			9CA7-71A7		****	
	DNAJ PROTEIN HOMOLOG	97.6	141	211 710						
	DNA LIGASE I (EC 6 1.1.1) (POLYDEUX YNUBUNULLEUT WE STRITASE (ATT))		15	100]]	
	DNA POLYMORASE ALPHA (EC 2.7.2.7)	230.3%								
-	DIVA POLITICACIONE DE LA CATALLITA CANANTACA ALTA C	2	114.148							
NAME AND AND AND AND AND AND AND AND AND AND	DOTE THE TENT DAYS IN (SE 24 IN 2) (SEC. 1.2) INDIASED	-								
TO THE PARTY OF	DECAMPANT IN TAMB PRECIDENCE DESMOSOWAL CLYCOPROTEIN II AND III)	101-01	355.398							
TOTAL PROPERTY.	DESCRIPTION I PRECIDENCE (DESMOSOMAL GLYCOPROTEIN I) (DGI)	3	271.298	105.79						
-	DESMOCHEN SPRECYTISON (130 KD PENDHIGUS VOLGANUS ANTIGEN) (PVA)	211.248	328-352							
-	DIVERGENT UPSTREAM PROTEIN (DUP)	\$84-618								
-	V-ERBA RELATED PROTEIN EAL-I.	533-550								
-	EBV-DOUCED G PROTEIN-COUPLED RECEPTOR 2 (EBI2)	44.78								
•	ELONGATION FACTOR 1-BETA (EF-1-BETA)	105-132								
-	ELONGATION FACTOR 1-DELTA (EF-1-DELTA).	84-118								
-	EPIDEBLAAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	6-9	440-467							
	EPIDEBLAL GROWTH FACTOR PRECURSOR, KIDNEY (EGF) (UROGASTRONE)	47.74								
PELFI HUMANI E	ETS. RELATED TRANSCRIPTION FACTOR ELF-1.	551-588								
	ENDOPLASMIN PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (GP96	47.74	246-273							
	RETROVINUS-RELATED ENV POLYPROTEIN	362-470								
	IG EVSILON CHAIN C REGION.	=								
	EPOACOUPHON	79-65	٦,	107-407						
PEATS HOMEN	PROTEIN DISCLANDE ISOMERASE-MELATED PROTEIN PRECURSOR (E.V. 1)	360 330								
PERCI MIDANN	PERCI HOMAN DNA EXCISION REPAIR TRUISIN ERICHI	2								

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PERCE HIMAN	EXCISION REPAIR PROTEIN EACC-4	202.09								1
PESTA HUMAN		П								
PETS HOMON	ENDOTHEL DK-2 PRECURSOR (ET-2)	133.160							-	
PETJ HUMAN		183-309								
PEVZA HUMAN	_	П								
PEZRI HUMAN		119-146	151.392	402-429	112.539					
TAS HOUSE	COAGULATION FACTOR V PRECURSOR	1103-2137								
PPAB HCMAN	COAGULATION PACTOR VIU PRECURSOR (PROCOAGULANT COMPONENT)	971-908	1007-1034	1194-1330						
PIAS HUMAN	_	271-298								
PFABI HUMON	FATTY ACID-BINDING PROTEIN, INTESTINAL		\Box							
PFASA HUMAN	APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS PRECURSOR (APO-I ANTIGEN)		106-92	106-111					_	
PFCE3 HUDALAN	LOW AFFINITY INDAUMOCLOBULIN EPSILON FC NECEPTOR (LYAPHOCYTE IGE	\$11-18								
PECEA HIDAAN	HIGH AFFINITY DOMINOCLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (FCENI)	140-134								
PFGRU HUMAN	FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112)	310-337								
PFIBA HUMAN	-	31:165	137-129						1	
PFIBB HIDAAN	-	911-611							-	
PFIBG HUMAN	FIBRINGGEN GAMMA-A CHAIN PRECURSOR	19-61	23:160						-	
PERH HUNAN		19.93	25.160		Ī	Ī	Ī	Ī	-	Ī
PEDIC HUMAN	FIBRONECTIV PRECURSOR.	2168-2199							1	
PFLLI HUDGAN		173-209					T			Ī
PENADO HUMAN		Т	356.203	301-328		T	T	Ī	Ì	
PFOS HUMAN	PIS-C-FOS PROTO-ONCOGENE PROTEIN	Г	T				İ	T	Ī	
PETAL HUMAN	FOS-RELATED ANTIGEN 1.	133.160	Ī	Ī	Ì	Ī	T	T	T	T
PETAS HUMAN	FOS-BELATED ANTIGEN?	149-110	ľ	Ī	İ	T	Ť	Ť	Ť	
PERCH HURSY	FERNITIN IGAVY CHAIN		Ī	T	T	T	T	T	+	T
PERT HIMAN		1	Ī	T	T	T	T	T	1	Ī
PESHON HUDALAN	OULICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH.R.)	364.395		Ī	T	T	\dagger	Ť	†	T
PEUCO HUMAN	ISSUE ALPHA-L-PUCOSIDASE PRECURSOR (EC.) 2 I SI) (ALPHA-L-FUCOSIDASE	308-335	T	Ī	T			Ī	1	T
PICKEL HUMAN	UMARATE HYDRATASE, MITOCHONDRIAL (BC 4 2 1 2) (FUNIARASE)	124-451	Ī	T	T	T	T		T	
PCOS1 HUMAN	NTATIVE LYMPHOCYTE GOGI SWITCH PROTEIN	36-63				Ì		İ	T	
POINT HUMAN	PROTEIN KINASE C SUBSTILATE, 10 KD PROTEIN, HEAVY CHAIN (PKCSH)	166-173	l		Ì				+	
POSPI HIDAAN	GLUCOSE 4-PHOSPHATE ISOMERASE (GPI) (EC 3) 1.9) (PHOSPHOGLUCOSE	16.30				T				
PG712 HUMAN	MAJOR GASTRODYTESTINAL TUMOR ASSOCIATED PROTEIN GATIL 2 PRECURSOR	111.315								
POAI2 HEREN	GALACTOKINASE 2 (EC 2.7.1 6).	154-201								Ī
PGAA! HEDAN	GANDIA-AMINOBUTYTUC-ACID RECEPTOR ALPHA-I SUBUNIT PRECURSOR (GADA(A	110-117								
POAL HEBRAN	GANDAA-AMDIOBUTYTUC-ACID RECEPTOR ALPHA-) SUBUNIT PRECURSOR (GABA(A)	311-255					İ			Ī
PGASR HIDWAN	GASTRINCHOLECYSTOKIND TYPE B RECEPTOR (CCK-8 RECEPTOR)	38.108				Ī		T	T	Ī
PCB01 HUBCAN	GUANDAE MUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT I	22.49			-					
NO HELEN	GUANDE NUCLEOTIDE BINDING PROTEIN G(O), ALPHA SUBUNIT 2	33-49								
PGBAK HUMAN	GUANDÆ NUCLEOTDE-BRODNG PROTEIN G(R), ALPHA SUBURIT (G(I) ALPHA-3)	22-49								Γ
CBAS HERAS	GUANINE NUCLEOTIDE BINDING PROTEIN G(S), ALPHA SUBUNIT (ADENYLATE	7.34								
MODAY HUMAN	GUANINE MUCLEOTIDE BINDING PROTEIN G(Y), ALPHA SUBUNIT (ALPHA-11)	95-133								
PCBB) HOLLY	GUANNE NUCLEOTIDE-BINDING PROTEIN G(INGS)G(T) BETA SUBLINIT)	┪								
TOWAY.	GUANGE NUCLEOTIDE BINDING PROTEIN BETA SUBUNIT LIKE PROTEIN 12.)	7	~ ??	38.38						
TOPICS HONOR	INTERPERON-INDUCED GOANTLATE-BINDING PROTEIN 2 (GUANINE NUCLEOTIDE.	22.486					_			
KORIZ HOMAN	GUANDAE NUCLEOTUDE BUNDUNG PROTEIN G(T), ALPAA-2 SUBUNIT (TRANSDUCIN	╗	7							
NOW HOW I	GC-UCH SEQUENCE DNA-BINDING FACTOR (GCF) (TILANSCHIPTION FACTOR 9)	_	29.330	167.3%	96:433	647-674				
MUNICAL MUNICAL	UIP CYCLOMYDRUCASE I (EL 1.3.4.19)	165.182	1	1	1					
PCCA HUMAN	CENTROCATION RECEPTOR ALTRA (GR)	167.194	1	1	1					
NAME OF THE PARTY	CONTRACTOR MELETION BEING (CA)	Z	1	1	1	1				
TOWN TOWN		460487	1				Ī	H		
POOL ROMAN	The state of the s	9	1							
NAME OF THE PARTY IN	CELECULAR FIRM A ACTOR PROTEIN ASTROCCTE	Ť	7							
PGI 65 MINAN	N.ACETYL CLIPOSAMOVE ASID EATASE PRECINCOLOGICAL INTRASS.	1	9.7.9							
POLPK PORKN	GLYCEROL KINASE (EC 1.7.1.30) (ATP. GLYCEROL 3-PHOSPHOTIKANSFEIASE)	7	311.331	T	†	†	†	†	1	T
PGLY: HUMAN	SEALME HYDROXYMETHYLTAAMSFEAASE, CYTOSOLIC (EC 2.) 2 1) (SERINE	Τ	16.30	T	\dagger	\dagger	†	†	1	T
		1		1	1	1	1	1	1	7

PCGENE	1671.18ad Motif Search on All Human Pratein Sequences	7 1 7 10 7	ARFAI	AREA 3 AREA 4	4 AREAS	_	AREA! ARE	AREA? AP	AREAL	AREAS
FILENAME		Т		_		J		1	+	
POL Y2 HUMAN		Τ	\$61.05				1	+		Ī
PURTH MUNAN		143-169	341-368		1	+	1	+	1	
MINA MUMAN		П	91.68		+	+	+	\dagger	1	
NAME OF TAXABLE PARTY.		128-155		1	+	1		\dagger	\dagger	Ī
NAME OF TAXABLE	CATHER THINNE C. TRANSFERASE HA SUBUNIT 2 (EC 2 5 1 18) (GTH2) (CLASS-				1	1	1	†	T	
		434.501	1012-1047		1	$\frac{1}{1}$	1	\dagger	1	Ī
MILL MUNICA		174-301					1	1	İ	!
MUMAN		173.200			<u> </u>					
POTES HUMAN	GLUCOSE TRANSPORTER 1778 J. DRAIN.	611.006			L					
POTR4 HUMAN					-					
PHIO MINAN	MS OWN HI	44-14			+		I	t		
NALE AND ASSESSED.	WASTONIS HILL IN	13.104					+	t	1	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	THE ALL AL	101-06						+	1	
MON BINA	HISTORIE HIS CALLED	31.103				_	_	_		
PIEC HIMAN	HISTONE HIC (ML3)	ļ			<u> </u>	<u> </u>		<u>-</u>	i i	
PHILD HUMAN	HISTONE HID (HI.2)	0.0			1				1	
PHIT HIDKAN	HISTONE HIT.	74-103			+			+	•	
HALPEO LITTLEAN	HISTONE H2B 1	20-47			<u> </u>	1	+	1	1	Ī
NAME OF THE PERSON	-+-	20-47			-	1		+	1	
1000	-	30-47			_			1	1	
		142-169				-	-	+	-	
STATE OF THE PERSON NAMED IN COLUMN 1		50-13					-	1	1	
PIGER RUNAY		50-77		_	H			-		
PERSON HUNCAN	MA CLASS II POSTOCOMPATIBILITY ANTICEN, DATA CUANDER CONTROL	110			ŀ		\mid		•	
PHEISO HEBACAN	HLA CLASS II HISTOCOMO AT BULLTY ANTICEN, DAWAY BELA CLASSIVE CONTROL			-	+		ŀ	-	•	
PIEZS HUDAN	HILA CLASS II HISTOCOMO ATIBILITY ANTICEN, SU BETA L'HAUM (PRAGMENT)				+	+		+	-	
PHBGI HUMAN	HEPARIN-BINDING GROWTH FACTOR PRECURSOR I (MBGF-1) (ACIDIC FIBROBLAS)	102-120		1	+		+	t		
PHROT HEDLAN		1			$\frac{1}{1}$	1		t	F	I
PHIRT H DALAN		╗	159.186		1	1	1	1	1	
		264.312			_	-		1	1	
		34-110						1		
A HOUSE		169-196			H					
FIELD HOUSE		67.22			H				-	
THE PARTY	THE STATE OF STATE OF AT BUY CLAIN PRECIETOR (C.) 2 52) (N. ACETYL.	356-383			L	_				
MEXA HUMAN	THE IA-MENUSALUM MASSER ALTHAN CONTINUES OF 121 STANDARD META-	388-415			\vdash		-			
MEXI HUMAN		172.212			L		-			
POCK HUMAN	INCHESTRAL TRANSPORT (STANSPORT)	2.5	ſ		H	L		┝	Γ	
PER HERAY	=1	101,234					\vdash			
THO! HUMAN	_				+		-	r		
HOPE HUMAN		27.2	10.4.00	1437 1444 9319	2714.228A 228	111 3115.015	1117.1144 144	1442.1475	Ī	
PHICK HUDGAN	_							l	Ī	
PHS1 HUMAN		27.7			$\frac{1}{1}$	$\frac{1}{1}$	+	t	T	
PHESS HUMAN		27	240-674		1	1	1	1	1	
PHSER HUMAN		\$ = =			1	+	1	1	1	
PHSFI MBAAN		113-140	168-209		1	$\frac{1}{1}$	+	†	1	
PHSF1 HIDAAN		117-198			1	\dagger	+	†	Ť	
PHY21 HEBAAN	-	67.108			+	$\frac{1}{1}$	1	1	Ť	
PHYST HUDGAN		47.74			+		1	1	1	
PHTEIN NO BALAN		261-289						1		
MAN COLUMN		135-162								
100		53.60			-	-				
A HIPTON		113.210			L	-	-			
PEPS HOMAN	-	351.234			t	-	-		Ī	
PICI HUMAN	_				ł	$\frac{1}{1}$	-	t	Ī	
PICAJ HUMAN	Ī	100 101	170		+	+	+	t	T	
PIDE HUDAN	INSIGEDIA DEGRADING ENCYME (EC.).4.99.43) (INSULINASE) (INSULIN	4/4-304	10.00		+	+	\dagger	t	Ī	
PD41 HUMAN	Н	212-238	122-348		+	+	+	Ť	Ī	
PG48 HUMAN		149-176	Î	_	+	1	ł	t		
PO HOMAN		304-349			+	+	1	t	T	
PUBA HUMAN	-	101-01	200	+	\dagger	\dagger	\dagger	t	T	
PILIA HUMAN	I INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR (IL. IRI) (PRO)	10-110	4.12	1	1	$\frac{1}{2}$	1	1	1	

PCCVNE	Hebrithad Marif Court as All Human Protein Separate				-	-	-	ŀ	
FILE NAME		AREAL	AREAZ	ABEA1 A	AREA 4 AR	AREA S AREAS	A AREA?	ABEAR	ABEAS
PILIR HUMAN	(P10).	437-467						_	
PILIS HUBCAN		159-166							
PILSR HIDAN		17.114			+	-		-	
PEG HUMAN	(B-CELL STIMULATORY FACTOR 2) (BSF-2)	112-139		1			1		
POAL HOMAN	INTERFERON ALPHA, I PRECURSOR	7	Т	Т		+			
THAN HUMAN	INTERPEROMALTINA RECEITOR PRECUASOR (IPN-ALPHA-REC)	1	3	X 125-005	(C. 10)				
PINE LIBRAR	INTERESTINATION DE LA PRECURSON (FIBNOSIAS)	221-1	Ī	1		+	1		
NVV PUPAVA	Т	T	300 310	A14 (4)					Ī
POYSE HIMAN		Ī.	7	No.		1		1.	
PERVO KIBAAN	PAVOLUCIUM	T	111.912	126-361	386-450	+	+		T
PUPIK HUMAN	ID-MYO-DAOSITOL TRISPHOSPHATE 1-KINASE A (EC 2 7 1 123) (TRIOSITOL	т	Т	т		1			T
POPSP HUDAAN	PLASMA SERINE PROTECTS OFFICE IN CHARACTER PRECINCOR (PC)	Ť	106.233	I	+	+			T
PIRRE HOMAN	NATERPHOTORICEPTOR BETTANIDANO PROTEIN PRECINCOS (12/2)	+				-			
PIREZ MINAN	NTEREGON REGIS ATORY FACTOR 3 (185.3)	107,193	1	Ť		<u> </u>	1		_
PITSP HUMAN	23 KD INOSITOL 1 4 STRISPHOSPHATE S-PROSPHATASE PRECURSOR	235.263				1			Ī
PITAS HIBAAN	PLATELET MEMBRANS GLYCOMODEIN IA PRECURSOR IGNATICOLLAGEN RECEPT	Т	600.027					1	T
PITAS HUMAN	FIREOMECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA.E)	Т	1_	765.792				1-	
PITAS HUMAN	INTEGRIN ALPHA 4 PRECIESOS (VIA 4) (INTEGRIN ALPHA-E) (CD49E)	Т	T						
PITAL HUMAN	LEUROCYTE ADHESION GLYCOPROTEIN L'A.: ALPHA CHAIN PRECURSOR (LEUROC	T		795-822				1.	T
PITAN HUBAN	CELL SURFACE GLYCOPROTEIN MAC. I ALMA SUBUMIT PRECURSOR (CR.) ALPHA	Ī	T			-			
PITAV KIRAN	VITE CANECTTAL RECEPTOR AT PILA CERCIANT PRECITACOR CHATECRIA AT PUA. VI	276.96	Ī						
PITE KILLAN	FIRECASECTIVE ECTEVIOR RETA SURFORD PERCHESOR (MITEGRAN RETA. 1) (CD29)	Т	16.18	t	-			1	
PITES HIMAN	Τ	T		l	+				
MANA IN INCAN	BETA.	+		1	1				Ī
PITTE KIBLAN	÷	147.169	T		+				T
PITTH HELLAN		17.7	T	l				-	
PITTE HIDAAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR	۴	101.03		ł	1	1		T
PITTES HUDGAN		Ť		\dagger	1	-			Ī
NAME OF THE	PLEX COMPONENT II PRECURSOR	۲	T.	772.411	-				Ī
PKIC HUMAN		L	T.	Т	428-462			T	Ī
PRICH HUMAN	KERATIK, TYPE I CYTOSKELETAL I) (CYTOKEIATIN I)) (KI))	112-142	Г	Т	-	-			
PRICH HUMAN	KEJATIN, TYPE I CYTOSKELETAL 14 (CYTOKEĀATIN 14) (K14).	133-151	306-335	193-424		L	-		
PKICO HUMAN	KENATBY, TYPE I CYTOSKELETAL 15 (CYTOKENATBY 15) (K15).	(1)-(1)							
PKICP HUMAN	KERATBY, TYPE I CYTOSKELETAL 16 (CYTOKERATIN 16) (K16)	106-339							
PKICO HUMAN	KERATIN, TYPE I CYTOSKELETAL. 17 (CYTOKEAATIN 17) (K17)	П		193.431					
PRICE HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18)	8 PH-68	151-298	337.365					
TKICS HELVE	KERATIN, TYPE I CYTOSKELETAL. 19 (CYTOKERATIN 19) (K19).	7	┪	170-197					
1	LECATION 11 FE I CT 10 MALE 1 (CT 10 CEANIN I) (AT) (CT 10 MALE 1 AL 0)	₹	┪	390-467					
	CALL TO A STATE OF ST		7	461-488	$\frac{1}{1}$	1			
HAVA MANA		77.	60.00	27.48					
PKOCH HIBAAN	80	Ť	1	433,440	+	+		1	
PKICE HUMAN	KENATIN, TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8) (K8).	+	Т	+	+		T		Ī
	KERATIN, TYPE II CYTOSKELETAL 54 KD (KKA KERATIN) (FRAGMENT)	7.7	191-02	217.244		<u> </u>			
	6-PHOSPHOPRUCTOKINASE, MUSCLE TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE)	,			-				
YKIN, HDKN	6-PHOSPHOFRUCTOKDASE, LIVER TYPE (EC 2.7.1.11) (PHOSPHOFRUCTOKINASE	Ħ	128-159			L			
PKARL HIDAN	PROTO-CHOCKENE TYROSINE-PROTEIN KINASE ABL (EC 2.7.1.112) (P150)	\$25-960							
PKAC HEBAN	IO KAPPA CHAIN CREGION.	37.68				H		ľ	
ALAL HOLD	KALLIKANN SYNDKOME PROTEIN PRECURSOR (ADMESION MOLECULE-LIKE X-LINK								
NAME AND ADDRESS OF THE PARTY O	CAMP DEPENDENT PROTEIN KINASE I YPE I ALPHA REGULATORY CHAIN	20.00							
TOTAL MONTH	CAMP-DEPENDENT PROTEIN KINASE TYPE FEETA REGULATORY CHAIN	٦Ť							
PERSON HIMAN	NAME FOR PACTOR KAPPA-B SIBINIT-I NE KAPPA-R PIOS SIRINIT	175.202	180.317	\dagger	+	+	1		T
PKCLE HIDAAN	T	101.101	1	+	+	+			•
PKECK HIDAAN	PRECY HIDAN TYROSDE PROTEIN KINASE ECK PRECURSOR (EC 2 7 1 1113) (EPITHELIAL CELL	164-493	T	\dagger	+	$\frac{1}{1}$	T	†	Τ
PKFER HUMAN		219.246	264.591	\mid	+	\mid	† †	1	T
		1				1	1	1	1

1000	TAXABLE SALE CALLED AND DESIGN COMMERCE		\mathbf{r}		H				1	
FILE NAME	ROTTIN	┚	TVIN	ANIAZ ANIA	ALEAS A	Allen 2	A PER P	4	4	7000
PKFES HUMAN	PROTO-ONCOCENE TYROSINE-PROTEIN KINASE FESTPS (EC. 2.7.1.113) (C-10.3)	208-235	18:31		T	T				
PENT HOACH	MECEPION RELATED IT RUSHING ATTION FACTOR I RECEPTOR PRECURSOR (CSF-1-R)	П					i		-	
PKSYN HUKAN	PROTO-CONCOCENE TYRIOSINE-PROTEIN KINASE FYN (EC 2.7.1.112) (PS9-FYN)	199-233			1		1	1		
PKCPB HUNCAN	COLO-DEPENDENT PROTEIN KINASE, BETA 1502 YAG (CCK) (EC 2.7.1.37)	Z .		+	1	†	1			
PKHEK HUMAN	TYNOSING KINASE HEK RECEPTOR PRECURSOR (EC 2.71.112)		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	431.443	9 089 119	8 914.914	173.800	Ī		
PKIDEH HUMAN	KINESIN HEAVY CHAIN	Т	Т	Т	Т	1				
MKKT HUMAN	KIT PROTOGONOUCEME TTROSINE KUNASE FRECOASOM (CC. 2.7.1.1.1.2).	750	T		T					
PICHET HUMAN	MEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PROTOCOLOGIC	253			T				-	
PKNH HUKAN	KINDOLEK DAW FRELLINGER (ALTHAS: INIOL PROTEINASE INITIALION)	11.100	T		T				_	
KYS HOLV	GALACTOSTITUTARS EXASTATED FADIEIN AUTOMATED PROTEIN KINASE	1	191.225	285.312	T	Ī				
PICHE HUMAN	MENEROPHINDUCED, DOUBLEST RANDED ANA ACTIVATED PROTEIN NIPASE	1	Т		T		ĺ			
PKP78 HUMAN	AUTATIVE SELIME/HOLEUMINE-FROI ELM KINASE F/8 (EU. 4.1.1.)		T		T	T	ĺ		•	
PKPCL HORAN	MOTEDI KINASE C, BIA TYPE (EC. 2.1.1.) (NTAC-ETA) (TAC-1.)	T	208-253		T	T				
E HOME	SERIOR FINE CALLES THE ANIMASE TO LANCE TO SELECT TO THE THEOLOGY	T			T					
PKPY! HUBAAN	TRUVAIR RIPASE MI (MUSCLE) SUCTIME (EC. L	20.20				Ī			-	
PICY HUNGA	TRUVALE RIMARE, MA LOVE I ME (SE S. 13-V)	۽			İ				١	
MONTH MONTH	TRUVALE KINASA, ISOZITME KILECATI. 1995	115.211			T				-	
PICE NUMBER	TACIOCAL COLLEGE TYPOSTAR PINASE REC 2.7.1.1121 (FRACIAL)	153.203								
TALES OF THE PARTY	PROTECTION TO THE PROPERTY OF THE PROPERTY RINASE SAC (EC 2.7.1.112) (160-5AC)	<u>0(1:5)</u>								
NAME OF THE PARKS	I THE RELIANTEDANTIGEN PROTEIN PTO (TO KD SUBUNIT OF KU ANTIGEN)	315.270								
NAME AND	LIFUS KIL ALITOANTIGEN PROTEIN PIG (16 KD SUBLINGT OF KU ANTIGEN)	158.791								
7778 17 3 35 48	PROTECTION OF THE COMPANY PROTECTION KINASE YES (EC. 2.7.1.112) (P61-YES)	t		_					• •	
MANUEL MINAN		Ī	17-144	152-163 21-	214-241	197.424	480-507	\$10-339	-	
ANA LABORA		Γ	114-165	192-343						
MANC MIDAN		Ī	114-165	292-343						
PLAB KIRAN	A (LEUKOCYTE ANTIGEN RELATED) (EC 3 3 48)	Н								
PLA HUDAN	[LIPUS LA PROTEDI (SJOCREN SYNDRONG TYPE B ANTICEN (SS-B))		3.73			1				
PLCAT HUBAN	PHOSPHATEDYLCHOLDVE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3) 43)								+	
PLDIEM HUMAN	LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.71) (LDM-B).	7	02:320		1	1	1		•	
PLDHOM HUMANIL	LACTATE DESIYDROGENASE IN CHAIN (EC 1.1.1.17) (LDH-A)	255-522			1					
PLDLE HUMAN	OW DENSITY LIPOPROTEIN RECEPTOR PRECURSOR.			1	T	1				
PLECH HIDAN		1	,	+	1					
NEW KINAN	P. SELECTIN PRECINSOR (GLANGLE MEMBRIAND PROTEIN 149) (UMD-144) (PADAM)	Ī		-	T	Ī				
M.COLL. MANAN	LACTOYLOLUTATIONS LITASE (EL 4.4.1.3) (METRICALTOANASE)	61.3		1	T	T	T		l	
N PERSON	LEUKARMA INPLICIUAT TACION PRELUNON (LE / DETENDITATION DE	T	232-263	296.354	869-169	134-901	1034-1066			L
	THINKS I AS CASE INVESTOR TO A PRESENTATION OF THE STREET	т		Т						
MANAGE SAT IN	-	305-332								
PLENA HIDAAN	LEUKOTRIEME A-4 HYDROLASE (EC 3.3.2 4) (LTA-4 HYDROLASE) (LEUKOTNIEME		290-324							
PLYA HUMAN	LAMMIN A CHAIN PRECIDEOR.	1311-1345					1965-1999	2026-2059	3091-318	
PLOS RUMAN	LANDRIN BI CHAIN PRECINSOR.			1597-1631 16	1651-1714	1722-1781				
PLACE HUMAN	_	≖া	1517-150		1	1				
PLYON HUMAN		23-65		1		1	1			
PLOXO HUMAN		341-368		1	1	1				
PLOXS, HUMAN		Ž,			1	1				
PLPH HUMAN	-				1	Ĭ				
PLEYB HOMAN	PROTEIN-TYROSINE PROSPATASE BELA FRECUNDOR (EU. 1.1.) 40) (Tir-Bela)	1-	100	\dagger	T					
	-		1997-1961	1071	T	Ī				
NAME AND ASSESSED.	-	44.114	448.480	***	T	T	T			
PLSHOT HUMAN		88-19		\mid	Ī	Ì	T			
NAMO MAAN		185.912								
PAZOM HUMA	NETOCHONDRIAL 2-0XCCLUTABATFAIA TE CARRIER PROTEDY (OCCP)	11-00	_							
PHACE HUMA		992-612		1		1				
PHANG HUMA	NINAMED ALPHA MANDOSIDASE (EC.) 21.1	77]	1	1	1]			

	1071.17414 Metil Scores on An Hember Present Schoeners	7								
	PROTEIN	AREA!	AREAL	243	AREA 4	AREA 4 AREA 2	AREA	AREA	ABEAI	AKEA .
PLANE HIDA MACROP	+		1147-1102	Ī	T					T
	EM).	т								
		408-449			Ī					
PINAX HIDAN MAX PROTED		117-144	l							
PLEASE HUNCA LABALE PA	-	235.288			Γ					
PHORI HUMAN MULTOR	-	\$61.188			Γ					
PACENT, HUMAN MERL IN (Т	332.566							
PLEAD HIMAN MEROSIN	1	11.105	136-173 4	431-458	319-167					
PHONE HUMA METHYL	Т	T	Т	Т						
PROCES HUMANIMOTOTIC		L	319-346 5	\$10-337	\$49.608					
PLO CH HIMANIMELANIN	Т	Т	Т	Т						
PLANT MEDIAN MIXED I		5	121,148	Ī						
TO SECURE	0947	Ť			T			$\left[\right]$		
4		7		1					1	
		1	100							
-	N PRECURSOR.	286-313								
PACIU HIBLAN MEPHASH	M-PHASE INDUCER PHOSPHATASE 3 (EC.1.13.48).	72.99							•	
	DUAL SPECIFICITY MITOGENACTIVATED PROTEDI KDIASE KINASE (EC 2.7.1.) 19-50	£.80							-,	
PAPIUL HUMAN CATION-I	<u>Noependent mannose 4-phosphate receptor precursor (CI Man 4-) (</u>	() 9651-695	2437-2478							
		386.423	507-548							
PHASHER HEIMAN MELANO	MELANOCYTE STDAULATING HORMONE RECEPTOR (MSH.4) (MELANOTAGPIN	31.65								
		Т	230-260	I				Ī		
	DNA (CYTOSINE-SPACTHYL TRANSFEJASE (EC.2.) LID (DNA	T	979-109			Ī		Ī		
-	TIEN	т		Ì					F	Ī
			1	1					-	Ī
7		A C	1	1	1				-	
7	INTEXPERION-REGULATED RESISTANCE GTP-BINDING PROTEIN MXA (INTEXPERON-	Т	1							
	ron reculated registance otp. Bandang protein Nob (ptr. rel a ted) 4		670-607							
MYBA_HIMA MYB-REL	(FRAGMENT).	999-619								
PAYED HUNANIMAPAET		111.11							F	
PANCH HUMA NAME	H-MYC PROTO-ONCOCENE PROTEIN.	Г	413-461	ľ						
PMYC HUMAN MYC PRO		193-422							-	
PMYF4 HUMAN MYDGEN	MYOGENIC FACTOR MYF-4 (MYOGENIN)	119-146							-	
PMYTS HUMAN MYOGEN		121.148	İ	Ī						T
		0-110	T						Ī	T
	ľ	41.70	Ì	T	Ī	Ī	Ī		T	Ì
	MYOSON PERVY CHAIN CARDIAC MUSCLE ALPHA ISOFORM FRAGMENT	Ť	111.71	117.171	314.35	100.114	140.484			T
		T	L	+	161	7		340 1400		
-		:	1	10		2	760		4/8/-74	700-1337
PMYSE HIMAN MYOSIN	PAYSE HIMAN MYOSIN HEAVY CHAIN FAST SKELETAL MUSCLE EMBRYONIC	-				1191-1216 1247 1340 1344-1411	07(1-1740)	1144.1411	1487 1487 1441 1474	1631
		334	3	+				2		
PMYSP HUMAN MYOSIN	PMYSP HIDAN MYOSIN HEAVY CHAIN, PERINATAL CARDIAC MUSCLE GEAGMENT	-	+	141.181	115.377	107-107	(0)	767 785	716 747	30.4 0.10
		<u>_</u>	Ĺ	34		Т	Т	Т	7	
PMYSS HUMAN MYOSDN I	PHYSS, HUMAN MYOSDI HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENT).	T	۳		423-460	468.526	\$11.464	187.579	741.704	100.014
		3	146-873		Г	Г	Т	T	Т	
PMYTI HUMAN MYELDI'I			П							
			394-621 T	205-735						
-	SOFORM	╗								
-	AUTOSOMAL CHRONIC	234-261	310-337							
-	J-PHOX).	Ę								
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7	REUKUPIL AMEN'I IKIN'EL MITROLEM (100 KU MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'IN MEUKUPIL AMEN'I PROLEMIN'I PROL	1	84	1						
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-	APPEAL CAUTEIN) [NP-M)	111.161		213-280	21.31	737.78	927	872-913	1	T
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FILE HAME	PROTEIN		j	50.59	2.0	116-203	1000-1133			
PNKCR HIDANN	MK. TIMOR RECOGNITION PROTEIN (MATURAL AT LEAST CELLS L'ACOMITIES	i	ī						.	
PHOCOA HUMAN	NKG1-A AND NKG1-B TIPE II INTEGRAC MEMBRACHE PROTEINS	l _e	116-1146	1292-1319						
PHOS! HUMAN		+								
PNOSJ HUBALN	Control.									
PATCI HUMAN	SODIUM AND CHEORIDE DEPENDENT GABA TRANSPORTER 1.		ŀ	T						
SASE REFE	WEUROTENSON RECEPTOR (NT-R.)		1		Ī					
PHTSE HUMAN	SODIUM DEPENDENT SENDTONIN TRANSPORTER (SHT TRANSPORTER) (SILTT)		1	T	-	-		!	: !	
PNTTA HUMAN	SODIUM- AND CILLONIDE DEPENDENT TAURINE TRANSPORTER	120-102	1							
PARTY MINIST	MADALIBIOLONGWE OXIDOREDUCTASE CHAIN 2 (EC 1 4 5 3)	7								
TAXABLE STREET	NAPALI (MICENSONE OXIDOREDUCTASE CHAIN 4 (EC. 1.6.5.1)	164-191	172.399						-	
	AND CARACITE COM	tt-73	360-367						I	
	NOTICE TO SECTION OF THE PARTY	462-508								
THE PERSON	NUCLEOCIA (FRO ELPERTOR TYPE 1 MPY1.B) (FB22) (NPYBL)	115-142				į	:			
THURK HUBANA	MINISTER AT THE TACK TON THE TANK THE T	10.00	-		:	i				
POAT INMAN	Continue	10.131	İ	Ī						
POCJA HUMBAN										
POCJB MISKAN	OCTAMER-BROTHG TRANSCRIPTION FACTOR 18 (OCT-18)		1							
POCEL MUNAN	LOWE'S OCULOCEREBRORENAL SYNDROWE PROTEIN	T	107 14.					Ī		
PODE2 HUSAN	LIPOAMIDE ACYLTIVANSFERASE COMPONENT (E.) PRECURSOR OF BILANCHED-CITAL	Т						Ī		
PODES HIBAN	DRINYDROLIPOAMIDE ACETYL TRANSFERASE COMPONENT (E1) OF PYRUVATE	72.99							-	
MANAR MIRAAN	ON ICODENDROCYTE ANY ELIN GLYCOPROTEIN PRECURSOR (OMG)	ε	1							
MANAGE ANDVAN	IN THE SENSITIVE OPERN (BLUE CONE PHOTORECEPTOR PICARENT).	_								
No. of Street, or other Parks	CHEEN CONCINTAR DAYS (CASEN CONE PHOTOMECEPTOR PICHENT)		239-266							
2	THE SENSITIVE DECIMAL TO COME PROTORECEPTOR PICHENT)	611.00	336-266							
NOT SELECT	STATE SECURITY SECTIONS AND SIAI DESCRED IN COUNTY STONE PROTEIN)	339-366							-	
No.	Γ	170.704							-	
NOT HOME	COUNTY PAINTE CALEMAN TELESCOPE AND PROPERTY AND PROPERTY BALLAND	133.307								
POTOC HIDAN	OSTEONECTIV PRECURSOR (BASEMENT PERMENONE FROIE	16.133	186.217	180-317	23.604				-	
DXT HUMAN	OXYSTEACL-BRODNG PROTEIN	150.177								
POYTH HUMON	OXYTOCIN RECEVIOR (UT-4)	159-126	422-449			L				
PPIOT HERAN	RETINGELAS ICOMA ASSOCIATED PROTEIN-LINE TO THE PROTEIN PL	97-61	637-464							
A HOLL	DRA PATINERASE ALTRA MALVAS I PRESIDENTE	298.335							7	
PAS HEREN	PLECKS HUM (FeV)	69.62	10:10						-	
PPCHA HUMAN	THULTI SHIPMAN INTERNATION SECTIONS OF THE VARIOUS PROTEIN	8.2	271-298	361.407						
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PPESA HUBANA	MOSPHATEURONI OF PARAMETERS RECORDING TO THE PERSON	3.10	Т							
TAN RUMAN	ANGLES IIII ANGCAN IN TANIE I SECTION FACTOR	187-187				L				
PPAXS HUBLAN	ALIED BOX PROTEIN PAX-3 (B-CELL ST CLAIR BOS OF BOOK ALCHAIN)	\$99							L	
PDGA HGMAN	A TREE LOCALVED GROW IN PACTOR, A COMMITTEE PRECINSOR (PECANII)	912-319								
PACE ROSE	PATER BOOK BOOK BOOK	142-176								
TATE THE PARTY	-	304-335								
TALL THE LAND	MENSON IN PRECIDENCE (PI) (LYAPHOCYTE PORE FORMOND PROTEIN) (PFP)	411-438								
PORAL LABORAL	IN A TELLET BASIC PROTEIN PRECURSOR (PBP) (CONTAINS: CONNECTIVE-TISSUE	21-55								
PPOCA HIBIAN	FARTEL AGE SPECIFIC PROTEOGLYCAN CORE PROTEIN PRECURSOR (CSPCP)	73.100								
PPCCS HIBAN	LARGE FERIORLAST PROTEOCLYCAN PRECURSOR (VERSICAM) (CHONDROITIN	£.9	130-1417	535.58						
PPGDH HUMAN	(IS-HYDROXYPROSTACE AND DEHYDROCENASE (NAD(+)) (EC 1.1.141) (PCDH)	97-118	-1							
PPODE HIDAN	BETA PLATELET DEMVED GROWTH PACTOR RECEPTOR PRECURSOR (EC 2.71.112)	- -	1	69.40						
PPGDS HUMAN	I ALPHA PLATELET-DEALVED GRÖWTH FACTOR RECEPTOR PRECURSOR	2.2	347.395	100	200	480-1038				Ī
PPGHS HUMAN	(PROSTAGLANDIN OM SYNTHASE PRECIDISOR (EC 1.14 99.1) (CYCLOOXYGENASE)	25.35								\prod
POSI HUMAN	BONEVCANTELAGE PROTEOCLYCAN I PRECURSOR (BIGLYCAN) (PG-S1)	18								
PPHAN HUMAN	픚	236.266					\prod			bracket
PPHS KOKAN	Ρ.	90								
PHIOS HEREN	_	£23								
PPHS! HUMAN	_	9								Ī
PPHS2 HUMAN	-	200				\downarrow				
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-		624-049	172-1003							
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_		146-890								
PPRIS HUMAN VITAMIN K-DEPENDENT PROTEIN S (BLOOD CLOTTING) PRECURSOR		176.766								
<u> </u>	2	39.62								
PPSOR HUMAN PSORTASON		26-59				Γ				
PPSPD HUBLAN PREJACHARY SUNFACTANT-ASSOCIATED PROTEIN D PRECURSOR (PSP-D) (SP-D)	Г	134-151							<u>.</u>	
		(11-98								
-		136-177							-	
PPTICE HUMAN T-CELL PROTEIN-TYROSINE PHOSPHATASE (EC.) 1.3.41) (TCPTP)	1	98-65	131-176							
	OPOLETIC	192-122	512-580						- 4.	
PPTND HUMAN (PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1 3.48) (PTP-2C) (PTP-1D)			310-345							
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PPIXO HUMAN PENTAXUA BALATED PROTEIN PIXO PRECUESOR.	1	101		1						
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PYTEO HUMAN (CTP SYNTHASE (EC 6.3.4.3) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE		613	100-334	T			Ī			
PPZP_HEMAN PREGNANCY ZONE PROTEIN PRECUISOR.			P201-066	6311.8911	1405-1432					
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PREST HIDAAN RESTEN (CYTOPLASMIC LINKER PROTEIN-170 ALPHA-2) (CLIP-170)		100317	333.330	445.477	\$71.619	144.771	714.152	1023-1050	1046-1139	1157.1184
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	605 RIBOSONIAL PROTEIN LV.	36.65	T							
==	SOS ACIDIC MISCOCHALL TRUILLY TO CHICAL A ANTIGEN (SCA)	T	338-365							
┱	SECURO PROTEIN (SOCIALIZATION FOR A ANTIGEN (SS.A.)	192-245								
7	BO KO KO ROJEN (SOCIETY STINDING FOR DISTORDING CIAC) HARBY CLAND HARAP	Ī								
7	REJEKTORENEOUS NICHESAN MEGNOCITO CONTINUE CONTINUE CONTINUE CONTINUE DE PROSENCI PORROLE CONTINUE CON	\$01-528	-							
	HE EXOCEMBED STRONG CONTROL OF THE STRONG CO	630-657								
PROU MUMAN	HETEROGENOUS AND WALLEUTHOUSEN OF	T	665.330	170.904	1314-1341	1331-1394				
	DNA DULET ED MA PULT MELASS II 213 AD POLITICALINE	T	12							
-+	DNA-DIRECTED RNA POLYMERASE II 140 KD POLYTEPTIDE	!		:			:		• •	
PRPD) IILDIAN	DNA-DIRECTED RNA POLYMERASE II 33 KD MALYPEFI IDE								-	
PRUCA HUMAN	RETINOIC ACID RECEPTOR BOXI-ALPHA.	711-752					T			
	RETINGIC ACID RECEPTOR RXR-BETA ISOFORM I	176.40)		; ;		į	1	1	:	-
	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM?	146-423	Ì		1					
PRESTO POPULAR	405 RIBOSOMAL PROTEIN S12	60.17								1
MAAA	ANG BIRDSONAL PROTEIN SIS	14.116								_
т	tor benofines benefits of	2							•	
PKS23 HUALAN	403 AIDCOCATAL TACHER 34.5	14:41		ĺ						
PIST HUNKY	405 KIBUSUMAL PROJEIN SITA	100		İ	i					
PRST HUMAN	405 PUBOSOMAL PROTEIN S7 (S8)		i		!	-			:	:
PRSI_HUMAN	405 RIBOSOMAL PROTEIN SO		1	i	:				1	
PRICI HUMAN	RAS-LIKE PROTEIN TC21									
PRUIA MUDIAN	UI SMALL MUCLEAR MBONUCLEOPROTEIN A (UI SMRNP A PROTEIN)									
PRUZE HUMAN	UT SALALL MUCLEAR NIBONUCLEOPROTEIN B"	┪							9191	8707 1507
PRYM HUMAN	RYANGOINE RECEPTOR, SKELETAL MUSCLE	-	403-575	2	1117-0-1		3	20.07.07		
MANUAL AND	C. IND PROTEIN ALPHA CHAIN	96-21								
301	S AND SET A CLASS	8.5								
PS 108 PUNCA	P-IO FROIEM, BEIN CINNIN	8:11								
75180 HGMAN	S-1900 MOILLY	717								
PSAPH HEBRAN		716 944	T							
PSATI HUMAN	DNA-BDODIC PROTEIN SATE									
PSCCA HIBMAN		601								
PSCF HUMAN	STEM CELL FACTOR PRECURSOR (SCF)	74-10								
PSEM! HUMAN	SEMENOCEL IN 1 PROTEIN PRECURSOR (SGI) (CONTAINS SEMINAL BASIC	8	9						,	
PSEND HUMAN	SENCED IN IT PRECURSOR (SCII)	M.		6	2	276-466				
PSET HUMAN	SET PROTEDY	60	2							
PSG HENEX	SECTIETOGRANTH I PRECURSOR (CHROHOGRANIN B)	6.7								
PSG1 HOLON	SECTIFTOGRAMIN II PRECITISOR (CHROMOGRANIN C)	_	200	26.80						
PSIAL ROBAN	BONE SIALOPROTEIN D'PRECURSOR (BSP II)	T	23:183	236-283						
PSW2 HONS	POSSIBLE CLOBAL TRANSCRIPTION ACTIVATOR SNF 21.	257-72	26.572							
PSINCE HUMAN		3								9366
PSPCA HUMAN		2 2 2	570.621	655.712	9211.0001	1461-1302	AX1.21	7707-924	× 17-07-17	237:077
		7	-1				100			
PSPCB HUMAN		_[316.350	486-520	60.0	101-102	1077-1083	7		1001-1601
PSPILE HUMAN	•	~ 8								
PSR HUNCH	SEXUM NESPONSE FACTOR (SAV)	2.0	480-307							
PSIUM HUMAN	-	9								
PSSRI HUDAAN		219-316								
PSTON MOMAN	ISTATIONEN (PHOSPHOPAOTEIN PIP) (ONCOPROTEIN PIB) (LEUKENIA-ASSOCIATED	47.74								
PSIDS HUMAN	SUCHASE ISOMAL TASE, INTESTINAL (EC) 2 48)/(EC) 2 10)	1748-1775								
PAYER MINAN	SYNAPTOBREVIN I.	19-16								
PAYES INDIAN		14-31								
BEYER LANAN			140-771		L					
Sevel Maria		380-442	206-890							
NAME OF STREET		140-167	130-277							
STATE TO STATE OF THE PARTY OF		497.524	658-685							
NAME OF THE PARK		230-257	413.440							
PSY'N INDALAN		93-127	196-223							
PTZEB HUMAN	THANSCRIPTION BRITISTION FACTOR IE-BETA CHAIN (TFIIE-BETA).	34.								
TAN MUNAN	PTADA HUMAN ITIANSCUPTION FACTOR AT 4 (FRAGMENT)	8 8	£							

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	OTEN TAIL	374.305			Ī		l	Ī	-	
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PIAUZ KUNIAN		20.00	130.357				Ī		Ī	Ī
		316-343								
-	-	61.95								
1	RECEPTOR TYROSINEIPROTEIN KINASE TER PRECURSOR (EC 2 7 1 112) (HITK-4)	144.678	369.996	MO1-10M						:
1=		135-162								
		8.5	123.149	178.236						
Т	1	36.56								
-	ATION FACTOR III)	148-175								
3		148-185					Ī			
	(GLIOINIASTO	241.270			:	!		:	`	
	TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGH 87-114	97.114								
	PROTEIN-GLUTAMME GAMMA-GLUTAMYLTRANSFERASE K (EC 2) 2 ())	\$88-388								
		110-165	284-314						-	
	J.KETOACYL-COA THIOLASE PEROXISOMAL PRECURSOR (EC 2). 1. 16) (DETA-	18-313								
	ITAINS SUBSTANCE P, NEUROKININ A	11:38							-1	
-		626-653								
I		94-125								
	TIVANSDUCIN-LIKE ENHANCER PROTEIN 4 (FRAGMENT)	394-331							1	
i		٦	203-532							
_	C 1 99 1.3).	٦	616-647							
PTPM3 HUMAN	tropomyosin, fibroblast isoform TMJ.	2	82-116	٦		╗				
PTPNIA HUMAN	IROPONIYOSIN ALPHA CHAIN, SKELETAL MUSCLE	3	47.74	91.2	27.1%	19:27	£	1	7	
PTPAGS HADAGN	IRDPOMYOSIN BETA CHAIN, SKELETAL MUSCLE	37.116	193-240						-	
PTPMC HUMAN	FOROMY DISK ALPHA LIMAIN, CALDIAC MUSICLE	,	97.71	117-141	Ī	1		Ì	1	Ī
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1		18-45	247.769							
•	MONE RECEPTOR (TRH-R) (THYROLIBERIN	144-383								
		19-9[
	(SOR (EC 2 7 1 112)	6.93	13.14							
PTRSR HUMAN	MANSFEREN RECEPTOR PROTEIN (TR) (ANTIGEN CD11) (T9)	(12-11)	106-191		1	1				
PISHON HOMON	HYADIROFIN MECETICA PRECURSOR (13H-R)			77.0						Ī
LINE LINEAN	MAINTENANCE TYPINGENESS PROTEIN KINAKE TYKY (EC.) 7 (113)	150-133	Т	1			İ	Ì		
	Ť	648-475		Ī					T	Ī
PUBFI HUMAN	INCLEOLAL TRANSCRIPTION FACTOR I (UPSTREAM BINDING FACTOR I) (UBF-1)	227-254					l			
-	IDP-GLUCURONOSYLTRANSFERASE PRECURSOR, MCCROSOWAL (EC 2 4 i 17)	227-254								
_	SE UFO PRECURSOR (EC 2.7 1 112)	416-522								
		33.793								
_	LAR ATP SYNTHASE SUBUNIT C (EC.) 6 1.34) (V. ATPASE C SUBUNIT)	П	13.63							
-		╗	23.461	11.74		Ì				
		901-61	233.760							
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-	- I) (TREBS PROTEIN)	97.138		T	T	Ī	T	1		
PXPAC HUMAN	DNA-LEPAIR PROTEIN COMPLEMENTING XP-A CELLS (XEXODERMA PIGMENTOSUM) 110-211	Г				Ī	T			
POOCC HUMAN	PYPCC HIMAN IDNA REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGNENTOSUM 134-168	Т	101.728			Ī	T	T	Ī	
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TABLE X

Search Results Summary for PCTLZIP, P1CTLZIP, and P2CTLZIP Motifs

LIBRARY FILE PENV POAMY FENV HVIMA FENV HVIMP FENV HVIRC FENV HVIEZ FENV	401-406 430-463 103-108 445-460	LIBRARY FILE PENV BIVOS	434-460			PENY BIVOS	626-642		
	11-496 19-463- 63-166	PENV BIYOG	434-460			PENY BIYON	626-642		
	11-496 18-453 15-450	PENV BIVOS					A R. A. R. 7.1		
	19-463- 13-198 15-460					PENV BIV27	1/0.00		
	15-188	The BIVA	403	***		PERV FENVI	30-47	630-047	
	15-460	PENV FOAMV	481-480	200.000		PENV PIVPE	781-798		
		PENY HVIKB	752-768			DENN FINED	770-706		
	186-201	PENV HVIMA	437-463			PENV PIVTZ	780-787		
	123-138	PENV HVIMP	163-166			DENV FLVCA	38-66	624-641	
	436-463	PENV HVIRH	44180			BENV EIVÜI	605-622		
	760-765	PENV HVIBI	738-764	j		Tana Tana	A28. A13		
	741.760	PENV HVIBC	186-201			PENV FLVLS	602.610		
	344.784	PENV HV1Z2	123-138			PENV PLVGA	200	100.00	
	279.763	PENV HV1Z3	117-133			PENV FOAMV	/2/2017	2/0//00	
		PENV HV12H	437-463			PENV FBVDA	20-070		
	761-760	DEUN UVSBR	750-768			PENV FBVOB	606-622		
	743-768	LENA HARD	344.754			PENV FBVBM	608-628		
PENV HV28T	745-760	PENV HVZDI	344.36.0			PENV HV10Y	123-140		
PENV JSRV	104-119	PENV HVZGI	20/216/			PENV HV122	410-427		
PENV MMTVB	616-633	PENV HVZNZ	/42-/0/			PENV HV123	164-171		
	616-633	PENV HVZRO	761-788			DENV WYZEA	760-787		
	139-164	PENV HV288	743-758			DENN MICER	900-617		
	139-154	PENV HV28T	746-760			PEROV MICES	601.618		
>	391-406	PENV JBRV	104-110	641-557		DELLA ALI VAV	630-647		
	301-400	PENV MOFF	397-413			TENT MENT	1000		
	301.406	PENAV MCFF3	307-413			PENV MLVCB	200		
1	200	PERV MIVAV	427-443			PENV MLVP6	000-000		
T	200-10	BENY MIVER	422-438			PENV MIVEF	639-655		
9	402-41/	1000 M	425.430			PENV MLVFP	639-656		
	403418	PENY MILVAD	130.463			PENV MIVHO	620-643		
	285-310	PENV MEVMO	377			PENV MLVKI	167-164		
	303-318	PENV MIVHO				PENV MLVMO	629-646		
	283-308	PENV MLVRK				PRIV MIVED	024-041		
	301-310	PENV MMTVB	010-033			BENV MIVEK	624.641		
	286-301	PENV MMTV0	018-033			DENN MANER	170-167		
	208-311	PENV BFV1	994-890			A PACEN	803-820		
	203-308	PENV BFV3L	661-677		-	SEUV ARVI	716-727	067-074	
	288-303	PENV BIVOS	93-109			SENV SEVI	707.724	964-971	
	200-314	PENY BIVMK	139-164	802-810		CONTRACTOR OF THE PARTY	246.783		
	302-317	PENY BIVML	130-164	801-817		TENV BIVE	245.782		
	202-307	PENV BIVB4	806-822		-	TENA STATE	344.341		
	200-311	PENV BIVEP	610-626			PENV DIVEL	360.388		
	288-303	PHEMA COVO	30-62			PENV BIVOS	207.007		
	301.318	PHEMA CVBLY	301-400			PENV BIVSP	08/4//		
	301.318	PHEMA CVBM	391-406			PENV BMRVM	20002		-
	408-313	PHEMA CVBQ	391-400			PENV BMSAV	42.08		1
	200	PARMA CONOC	391-408			PHEMA COVO	30-53	2002	
	784-308	BUENA CVIAR	402-417			PHEMA CVBLY	391-408		
1	700-301	THE PARTY OF THE P	402.418			PHEMA CVBM	391-408		
PHEMA DIBVK	303-318	PREMA CVMB	227.00			PHEMA CVBD	301-408		

				SULLY CAUCE	391-408	Γ
PHEMA MUMPM	133-148	PHEMA LABAN	221-237	CONTO CARRIED		T
PHEMA MUMPA	133-148	PHEMA IABUD	234-260	THE PARTY AND ADDRESS OF THE PARTY AND ADDRESS	106.101	
PHEMA MUMPS	133-148	PHEMA IACKA	234-260	MEMA MANA	220.223	T
PHEMA PITHW	346-360	PHEMA LACKO	231-247	LHEWY IVER	755 535	Ī
PHEMA PIZH	09-99	PHEMA IACKV	230-248	PHEMA INCK	100000	
PHEMA PIZHT	98-90	PHEMA LADA1	234.280	THEMA IACKO	600.000	
PHEMA RINDK	366-383	PHEMA IADAS	237-263	PREMA IACAP	302:316	Ī
PHEMA BV6	7.84	PHEMA IADCZ	234-250	PHEMA IACKO	304-316	
PHEMA AVECM	7.04	PHEMA MOHI	221-237	MEMA MCKB	316-330	T
PHEMA RVSCP	7.54	PHEMA IADH2	221-237	PHEMA LACKV	316-332	T
DUENA AVRIN	7.04	PHEMA MOHS	221-237	PHEMA LADA1	320-337	
THEMS OF CH.	13.67	PHEMA IADHA	221-237	FHEMA MOAS	322-339	
LAKAY CAVI	20.00	PURMA IABME	221-237	PHEMA IADCZ	320-337	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	50.00	PUBLIA IADRO	221-237	PHEMA_IADH1	306-323	
PVFUB VACCO	70.77	PUELLA IADU?	221.237	PHEMA IADH2	306-323	
PVGO1 BPP22	/02-292	FORMA LADIA	217.283	PHEMA LADHS	306-323	
PVGO1 HBVEB	1	7	234.250	PHEMA IADH4	306-323	
PVG01 HSVI1	210-226 210-325	+	200.00	PHEMA IADHO	306-323	
PVG08 BPT4	184199	PHEMA LAENO	727-237	BAIELLA LADUT	20A.393	
PVG07 BPT4	685-900	PHEMA (AEN7	237-263	COLUMN CO	975,430	Ī
PVGOB HBV1	134148	PHEMA LAFPR	230-246	PHEMA IAUMZ	355,335	T
DVOTO RPM2	183-108	PHEMA IAHAL	230-262	PHEMA IADNZ	320-337	T
AVOID 0807A	187.108	PHEMA MAHAN	236-261	PHEMA (ADUS	322-339	1
1000	100.134	PUEMA IAHCO	230-248	MEMA IAENO	306-323	
PVGIO ROVO	00.00	PHEMA IAHC?	230-246	PHEMA_LAEN7	322-339	1
rvala Brr	207.007	BURNA IANCO	230-248	PHEMA, LAFPR	316-332	
PVQ18 BP14	400-403	PACITA LANDE	230-248	PHEMA IAGRE	320-337	
PV0ZB BF14		OUTLA IAVEO	230.282	PHEMA_LAGU2	320-337	
PVG29 HSVII	36.38	PURE INTE	216.252	PHEMA IAGUA	310-336	
PVQ30 BPPHB	11:04	POLICE A LAUNCE	224.283	PHEMA LAHAL	321-338	
PV036 BPOX2	72.37	PREMA MAIN	270.348	PHEMA IAHCO	316-332	
PV036 HEVSA	108-123	THEMA WALE	820.240	PHEMA IAHC7	16-332	Γ
PV037 BPT2	1263-1208	PHEMA IAHLO	276.763	PHEMA IAHCD	316-332	
FV037 HBVII		+	4040404	PHEMA (ANDE	316-332	
PVGSE HØVII	22.37	7	236.363	PHEMA (AHFO	321.338	
PVGEG HBVII	208-283	PREMA LATINO	400 404	OWEMA LANKS	921-338	
PV080 HBVII	102:117	PHEMA IANDA	970.000	PURILA IAHE?	321.338	
PVDE9 M6VII	207-202	Mana astan	220.246	PHEMA IAHLE	318-332	
PV065 HBVII	610-633	THEMA INTO	316.363	PHEMA IANIO	316-332	
FVGB BPH2	234-248	PIERS INTE	200 000	INNA IANNI	321.336	
PV08 BP7ZA	234-240	PREMA IANIE	916,363	PHEMA LANIM	321.338	Γ
PVG9 BPV1R	7//8	PATE TANK	226.284	MAKIN WINK	A15-332	
PVOF BPPHX	234-240	PARENT INTE	226.261	PHEMA LAMPR	316-332	
PVOL2 CVBF	284-278	FREMA IALEN	20000	COURT ALIEN	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
PVOLZ CYTE	204-279	PHEMA IAMAA	233-240	A COLOR AND	025-140	Ţ
PVOL2 CVBLY	264-279	PHEMA IAMAB	238-254	PARMA LANGA		T
PVOL2 CYTH	204-270	PHEMA IAMAO	237-263	PHEMA LANGE	210-22	T
באסוז כאשם	264-279	FHEMA LAME!	237-253	MEMA IAHEW	316-332	
PVGL2 CVBV	264-270	PHEMA IAME2	237-263	PHEMA IANTE	321-339]

			600 000			LUCKY PAINS		
442-467	╗		241:43/	24. 343		PHEMA LANUR	321-330	
440-455	504-519 PHEMA IAMIN		101-48			PHEMA IAJAP	317-334	-
216-233	PHEMA IANTO		237-263			PHEMA IAMAA	319-336	
218-233	PHEMA IAGU7	1	221-237			PHEMA LAMAS	324-341	
1066-1071	PHEMA LARUD		234-250			PHEMA IAMAO	322-338	
1065-1070	PHEMA IABEZ		234-260			DUEWA IAME!	322-338	
1066-1071	PHEMA IASH2		234-260			PHEMA IAMEZ	322-330	
1066-1079	PHEMA IASTA		230-248			DUELLA IALIER	306.323	
1066-1070	PHEMA LATA!		235-261			PUEMA IAMIN	316-333	
701.218	PHEMA IATION		234-260			CASE LA LANTA	322.330	
202.218	PREMA IATKO		233-240			PREMA LANGE	250.23	+
136.400	PHEMA IATKR		230-248			LINE WAY	100 900	-
937 777	PHEMA IATKW		220-246			PHEMIA INDO	10000	
	OULIVI ALIANA		237.263			PHEMA LARUD	320-333	1
427-442	BALLA ALIANA		238.261			PHEMA WAE2	320-337	
440-461	A VMSMA	2001	316.9K4			PHEMA IABH2	321-336	+
70.04	THEMA IAVIA	Ī	216.261			PHEMA LASTA	316-332	
70-04	MEMA LAND					PHEMA LATIKM	320-337	
265-260	PHEMA IAZCO		23.7.20			PHEMA LAUDO	322-339	380-397
268-280	PHEMA LAZHZ		/62-122			PHEMA IAVIT	323-340	
286-280	PHEMA IAZHE	ZX2	221-237			BUELLA 1A7CO	322-330	
268-280	PHEMA IAZUK	(ZUK	237-263			ENERGY 14743	106.123	
248.280	PHEMA BIBAA	KBAA	116-131	296-310		PUENT 14914	206.323	-
AR 380	PHEMA DIGBE	1995	123-130	303-318		PREMA LAGRA	222,230	
207-007	PARTA INRIO	CERC	110-132	293-308		PHEMA IAZUK	346.338	
765-760	DATE OF STREET	NAUN	123-130	301-318		PHEMA MUMPM	101-110	
6.94	TOTAL CHIEF	1997	100-124	286.301		PHEMA MUMPR	101:116	
276-293	LINEMA	200	11011	206.311		PHEMA MUMPS	101-118	
900-016	PHEMA INBUT	MOOF		201.108		PHEMA NDVA	03-110	
743-768	PHEMIA INDHA	NEWK	110-136	200		PHEMA NDVB	03-110	1
901-910	PHEMA INDIB	NO 10	105-124	488.303		PATUA NOVO	93-110	
900-918	PHEMA INBID	NBID	120-130	200 214		BUTUA NOW	03-110	
420-441	PHEMA INDLE	NOLE	123-130	302-317		CLICATE MOVE	02110	-
427.442	PHEMA INBMD	NBMD	113-129	202-307		WIELLA MOVAL	04.110	
498-440	PHEMA INDIME	NOME	110-132	200.311		EACH VENT	91.50	
A21.638	PHEMA INBNA	NBNA	10B-124	200-303		THEM HOLD	01.10	
380-385	PHEMA INBOR	NBOR	123-130	301.316		PUREN NOVI	93-110	
187-202	PHEMA INDE	NBBI	123-130	301-318		STOCKE WILLIAM		
378-303	PHEMA INBOJ	NB9J	119-138	208-313		ACCULATION OF THE PERSON OF TH		
202.200	FKEMA INBUS	NBUS	116-132	284-308		PARMA FULL		
200	INEMA MIBVI	NBV	116-132	206-311		PHEMA PIDB	111120	
200	PHEMA	NBVK	123-139	303-318		PHEMA PISHA	111:128	
2000	BURNA MEYA	MEYA	108-124	286.301		PHEMA PISHA	111:128	
363-380	Marata Adams	Martin	137.148			PHEMA PICHT	111:120	
234.248			97.56			PHEMA PICHU	111-120	
28-40	PHEMA MUMPH	MOMPH	01.75			PARMA PIDAY	111-120	
26-40	PHEMA MUMPS	MUMPS	33-148			DUFLIA PENNA	111.128	
26-40	PHEMA PITHW	MEN	26.380			PACENT PRINT	111.128	
28-40	PHEMA PIZH	PIZH	96-81			PATENTA PATENTA		
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																																															-			
	1													621-638																				803-820	903-820															
06-102	101-20	84-101	64-101	101-101	280-297	280-287	281.208	174.103			209-226	173-180	646-668	109-126	171-168	1252-1260	2072-3000		100	(30-70)	676-682	736-753	736-753	736-753	597-614	607-624	607-624	180.187	100	408-400	401-418	366-382	364-381	245-262	246-262	43-60	61-96	81-98	712-720	712-720	344-361	344.361	12.04	12.04	19.04	10.5	10.00	12-04	280-287	250-287
PHEMA 8V41	PHEMA BV6	PHEMA SVBCM	PHEMA BV6CP	PHEMA BV6LN	PVF05 VACCC	PARTS VACCP	PUTOR VACCV	COURT OFFICE	TANA BOAL	PVPOB VACCV	PV027 H8V8A	PY028 HBVII	PVG39 HBVII	PV043 HBVII	PVG67 H8V11	MAN COM	F10.50	DAGI LIDAL	rval z lavo	PVGLB HOVET	PVOLB HEVE4	PVOLB HOVEA	PVQLB HBVEB	PVOLB HBVEL	PVGLB ILTV8	DVOIR NTVA	TALL BOW	200 C 100 C	PVGLC PAVIL	PVOLE VZVO	PVOLF 6V6	PYOUN HCMVA	PVOLH HCMVT	PVGLH HBV11	PVOLH HISVIE	PVQLI HBV11	PVOLM BUNL7	PVOLM BUNGH	PVOLM PUUMH	PYOLM PUUMB	PVG1M RVFV	PVOLM RVFVZ	PVOIV LASED	DVOLV LARRJ	M.010 1004	PVGLY LYCVA	PVOLY LYCVW	PVOLY MOPEI	PVM1 REOVD	PVM1 REOVI.
																						Ĺ																												204-270
																																														204-279	264-270	204-279	284-270	174-100
																					317-332													143.168			330-346		618.633							174-180	174.100	174.180	174-180	123-138
324.340	374.740	324.340	200		324-340	324-340	324-340	324.340	306-383	7.84	2.04				42.D/	20-41	104	89-104	72-87	169-164	209.228	124.140	100.00	900	11.50	270-280	70-02	20-35	22-37	108-123	284-200	244-260	1244-1260	22.37	246-263	101.117	130-146	287.282	169.178	100.00	201.00	224-240	******	2/-/2	2210-2220	123-139	123-139	123-139	123-139	31-47
DUELLA DITR								PHEMA PISHX	PHEMA RINDK		Į	Ī			2		PVFP2 FOWITY	PVFP7 CAPVK		PVOOT HEVER			MACO HOLL	Valo Have	PVG11 H3VII	PVOR 2 HBVII	PVQ1 SPV1R	PV029 HBVII	PVQB6 BPOX2	PV036 HBV8A	PVCC37 HBVII	PVAA1 HBVII	PVOLA LIRVII	PVORK MRVII	PACE DEVI	SVOKS NEW!	PVORA HAVSA	AVARD LEVIL	AVORE DOVA	TACK DEPAR	PVG/1 MBVBA	PV08 BPPHZ	FVG Brrz.	PV00 SPV1H	PVOF1 IBVE	PVOL2 CVBP	PYDL2 CVBLB	PYOLZ CYBLY	PVOL2 CVBM	PV6[2 CV80
		+						_	-	-										-	+									-	-	+		1	1	+		-	1			1		-		_			_	
	26.40	28.48	26.40	26.40	25-40	26-40	25-40	226-241									_											_		-			-				1				1					_		-	-	
	PVMT2 IALE1	PVMT2 IALE2	PVMT2 IAMAN	PVMT2 IAPUE	PVMT2 IABIN	PVMT2 1AUDO	PVMT2 IAWIL	PUMTS MYXVI																																						-		-		

VANC - 10/20	123-130	174-180	404.47		10000	100	_
1000	08.111	1207-1283			PVMAT MEAB!	31.70	1
		1916-1231			PVMP CAMVC	14/-19	
PVOLZ CVMAS		1124.1142			PVMP CAMVD	167-164	1
VOLZ CVIKAR	449.487	600-610	1274-1290		PVMP CAMVE	147-164	+
Mary Course	440-486	604-618	788-814	1272-1288	PVMP CAMVN		
EVOL 3 CVPRB	210-233	570-592	1050-1066		PVMP CAMVS	147.164	
PVGL2 CVPRM	216-233	676-692	1050-1066		PVMP CAMVE	11.04	
PVGL 2 FIPV	803-819	1277-1203			SAN TINES	186-202	
PVGL2 MV8	1066-1071				DVMAA HPRV4	165-202	
PVOL2 IBVB	1086-1070				BVIJRA HPRVA	174-191	
PVOL2 IBVD2	1066-1071				OVMAA MPRVD	10.0	
PVOL2 IBVK	1055-1070				PVMBA HPBVJ	174-101	
PVGL2 IBVM	1066-1070				PVMSA HPBVL	174-101	
PVGLB HSVBA	701-710				PVM8A MPBVN	11.04	
PVOLE PRVIP	203-216				OVERA MPRVO	174.101	
PVOLB VZVD	622-630				EVMAA MPRVP	185-202	
PVOLC HINDS	476-480				DVALA LIBRAD	186-202	
PVOLC HSVE4	444-460				TANKS AND AND AND AND AND AND AND AND AND AND	19.04	
PVOIC MBVED	427-442				TAMES ALDER	134.101	
PACI C PRVIE	440-401				PVM3A HPBVW		
avole vavo	160-166				PVMBA MPBVY		
SVOI C VOVE	160-166				PVMBA MPBVZ		
2000	79.94				PVMT2 IAANN	ZB-42	-
	19.00				PVMT2 IABAN	28-42	+
Main Heve	100				PVMT2 IAFOW	28-42	1
VOLE PRVM	100	245.280	_		PVMT2 IAFPR	26-42	+
PVQLF BRISVA	200-241	186.280			PVMT2 IAFPW	26-42	1
TVOIS BRBVC	2002	202.202			PVMT2 IALEI	26-42	
PVOLE BRBVR	206-221	097.907			PVMT2 IALE2	28-42	
evale covo	388-414				PVMT2 IAMAN	26-42	
PVOLF HRSV1	205-221	200-200			PUMT2 LAPUE	26-42	
PVOLF HRBVA	206-221	200-200			DVATT (ASIN	26-42	
PVQLF KRSVL	205-221	265.280	-		PVMT2 IAUDO	26-42	
PVOLF HRBVR	206-221	285-280			DVACTO (AWIL	26.42	
PVOLE MEABE	266-302	1					-
PVOUP MEAS!	200-306						
PVOLF MEABY	286-302						
PVOLE MUMPIN	276-292			-			
PVOLF MUMPR							
P MUMP	Γ	276-202					+
AVON BIOVE	273-289						
SVOIS NOVE	T						
	979.980						†
2	237.380	1			- :		
NON TIPM	377.280		-				+
אמר אסאופים	277.280						

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280	280	101	283	371 000-016	816	516	516	756	526	528	371 801-916	371 600-016	Γ	988	420.441	Ī	T		7.00	T		1021-1037	536	207	161	161	205	205	14 132-148	134	134	134	134	134	101	131	308	202	203	398	398	396	966	248		0	0
	1 282-288	176.191	278-203		TH 409-515	T 400-616	TV 489-515	743-760					Γ		T				T				D 621-538	APS 191-207	136-161	135-161	100-206	1 189-205	98-114	118-134	116134	110-134	119134			116-131	09 360-368	VB 187-202	V1 376-383	V69 383-388	V7 383-398	V8 383-398	VBI 383-388		4N 26-40		
PVQLF RINDK	PVGLF RINDL	PVOU TRIV	PVGU VZVD	PVOLM HAN	PVOLM HANTH	PVOLM HANTL	PVDLM HANTY	PVQLM PTPV	PVOLM PUUMH	PVOLM PUUMS	PVOLM SEOUR	PVOI M AFOUR	PVOI IN CITIES	I BYOLD BEV	PVOIN LARGO	0/01 / 1 / 44	2000	1000 N	באקרו היי	PVQLY MOPEI	PVQLY PIARV	PVONM CPMV	PVM3 REOVD	PVMAT MUMPS	PVMAT NDVA	PVMAT NDVB	PVMAT PI2HT	PVMAT BV41	PVMAT BVB	PVMP CAMVC	PVMP CAMVD	PVMP CAMVE	PVMP CAMVN	PVMP CANVS	PVMP CAMVW	PVMP, FMVD	PVM&A HPB09	PVMSA HFBVB	PVM9A WHV1	PVMSA WHV69	PVMSA WHV7	PVMBA WHVB	PVM9A WHV8	PVMBA WHVW6	PVMT2 IAANN	FVMT2 LABAN	PVMT2 IAPOW
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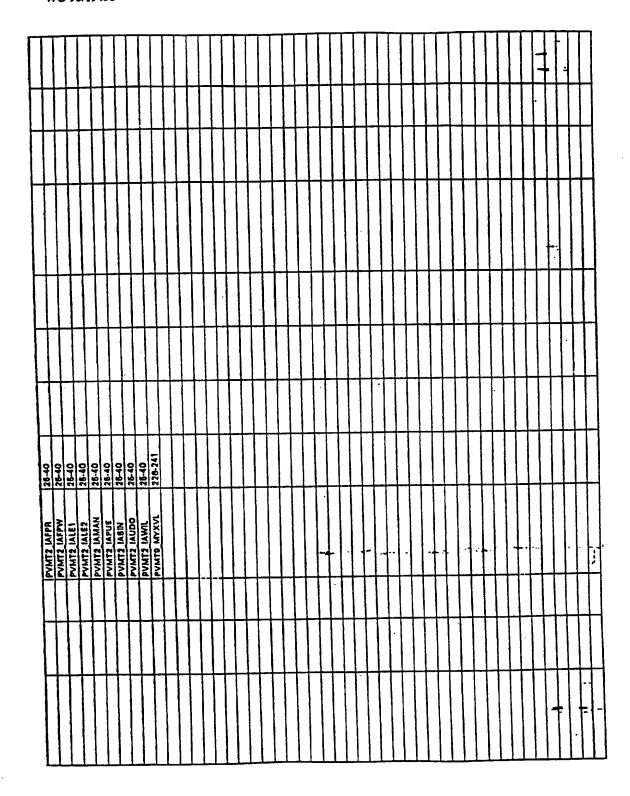


TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP, P5CTLZIP, and P6CTLZIP Motifs

POCTIZIP			PACTIZIP								.:	
LIBRARY FILE		_			•	HEBRITY FILE			LIBRARY FILE			ĺ
			LIBRARY FILE			DESIZE EDED	380-400		PENV BIVOD	47.09	626-640	
DENV RIV27	147.106		PENVI FRSFV	360-366		FENVI CHOLV	200.400		PENV BIV27	47.68	147.160 56	564.575
DENV CARVE	810-828		PENV AVIBU	08.117		PENVZ PHOFY	200		DENV FENVI	226.240	630.061	
DENY CARVO	808.828		PENV BIV27	147-188		PENV BAEVM			PENV 61 VCA	824.645		
ביייי יייישני	7KQ-7AB		PENV HVIZH	1123-142		PENV FIVPE	100.107		DENIN ELVOI	447.488	805.828	
TOYAL AND	741.380		PENV HV2D2	0.20		PENV FIVSD	1/8-1/80		PENY CENT	467.486	625.848	
OZAH ANJA			PENV HV258	778-707		PENV FIVT2	700-000		FERN FLVED	307	100	Ī
PENV HV201	20/.10/		PENV JARV	641.680		PENV FLVOL	0.20		PENV FLVSA	444-400	50.700	Ī
PENV HV2NZ	742.780		PER CONT	K 3 2. KK 2		PENV FOAMV	266-276	924.944	PENV FOAMV	163-174	8/8/98	T
PENV HV2RO	761.769		PENV ROVE			PFINV FSVOA	0.20		PENV FSVOA	467.488	026-040	1
PENV HV258	743-781		PHEMA VACCC	1/3:182		SENV MANCE	420-448		PENV PEVOB	447.460	605-626	
PENV HV28T	746-763		PHEMA VACCI	173.102		TOUR MALE	360.330		PENV PSVSM	460-471	808-828	
PENV JSRV	376-304		PHEMA VACCT	173.102		PENV HVZCA	2/200		PENV FRV&T	467.488		
76.00	118.136		PHEMA VACCV	173-182		PENV MIVED	2		7100	89.33	K10.640 :	
THEMS THE	96.0		PVENV BEV	62-61		PENV MMTVB	043.003		בניין היינים	340.331	-	
PHEMA PIZH	27.01		PUENV MCV1	91.80		PENV MMTVO	043-063		PENV HVZBE			٠
PHEMA BV41	66.73		BVENV MCV2	91.60		PENV OMVVS	76.96		PENV HV201	/41-/07	1	Ī
PVENV THOOV	473.481		PARTIE ABOVE	79.4R		PENV RSVP	42.62		PENV HV2NZ	742-783		
PV010 8PP22	93-101		TANGO COMA	1.00.100		PENV SFVI	024.044		PENV HV2RO	761-772	+	
PV024 BPT4	116.133		PVG01 N3VC0	376 306		PENV BFV3L	921-941		PENV HV28T	746-766	-	
PVG36 H6V8A	344-362		PVGOI VACCE	310.50		DEMY SIVIN	768.786		PENV MCFF	900-621		
PVQ40 HSVII	14-32		PVG01 VACCV	316-334		WALL STATE	74E.786		PENV MCFF3	901-622		
BYOKO MEVEA	16.94		PUDOI VARV	376-305		PENV DIVINA			BENY MIVAV	630-651		
2000	19.0		PVG08 BPT4	627-846		PENV BIVML	5		BEAN MINES	A28.A4A	_	
PVG61 BP 14	200		PVG10 H6VII	36-64		PENV GIVB4	769-769		LENV MLVCB	200	-	
PVGE1 MEVIT	201.3		INSTITUTE	103-122	160.109	PENV SIVBP	773-703		PENV MLVF6	038-000	+	
PV065 HSVII	166-173	- 1	C. 00.00	31.60		PHEMA COVO	403-613		PENV MLVFF	639-660	1	İ
PVOF1 IBVE	2788-2505	33/4.3384	01/00 10/10	059.678		PHEMA CVBLY	391-411		PENV MLVFP	038.000	-	
PVQL2 CVH22	1083-1071		ELAID INA	036.166		PHEMA CV8M	301-411		PENV MLVHO	026-647	-	1
PVQL2 IBV8	1056-1074		PV020 8FT4	231:480		PUEMA CVRO	301.411		PENV MLVKI	107-108		
PVGL 2 IBVB	1066-1073		PY032 VZVD	201.08		PUENT CAUD	101.411	_	PENV MLVMO	059-629		
PVGL 2 IBVD2	1060-1074		PVG36 BPK3	132.161		DISCOURT CANAL	403.433		PENV MLVRD	024.046		
BVGI 9 IRVE	1066-1073		PV037 BPT2	10.38	620.640	PHEMA CVINA			PENV MIVER	024.046		
PVGL 2 IBVM	1066-1073		PV037 8PT4	10.39	929.920	PHEMA IACAU			PENV MSVFB	170-101	<u>-</u> .	
PVOI B MAVAI	660-678	989.707	PVG30 H9VII	1038-1067		FHEMA IADMA			PENV BULEV	803-824	-	
OKON WINDOW	602.710		PUD41 HSVII	62-81		PHEMA MUMPM	1		DENIV ORVI	057.078		
10,00	E84.802		PVO43 BPPF3	360-300		PHEMA MUMPH		-	10000	167.170	054.076	
SACE BOAL	740-768		PVO48 BPPF1	337.350		PHEMA MUMPS	307.417	1	PENY BRANC	41746	-	
באמום וריים	360.700		PVOGO HOVII	142-101		PHEMA PHODV	403-613		PENV BIVA		+	
אמום ורואם	360.388		PVD61 HBVII	117-138		PHEMA PITHW	322-342		PENV BIVAL		+	
אמום ורואו			PVOS7 HSVII	316.337	1072-1001	PHEMA PIZH	13.33		PENV BIVAL	7	1	
PVOIC VZVD	201.16		PVOF1 18VB	1587-1606	2108-2127	PHEMA PIZHT	13.33		PENV BIVAT	430-400	+	
PVOIC VZVS	43)-440		BVAL 2 CVRF	0101-100		PHEMA RINDL	407-817		PENV BMSAV	62-03	-	1
PVOLF PISH4	2.04		1870 - 1018	0101.100		PHEMA SENDS	322-342		PHEMA CVMAS	402-423	+	
PVOLH HEVED	314-332		2007	0101		PHEMA BENDE	322-342		PHEMA IADE1	200-207	-	
PVOLH HBVE4	014-032		PVQLZ CVBLY			PHEMA BENDH	322.362		PHEMA MUMPM	226240	-	١
PVOLH HEVER	807-826		PVQL2 CVBM	0.00		DUFMA MEND	322-342		PHEMA MUMPA	226-240	_	-
PVOLI HSV11	6.04		PVGL2 CVB0	0101-1010		PUEMA BENDY	322.342		PHEMA MUMPS	226-246		
VAN MANOVA	676-696		PVGL2 CVBV	001-1010		CHEMIA BENDA	27.43	146.168	+	213-234		
PVIANI VACCC	134-162	177.186	PVDL2 CVH22	766-787	11116-1134	PVENV LELV	14,77	***	7			

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		370-400	378-400	379.400	379.400			-			+	-	_			-				-	-		+	-	-			J							1										<u> </u>	†		-		463.474
13.34	13.34	7.20	7.28	7.28	7.28	160.160	688.610	314.336	98.99		167-178	268-309	86-106	1165-1170	266-287	30-61	238-269	1866-1877	167.178	200	1400.1400	1268-1260	1269-1200	1269-1260	1260-1200	1269-1280	1317-1338	1266-1288	1170-1187	83.104	100	501.50	20.10	501.68	130-100	440-40/	330-307	224.246	227-240	224.246	440-497	446-467	440-407	306.326	15.4 45.	460-477	460-471	460-471	460-471	405-426
PHEMA PIZH	PHEMA PIZHT	PHEMA 6V6	PHEMA 6V6CM	PHEMA BV6CP	PHEMA SVBLN	PVGO1 MSVEB	PVG01 HEVII	DV034 MAVII	1000 TOOM	- CO.	PVO43 H9VII	PVG56 HSVII	PVG66 HSVBA	PVQ56 HBVII	PVGEB HSVBA	PVG80 HSVII	PVG63 MSVII	BVGE INVE	BYOUR UCINA	TAGES SCHAP	באמרק באפו	PVGL2 CVBLB	PVOL2 CVBLY	PVOL2 CVBM	PVOL2 CVBG	PVQL2 CVBV	PVQL2 CVM4	PVQL2 CVMAS	PVAL2 CVMJH	DVOIR WAVII		אלום שפאלו	PVGLB HBV1K	PVGLB MBV1F	PVQLB MCMV5	PVOIC PHVP	PVOLF COVO	FVOLF MEASE	PVOLP MEAB!	PVOLF MEABY	PVOLF MUMPM	PVOLF MUMPR	PUNIT MIMPS	PACE BUON	FVGLF FRUET	PVOLF PITHC	PVOLF PIZH	PVOLF PIZHO	PVOLF PIZHT	PVOLP PISB
1									000	+										7	378-39B																							T	1					
360-370	298-318	237.267	208.318	11.61	31.61	36.4E	181.171		300 350	040-000	20-40	336-356	117.137	124-144	328.348	127.747	976.946	2000	010.075	327.347	327.347	310-330	732-752	760.770	751-771	70.09	70.00	98.98	29.03	410.000	207.0/7	63-63	738-768	283-303	464-474	464-474	464-474	464.474	464.474	670-680	1326-1346	135C.134K	4.0.	200	000-1010	1000-1020	1001-1001	1001-1021	1166-1170	1000-1020
PVENY THOOV	PVOOT VACCC	BVOOT VACCV	VABV	20047 60070	200 VAND	TVGO CON	1000 POON	VOIS HOAII	PV022 HBVII	PVG38 HSVII	PVGE1 HOVII	PVG63 H9VII	DVCAS MSVII	PVOTA HSVSA	DVC: 9 IRVA	9/10/ 10/10	VOL 4 1970	אחרק ופאחק	PVGL2 IBVD3	PVCL2 IBVK	PVGL2 18VM	PVGL2 IBVU2	PVGLB EBV	PVGLB HCMVA	PVQLB HCMVT	PVOLE HSV23	RCASH SIDA	NAVA MINOS	DAVE BUSINES	2000 0000	PVOLE HSVBZ	PVGLB HBVBA	PVOLB MCMV8	PVGLF PI3H4	PVOLO RABVE	PVOLO RABVH	PVOLO RABVP	PVOLO RABVE	PVOLO RABVT	PVOLH MCMV8	DVOLM RUNL?	NACT A STANSM	TACLE BOTTON	PVOLM BUNYW	PVOLM HANTE	PVOLM HANTH	PVOLM HANTL	PVOLM HANTV	PVOLM RVFVZ	PVOLM SEOUR
٩			. 30. 000	1	7			١		770-789 P	771.700 P	Γ	Γ	T								407.486														_														
B00.1018	0101.000	000./		†	84.83	814-833	814-833	Q	٦	-		T	T	T	100/	10/./00	117.130	266-276	266-285	266-266	3.04	3.04	1	414.466	192.761		64.03	7/8-7/2	11/130	162-171	997-1019	166-174	166-174	830-849	630-649	865-874	60-108	1166-1104	621-640	131.100	146 466	001.00	174.183	174-103	174.103	171.100				
******	CVM4	CVMAB	CVMJH	CVPFB	CVPPU	CVPRB	2		PVGL 2 IBV®		P IBVD 2		YAB.	MARI	PVGLB HCMVA	PVGL6 HCMVI	PVOLB HSV8U	PVGLB ILTV6	PVGLB ILTVS	PVOL8 ILTVT	PVGLC HEVII	PVGLC MSV1K	PVDIC MSVBC	NAID CUAN	שונים משמת	PVDLU NABVO		שאמון אמאם	PVOLM BUNGE	PVOLM PHV	PVOLM PTPV	PVOLM PUUMH	PVQLM PUUMS	PVOLM RVFV	PVOLM AVEVZ	PVOLM UUK	PVOLY LYCVW	PUDNB CPMV	PVM1 REOVD	AND DECK	P.V. C. C. C.	PVME1 CVHZZ	PVME1 CVPFB	PVME1 CVPPU	PVME1 CVPRM	PVME1 CVTKE			 	
	120-144																																		-							_			-	<u> </u>		<u> </u>	-	
	83-101	227.246	227.246	11.02	100-208	100-208	183-201	183-201	183-201	102.501		107.50	163-201	160-106																																				
	,	PVM1 REOVD	PVM1 REOVL	PVMAT HRBVA	PVMAT NDVA	PVMAT NDV8	PVMP CAMVC	PVMP CAMVO	PVMP CAMVE		TVMP CAMVI	PVMP CAMVS	PVMP CAMVW	PVMP FMVD																																				

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	220-261	220-241	460-481	460-461	460-481	460-481	180.481	200	403-4/4	446-407	801.712	600-711	304-326	207.318	666-670	2.23	2-23	107.218	180-211	180-211	103-214	237-269	236-269	99-20	261-302	230-251	189-160	200-221	122-143	64-66	201-222	70-01	244-205	244.288	244-268	233.284	70-01	233-264	233.264	233-264	70-01	233-264	244.256 1	244.208	70-01	233-264	233.964
	PVQUE RINDX	PVOLF RINDL	PVOLF BENDS	PVOLF BENDF	PVOLP GENOH	DVOIR ARMS		LVOIL BENDA	PVOLF 8V41	PVOLF BVB	PVOLH HCMVA	PVOLH HCMVT	PVOLM MBVE4	PVOLH HOVED	PVOLH HBVSA	PVOLI HBV2	PVQLI M9V23	PVOLM BUNDE	PYOLM BUNL7	PVOLM BUNSH	PVOLM BUNYW	PVGLY LABBO	PVOLY LABOU	PVGP8 EBV	PVMO1 VACCC	PVM01 VACCV	PVMAT HRBVA	PVMAT RINDK	PVMAT TRTV	PVME1 CVHOC	PVMBA HPBDB	PVMBA HPBVO	PVMGA HPBV2	PVMBA HPBV4	PVMBA HPBV0	PVM8A HPBVA	PVM6A HPBVD	PVMSA HPBVI	PVM9A HPBVJ	PVMBA HPBVL	PVM9A HPBVN	PVMBA MPBVO	PVMBA HPBVP	PVMBA MPBVR	PVM8A HP8V8	PVMBA HPBVW	WINDS LIBBIA
101-000	926-946	12-32	12:32	13.32	197.19		310-330	309-329	309-320	308-328	312-332	312-332	308-328	306-328	74.04	74.04	74.04	74.04	201-221	209-228	203-313	207-227	212-232	212-232	919.932	212.232	63-63																	:.			_
PVOLM BEOUS	PVOLM UUK	PVOLY LYCVA	PVOLV LYCVW	VOLO BIABV	PVOLT PICATE	PVGNB CTMV	PVMAT MUMPS	PVMAT NDVA	PVMAT NOVB	PVMAT PIZHT	PVMAT PICHA	PVMAT PIAMB	PVMAT 9V41	PVMAT 6V6	PVME1 IBV6	DVAET IRVE	PVME1 IBVB2	PVME1 IBVK	PVMSA HPBDB	PVMSA HPBOB	PVMSA HPBHE	PVMSA WHV1	PVM9A WAVED	PVM8A WWV7	DVIMA WHYA	PVMBA WHVBI	PVM9A WHVW8																				
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233-264	26-46	26.40	26-46	25.40	28.48	26.40	26-40	26.40	26.40	26.40	26.40	26.40																		+				
PVMSA HPBVZ	PVMT2 IAANN	PVMT2 IABAN	PVMT2 IAFOW	PVMT2 LAFPR	PVMT2 IAFPW	PVMT2 IALES	PVMT2 IALE2	PVMT2 IAMAN	PVMT2 IAPUE	PVMT2 IABIN	PVMT2 IAUDO	PVMT2 IAWIL																						
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WO 96/19495 PCT/US95/16733

TABLE XII

Search Results Summary for P7CTLZIP, P8CTLZIP, and P9CTLZIP Motifs

			PACTI 7:P			POCTLZIP				
PZCIIZE	+		LIBRARY FILE			LIBRARY FILE				
LISKANY PILE	100 000		PENVI FRSEV	380-403		PENV BLVAF	303-327			
PENV BAEVIA	202-224		PENV3 CREEV	300-403		PENV BLVAU	303-327			
PENV HVIBI	486.020		DENV BLOA	178.201		PENV BLVAV	303-327			
PENV HVIBB	403-010			00.00		PENV BLVB2	303-327			
PENV HVIBN	484-510		PENV BOALIN	804.687		PENV BLVBG	303.327			
PENV HVIBA	603-626		TENY COMME	176.109		PENV BLVJ	303-327		-	
PENV HVIEL	485-517		FENV NVIAS		301.804	DENV FIVE	781-605			
PENV HV1H2	400-620		PENV HV20E	350.33		PENV FIVED	770-803			
PENV HV1H3	488-820		PENV MVZCA	7/10/	300	SELVY CIVITS	780.804		ŀ	
PENV HVIJ3	610-632		PENV HV201	3.20	5	DUESTA CUBIN	301.415			!
PENV HVIJA	480-612		PENV HV201	58/.2//		LIKE CARL				
PENV HVIKB	604-620		PENV HV2NZ	777-800		PHEMA CVBM	301:410			 -
PENV HUIMA	600-622		PENV JSRV	641.664		PHEMA CVBO	301-410			
200000	48A.K16		PENV BFV1	864-667		PHEMA CVHOC	301-416		1	
LEWA MAIN			PENV 6FV3L	861-004		PHEMA INCCA	442-406			
PENV MVIND	01000		DENV NVM1	603-626		PHEMA INCEN	430-464			
PENV HVIPV	488.970		PERSONAL PROPERTY.	802.825		PHEMA INCOL	430-464			
PENV HV181	7		LENA BIAMIN			PHEMA INCHY	420.463			
PENV HV122		406-617	PENV BIVML	200		PLEMA INC. TH	443.467			
PENV HV128	407-610		PENV BIVSA	879-909		THE PARTY OF THE P	100 163			
DELIV MV178	606-627		PENV BIVSP	610-633		PHEMA INCKY	20-02			
APM MUTAN	406.820		PHEMA COVO	200-223		PHEMA INCM	428-463			
100	474.100		PHEMA PIZH	99-99		PHEMA INCNA	420-463			
PENV Janv	350		MAEMA PIZHT	66-68		PHEMA INCPI	430-464		-	
PENV MIPMV	20000		PVE11 VACCC	101-104		PHEMA INCP2	430-464			
PENV SHVI	213-230		PVB16 VACCC	26-48		PHEMA INCP3	430-454			1
MEMA MAIC	20.75		SAME VACO	3.28		PHEMA INCTA	430-464			
PHEMA IABAN	21:43		שינים השינים	112116		PHEMA INCYA	430-484			
PHEMA IADAS	37.50		FVGIL AMERY	200		PUEMA MIMPM	101-126			
PHEMA IADH2	21-43		W028 HSWI	401.014		SURIAL MINER	101-126			
PHEMA LADHS	21-43		PVG43 HEVII	322-346		PARTY MONTH	101.126			
PHEMA LADH4	21-43		PVG62 H9VII	728-762		PHEMA MUMPS	200			
PHEMA IADHS	21-43		PVG67 HBVII	722-746		PHEMA FILM				
PHEMA IADHO	21.43		EVOL2 CVBF	10-33		PVENV BEV	02-20			
PHEMA IADA?	21-43		AVOL2 CVBLB	661-674		PVF08 VACCC	280-304			
PHEMA IADM2	37.60		PYOLZ CVBLY	10-33		PVF08 VACCP	260-304			-
PHEMA IADMA	28-60		PYOL2 CVM4	1207-1290		PVPOB VACCV	201-100			
PHEMA IADUS	37.69		PYOL2 CVMAS	1216-1230		PVF09 VACCC	1/6-200			+
BURNA IARNA	21.43		PVOL2 CVMJH	1126-1140		PVFOB VACCV	176-200			-
BUCKLA IAFU?	37.60		PVOL2 CVPF8	1274-1207		PV001 VZVD	60-02			-
Called Angel	13.60		PYGL2 CYPU	1272-1285		PVG10 HBVBA	366-370			-
PHEMA IAMAN	23.60		PVOL2 CVPR8	1060-1073		PVG12 HBV9A	GB-02			
FREMA MARE	3.6		PVOLZ CVPRM	1060-1073		PVG16 HBVI1	00-112			-
PHRMA LAMEA			PVQL2 FIPV	1277-1300		PV028 HSVII	173-107			4
PHEMA HIMEO			PVOL 2 MVA	186-219		PVD43 HEVII	108-133			-
PHEMA IANTO	34.75		PVDI 9 IRVB	106.210		PVOB7 HBVII	108-132	1006-1020		-
PHEMA JAOU7	27.72		EVAL 3 IBVD 2	106-210		PVG72 HEVIT	720-744			
PHENA MTM	27.00		A (0.0)	100.210		PVGF1 IBVB	3601-3628			
PHEMA JAUDO	37.68		ירעטול ומביני							

19-60 PV01.2 BVM 18-210					91, 95,	PVal	PVGLB H9VMD	689-613				
19.58 VVGI_2 BVVI 19.210 VVGI_2 BLV1 19.210 VVGI_2 BVVI	PHEMA LAVID 3	8	2	JLZ IBVA		PVG	B RTV6	697-621				
17-89 PVOLIZ BNV13 179-201 PVOLIZ BLV17 413-427 21-43 VOLIZ BNV19 413-460 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 413-460 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 413-460 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIM BLV17 413-47 21-43 PVOLIZ BNV19 12-36 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 413-47 PVOLIZ BNV19 413-47 21-43 PVOLIZ BNV19 A13-47 PVOLIZ BNV19 A13-47 21-43 PVOLIZ BNV19 A13-47 PVOLIZ BNV19 A13-47 21-43 PVOLIZ BNV19 PVOLIZ BNV19 A13-47 21-43 PVOLIZ BN		7.80	<u>∑</u>	11.2 (8VM	20.00	2	SVT II &	100.00				
11-13 PVOIL BIAVI 178-201 PVOIL BIAVI 113-137 17-14 PVOIL BIAVI 178-201 PVOIL BIAVI 113-137 17-15 PVOIL BIAVIA 125-56 PVOIL VIOL VIOL 101-145 17-15 PVOIL BIAVIA 125-56 PVOIL BIAVIA 125-56 17-15 PVOIL BIAVIA 12-36 PVOIL BIAVIA 12-36 17-16 PVOIL BIAVIA 12-36 PVOIL BIAVIA 12-36 17-16		7.60	ĭ ∑	112 BVU1	176-201		200	807.631				
1143 PV011 BIVAT 198.01 PV011 CATA 199.01 PV011 CATA PV011		1.43	Ž	11.2 IBW2	176-201			417.417				
17-56		143	Ž	31.2 IBVU3	178-201		ONCY S	449.403				
1966 PVGLB HCMAT 658.866 PVGLH HCMAA 617.60		7.60	Ž	118 HCMVA	635-568		200	401.426				
Color Colo		996	ž	SLB HCMVT	630-660	2	DATE OF	E24.500				
17-219	Ī	6-07	PVC	DIB HBVBA	483-606		TOTAL ST	677.607		-		
12-34		8.07	Ž	DIB MCMV8	660-660	DA	H HCMVI	100.010	601.633			
17-316	Ī		Ž	DIC HOVII	487.480	0	H HEVII					
17-316			Ž	DIC H9VIK	467.480	PVQ	H HSV1E	443-407	203:02/			
17-339	J			ALC LIEVS	435-460	PVO	M BUNL7	31.66		1		
60.72 FVGLM BUNST 1397-1410 PVGLM HANTH 11-33 FVGLM BUNST 1397-1410 PVGLM RVFVZ 11-33 FVGLM BUNST 1397-1410 PVGLM RVFVZ 11-33 FVGLM BUNST 13-36 PVGLM UNK 10-21 FVGLM LUK 86-889 PVGLM UNK 10-22 FVGLM LUK 12-36 PVGLM UNK 10-23 FVGLM LUK 12-36 PVGLM UNK 10-24 FVGLM LUK 12-36 PVGLM UNK 10-25 FVGLM LUK 12-36 PVGLM CRW 10-26 FVGLM LUK 12-36 PVGLM CRW 10-26 FVGLM LUK 12-36 PVGLM CRW 10-26 FVGLM LUK 12-36 PVMR REOV 10-26 FVGLM REOV 12-36 PVMR REOV 10-26 FVMR REOV 12-36 PVMR REOV 10-26 FVMR REOV 12-36 PVMR REOV 10-26 FVMR REOV 12-36 PVMR REOV 10-27 FVMR REOV 12-36 PVMR REOV		17:338		Never of	436-469	DAd	M BUNSH	31.66			1	
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TABLE XIII

SEARCH RESULTS SUMMARY FOR PIZLZIPC MOTIF

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BOVINE MALYONA VIAUS	21.20		-				i		!
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PCOAT TAMO	GENOME POLITHOTEIN	TAMABILLO MOSAIC VIRUS	221-237		- i					İ	
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POWER EBY	MAJOR DNA-BRODNO PROTEIN	EPSTEIN-BARR VINUS (STRAIN 895-8)	640-673								
ž	MAJOR DNA-ED-DOUG PROTEIN	HICKLAN CYTOMEGAL OVINUS (STRAIN AD149)	481.708								
Product Literal	MAKOB DNA BORDNO PROTEIN	ICAPES SUGLEX VIAUS (TYPE 1/ STRAIN 17)	23.476	\$67.610							
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	DNA POLYMERASE	PSTUIN BARR VIRING (STRAIN DOS B)	1	_	224 342	M7.687	62.62				
	DNA POLYMERASE	FOWL PURIUS	1	10.00							
Poro Toliva	DNA POLYMERASE	HUMANI CYTOME GALOVIRUS (STRAIN AD169)	اء	200	=					i	
PDPOL HEEDS	DHA POLYNG RASE	DAKK HEPATISIS BYTHUS (BPOWN SHANGHAI DIKK ISOLATE SA)	Ī	- ;	\neg	<u> </u>	-				
Dec -	DNA POLYLERASE	DIXCK HEPATHUS & VIRINS (STRAIN CHINA)	1	:	21.50	21:32					
DOG SEDE	DNA POLYMERASE	OUCK HEPA HIS & VIRUS	8	_	-						į
POPOL HOBDW	DNA POLYNŒRASE	DUCK IEPATITIS B VIRUS (WILLE SHANCHALDUCK ISOLATE \$11)	2	21.12	13.54	24.53					
POPOL 18 BCS	DNA POLYMERASE	GROUND SQUIRREL HEPATHIS VIRUS	441.475			_					
POPOL 10 BHE	DNA POLYMERASE	IEROM (EPATITIS IN VIRUS	_						!	<u>.</u>	:
PIDEOL IDBV1	DNA MILYMERASE	INFATITIS DVINIS (SINI) PE AINVI		:	100	:	:	:	:		
PLINCE. IPBV	DEA THE YAGEN SE	INPARING I VIEW NATION OF ALTRA	=======================================		_						
PLYCE CERVA	INA MA YARINASII	IDSPANIES IN VIRIES CALIDIVER, ADMINISTRATIONS	413.414	1.35	26.1 140	•					
_	DEA POLYMERASE	STATES TO VICTOR AND ALPHA IN	ï	106.474	:5	340.346			i	1	!
_	DNA POL YMERASE	TOPATITIS IN VIRGIS (SURE YOF ADM / STRAIN INTONESTAPIDING 200)	Ī	0.41	Ţ	141.376				İ	
	DNA POLYNGASE	TEPATITIS E VIRUS (SUBTYPE ADV.) STRAIN IAPANTIDAY	Ī	10 411	i	161.378					
	DAY BOT VACE A CE	INDATES CONTRACTOR CONTRACTOR SERVICE AND	Ī	. 15	1	7.0		Ī		!!!	:::::::::::::::::::::::::::::::::::::::
1	THE PARTY OF THE	THE PASSES CHARLES OF THE PASSES AND THE PASSES OF THE PAS				- - - -					
	TO SHEET WAS A STATE OF THE PARTY OF THE PAR	THE A LOCAL TO SELECT THE CASE OF THE CASE	i				:		•	:	į
	UNA PULT WELLASE	THE FAILUS & VIRUS (SUBLISHE AND A STRAIN URINAWA/TODOW 201)	ī	10.00		10.77					j
	DNA POLYMEJIASE	REPATITIS B VIAUS (SINBIYPE ADW / STRAIN PRILIPPINGPEDWYM)		3							
- 1	DNA POLYMEJASE	EPAITHS B VIRUS (SINBI YPE ADR)	Ī	410 437	761.778						
	DNA POLYNŒRASE	IEPATITIS B VIRUS (SUBTYPE ADW)		£05.432	440.456					ĺ	
	DHA POLYMERASE	IEPATITIS & VIRUS (SUBTYPE AYW)	2 9	14.41	15:51	7197.00			-		i I
	DNA POLYNEJASE	ICEPATITIS B VIRTIS (SUBTYPE ADYW)	26.02	199.426	434.457				Ī	<u>-</u>	
~	DNA POLYNERASE	HERPES SUPLEX VIRUS (TYPE 17 STRAIN 17)	L	877.897	0001.100	1			İ	İ	İ
1	DHA POLYNGAASE	HERPES SUDIEX VIRUS (TYPE I / STRAIN ANGELOTTI)	ī	177.007	080	-				<u> </u>	i
	DNA POLYKERASE	HERPES SINCHEX VIRUS (199E 1/ STRAIN ROS)	т	111.001	100	İ	Ì		ļ	: -	ì
POPOL HEVIL	DNA POLVMERACE	TERPES SILCH SX VIRIS / TVPF I / CIDAIN (CIA)	Τ	11.69	100	1		i	:	İ	:
	DNA POLYMERASE	HERPES SIACH EN VIEWS (1 VPT 2 / STEAKS 196)	ī	18			1	İ	:	:	•
POPOL INVAL	DAYA BOLL YAKE BAKE	LICEPEC CHAPLE IN VIBILS (FVPE & / CIBAIN INTANA - 103)	Т			Ť			Ī	i	ĺ
POOL INVEN	DAY BOX YAGE A CE	POLITICAL DESCRIPTION OF THE PROPERTY OF THE P	T	ì	1			Ī	İ	İ	
1531	DAY BOX VALEBACE		ī	4	i						İ
POPOL MSVSA	DNA POLYMERACE	TERPERCIENCE CATEAN III	ī	ī	ī	T		1		Ì	
	DNA POLYAGRASE	ACIDINE CYTOMECALOVIBIS (STRAIN SAITTI)	Т	i				Ī	Ī	İ	İ
_	DNA POLYMERASE	LEDROSIS VIRUS	ī	ī	-				İ	İ	
PDPOL VARV	DNA POLYMERASE		Т			Ī	Ī		Ì	İ	
PDPOL VZVD		VARICELLA-ZOSTEA VIRUS (STRAIN DUNIAS)	10:11	16.18	460-463	713.740	157.781	1006-1324			
POPOL WITH	DNA POLYNERASE	WOODCHUCK IEPATIFIS VIRIIS I	146.473		i				İ	İ	
		WOODCHUCK IEPATITIS VIRIIS 59	11715						Ī	ĺ	
	DNA POLYNGRASE	WOODCITUCK IEPATITIS VIRISS 7	117150	İ							
PDPOL WHYE		WOODCHINCK HEPATITIS VIRIES I		356.571						İ	Ī
	DHA POLYMERASE	WOODCHUCK HEPATHIS VIRUS B	451-478								
		WOODCITUCK HEPATITIS VIRUS WEG (150), ATF. PW523)								İ	İ
POPOM HOBIN	잌	IEPATTIS B VIRUS (SUBIYPE AYW)		14.450	750.767						<u>.</u>
_1		HIDAAN CYTONEGALOVIRUS (STRAIN AD169)	107.126		Ī						i
- 1		EQUINE IEARESVIAUS TYPE 4 (STRAIN 1942)	× ×		İ				İ	İ	
_	DUTIPASE	EQUINE HEAPES VINUS TYPE I (STRAIN ABAP)	130-14							İ	
- 1		ICTALUNID HERPESVIPUS I	13.15							<u>i</u> i	Ì
١		PERFESVIRUS SAINIEI (SIEAIN II)	\$	104 104	10.10						!
1		MAJASE ADENOVIRUS 1YPE I	14.47		i						:
_	EARLY ELA 6) NO PROTEIN	HAMAN ADENOVIRIS LYPE 7	3								i
PEIA ALEON		III INDAM ADENDVIALIS 1 TTE 4	2								
L		RUMAN ADEROVIRUS 177F 7	П								
SEIN ACES	EST ELA JUNIO ROLEIM	SOMEON ADDRESS 177E		ž.	-	Ì				ĺ	
1200	The same of the sa	Interest State of the Control of the	1431:463								7

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1	PHCTLZIP	All Virare (No Bacteriophoges)	ī	1		- 17117	ABEAG	ABIA	A BY A V	ABTAL	ANTA
	1	CANNE ANEWOVIDIE 11PF 3	2	ı	7		Ī	ī	Ī	į	7
TELEST ANEX.		TOTAL ADENOVICE	101.52		İ	T			-	-	-
PEIBL AUTH		UTAIN AUCHUMING		Ì	İ	-		Ī	1		
reins Apeca		CANINE ADEMOVIRUS TYPE 2							-	-	1
PESSS ADEM!	EIB PROTEIN, SMALL T. ANTICEN	MOUSE ADENUVIRUS LYPE 1			i	Ī		į			-
PESIO ADEOS	EASLY EID 10 4 KD PROTETN PRECINSOR	INPLAN ADENOVIBLES TYPE, 2	-	3							ĺ
PEJIO ADEOS	EABLY ESB 19 4 KD PROTEIN PAFCURSON	IIMAM ADENOVIALIS TYPE S	=	8					j		İ
FEJIO ADEO!	EARLY EUD 10 4 KD PROTEIN PRECURSOR	RINGAN ADEMOVIALIS 1 YPE 7		!	-				-	-	_ !
PEJII ADE03	8	RIMAN ADENOVIALIS TYPE 1	13.51	7						į	-
PEJII ADEOI		IIMAN ADENOVIAUS TYPE I	19.45							-	_
PEN ADES		INDIAN ADENOVIRUS IYPE S	10.44								
ī	EARLY ED 77 KD PROTEDA	TIMAN ADENOVIRUS TYPE 1	16.62								
i		DAAN ADENOVIALIS TYPE S	20.00			1					:
Ī		DEAN ADENDALIS 1 YPE 1	2.0		:	-			<u> </u>	į	1
ī				-	-				1	İ	:
		HAMAN ADENOVIATION TITE 7		İ		-				1	1
٦		ILIMAN ADENOVIRUS TYPE 1	2		1	-		†		-	!
		HALAN ADENOVIRIIS 17PE 3	96.	į		-					-!
		~	14:15								
Ī		CAMINE ADEMOVIRUS TYPE I (STRAIN GLAXU)	135.177							<u> </u>	
Ī		MOUSE ADENOVIRUS TYPE I	105.131						İ		
İ	PROPAGIE FABILY FA 11 KD PROTEIN	ILIDAAN ADENOVIRUS TYPE 1	10.3	-		-			 	<u> </u>	-
ī	201044 Ca 1 1 1 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	BALAN APENDOLETIC TVPC (15.75				Ī	!		i	!
	THE PARTY OF THE P	COLUMN TO THE PARTY OF THE PART				1	Ī		 	<u> </u>	
7	TAUDABLE EASE, TO 37 R.D. PROJECT	MODEL ADELLO MANAGE & COMP.			1	-		į	-		!
27	EALT IS JUILD TRUILIN				1	Ī				i	1
VEAD EDV		EFSTEIN-BARR VIKUS (STICAIN BY)-II)	97.64		1	-			1		
		EPSTEIN DARR VIRUS (STRAIN 895 6)	-			-	Ī	İ	i		
PERMI ENV		PSTEED DARK VIRUS (STRAIN 841 B)	1		i				i		-
PEBRO EDV		PSTEDI-BARK VIRUS (STRAIN BY) 11	10:01	663.683		_					
PETTI VARV	S C PATE	VALUOLA VIRUS	7								
PENNI FREEV		ALEND SPLEEN FOCUS FORKING VIRINS	100.001			-				İ	
Τ	ENV POLYPROTED PRECIASOR	PAIESTS SPLEEN FOCUS FORMING VIRUS	100.001		i			Ī			!
ī		AVIAN RETROMBUS APL 30	106.333			-	Ī				!
PERIV AVICE	COAT PROTEIN CP12	AVIAN SABCOMA VIRUS (STRAIN (IR.))		Ī	-		Ī		İ	İ	i
ı.	THE PARTY OF THE P	ARCOM SOCCEMENT VIRILE (CITATINES)	Ī,	71.00	-	İ	T	Ì			!
		NOON THE PROPERTY WILLS AND THE TANK	ī		7			İ	 		;
ı		BOARS MANAGER LINE VIEW VIEW AND	Ī	:				Ī	i	i	!
		BOARD INTERCOMMENTAL COLOR OF STATE OF		i	7			Ī		i	
ŀ	EN POLITICISM						Ī		İ		
	CAN CHANGE OF THE PARTY OF THE	COUNTY FINE CALCAST CALCAST AND ASSESSED.			Ī	Ì				İ	i
100	The second second	DOVINE LEGISLA UPING MET CHEN ICOLATE COLORS				İ		Ì	İ	Ì	
	EAV PALITACIENT	TOTAL LECKENS OF SELECTION SOLATER LECKES						1	1	i	
Ī	EN PALITAGIEM	SOUTH LEGACIAN VINOS (SELECTION 130 ACAIS LEGAL)		Ì						-	1
	ENVIOLEM STATES	SOUTH ELONEAUM VINOS (INC. AM 23 ISOLATE BL.V.1)	j	:					<u>-</u>		-
J	ENVIOLENCE CONTRACTOR OF	EL DAS EMPOCEMBLE MINIS EVEL							i	<u>-</u>	:
T	CAN THE VALUE OF THE CONSUM	CLANE CALCACIANTS VIACO FLET		.!	0.00	i	1		-		•
2	EAV POLYROLE OF PRECURSUR	ELING LEUNGAUA PRINCIPLIO (L. L. E. D.)					::		. :	;	:
DA LI NOL	ENV POLYPROTEIN PRECUASOR	ELINE LEUREMIA VIRUS (STRAIM AGILASCOW.)	ī		1 4 7 6 F				-	:	:
מא אנא	ENV POLYPROSEIN PRECURSOR	ELIME LEUKEMIA VIRIS (SIRAIN LAMBOA III)	ī	475 646	j						
YOU ILVA	ENV FOL TPROTEIN PRECURSOR	ELINE LEUKEMIA VIPUS (STRAIN SARKA)		102-623							
TENY TOALN	ENV POLYPROTEIN	o,		22.53	50 00	11.196	110.111		0 150 060	875.978	
PDIV ISVOA	ENV POLYPROTEIN PRECINSOR	333		625.644						- !	-
PERV PSVCB	ENV POLYPROTERN PRECINSOR	EI IME SARCOMA VIRUS (SIRAIN GA)	447.468	929-509						<u> </u>	!
_	ENV POLYMOTERY PRECIASOR	2	Ì	60.00					-	:	: !
	ENV POLYPROTEIN PRECIMSOR	EL DE SARCONA VIRUS (STRAIN SNITTR. 1111, 11 + 11)	467.488		:	!	!	!	<u> </u>	— і	:
PEN OALV	ENV POLYPROTEIN PRECURSOR	IIA VIRUS	20.50	<u>-</u>	!				<u> </u>	:	
	GP140 PRECURSOR	STIENCY VIPIUS	498-520		:	!	i !		:	<u> </u>	
	GP160 PRECURSOR	CIENTY	403 515		:		:	i		i i	•
PENY HYIBN	GP160 PRECURSOR	RAMAN BOMINODEFICIENCY VIRUS TYPE I (DRAIN ISOLATE)	494-516		<u> </u>	İ		1		i	!
PENV HVIBA	GP160 PRECURSOR	INMAN INMANITED BEN'T VIRUS TYPE I (MRIJISALATE)	503 533						<u> </u>		İ

1000	10110741910										
FILE NAME	PROTEIN	Vinite	1			!					
PENV IIVICA	C.P.140 PRI CLIMSOR	TOPIAN INDICATED THE TAX CONT. THE TAX AND TAX AND TAX									•
	Gried PACCURSOR	VIBILIS LYES LO				_					
PENVIN IN	GP 146 PRECURSON	NCY VIRUS INFL	0.0	:		:	:				
	GPI60 PRECINSOR	NCY VIRIS TYPE	458.520		:	!!		! !	<u> </u>		1
	GP166 PRECITISON	VIPUS TYPE 1 (1)	200		-			1			-
	GP 100 PRECURSOR		200	İ		!	-	!	:	:	•
	Chies PRECURSOR	DIEMAN RIMIDMODITIECTINGY VINIS TYPE I SSTRAIN KIT TOP TO	504.55	100	111.76.	•	:		_		
	GP160 PRECURSON	INDIAM INDICHOLLICII NCY VIRIIS IVFI. I (AIA). 15(1), A 11.)	3	:							
	GP160 PAECURSOR	YPE	117.85	İ				-	1	: !:	!
	CP 140 PRECURSOR	HUMAN INDALINODEFICIENCY VIRIS TYPE I (NEW YORK STROLATES)	171.703		-	1			-	-	!
	CPIEG PRECIMSOR	À	9	•		:					i
Į.	Chies precurson	YFE	9		:	-		İ	!	i	;
	OP 100 PAECUR SOR	CHACK VIRING IVE	100		:	i	:	:			
	CP 160 PRECURIOR	THE PROPERTY OF THE PARTY OF TH		-	:	-	-	1		: i	;
	CP 140 PRECISE COL	THE PERSON NAMED IN COLUMN	3		1	4			<u> </u>	1	
PEN INITI	TO SECTION OF THE PROPERTY OF	CHEMICA VIRGIS CAPE		2							
1	Colinor and Colinor	INCREMENDED IN THE PROPERTY OF THE PARTY OF	8			-					
1	Carlot San San San San San San San San San San	1776	3	410-23	21.50						
ı	COLON PARCUASUR	VIRUS 1YPE I	113:13	35.10							İ
1	CATIO PRECURSOR	MARITHODEFICIENCY VIRU	497.519		-				-	İ	1
	CP 140 PRECURSOR	IVPE	\$61.533			-				İ	
. 1	GP140 PRECURSOR	DOMUNODEFICIENCY VIAL	7	100	101 5 20					İ	
PEN HYBE		HUMAN INDRANCOEFICIENCY VIRIIS TYPE I IISOLATE BENI	+-	750 735	8						
		INDIAN BORNODEFICIENCY VIRUS TYPE 3 (1501.ATE CANIZ)	_								
		INDIAN BOMBODEFICIENCY VIRUS TYPE THEOLATE DISA	•	741.766	111.795	-	j				;
•		HEBANN BOARDODEFICIENCY VIRUS 1YPE 2 (150) A 1E DJOS 23	Ŧ			+				:-	
		INDIAN BEADVODE ICIENCY VIRUS TYPE 1 (SOLATE GILANA. 1)	_	171, 304							i
1		INDIAN BACODE POTENCY VIRIS TYPE 3 (1901 A 15 MILL 2)	- 7								-
L		INDIAN DEADWOODERCIENCY VIRUS TYPE 2 JISOLATE BODS	•	3		-			İ	İ	
L		INDIAN BORNODE FICIENCY VIRUS TYPE 1 (SOR ATE CONTINUE)	_	3.70		-			-		
L		HUMAN MORINODE FICIENCY VIRUS TYPE 3 LICOLATE CT.	-					Ì		j	
PENV JEAV	N PRECURSOR	SIGEP PULMONARY ADENDALATOSIS VIRIIS	_	1							
	ENV POLYPROTEIN PRECURSOR	MINIST CELL FOCUS FORMING MINISTER FINE MELLE VIBILE	_			# N					
L	ENV POLYPROTEDY PRECTINSOR	NOR CELL FOCIS FORMAC AND ONE FINERALA VIBILE (150) ATE CT	-							İ	
L	ENV POLYPROTEIN PRECISION	AKVAGANE LEUKEMIA VIRUS		İ	-						
l	ENV POLYPROJEIN PRECINSON	Ī			į	1	İ				i
	ENV POLYPROTEIN PRECINSOR	Ī		-					j	-	į
PENV ME.VEF	ENV POLYPROJEDI PRECIMSOR	FRIEND ARTHUE LEINENIA VIRITS (ISOLATE FD29)	9				İ			1	
- 1	ENV POLYPROTEIN PRECURSIN	FRIEND MURLIE I EUXEMIA VIRUS (1501.A TE PVC. 211)	039 619		- i		İ	1	-	Ì	
PEN NAME	ENV POLYPROTEIN PRECURSIN		676-447		İ	İ				İ	
	ENV POLYPROTEIN	Γ	167.188	İ							
VENT HE WAS	EW POLYMOTEIN PRECURSOR	MOLONEY AIUMNE I EUKEAIIA VIRUS	629-650								Ī
	ENVIOLENT TRECUSOR		624-643								
	ENVIOLENT THE CASON	CAPLAM	624-643								
	ENV TO COROTE OF	PROUSE PROPORARY LUMOR VIRUS (STRAIN BR6)	13463								
T	THE PART OF THE PA	MUDDE PLANDRAKY TURION VINUS (STRAIN GR.)	3							Ī	
PENN MANER	PARTON NO PER	SUMMA MASUR-PPIZER VIRUS	10.235								
1	ENV POLYPROTE TARGET TRACES		20.00								İ
Ī	DAY POLYPROTEIN PRECIPEON		5								
T	ENV POL VPROTEDA	MOUSE CARCOAR SOLLS FOR STANDAR PIROS	601426								
T	ENV BOX VERGIERA	CONTRACTOR VICTOR PRACTICAL	47.49	513-552	П	_					
].	ENV POL VEROLETA	SPACE TO THE STATE OF THE STATE	2	110.71		_	953.938				İ
PAV SIVA		SOUTH POART VINIS (177E) / STRAIN (K.)	22.23	2	301.776	101.181	931.048	934.011			i !
1	GP140 PRECIESOR	COURT DESCRIPTION OF THE PARTY STATES AND ASSESSMENT OF THE PARTY STATES AND ASSESSMEN	7								!
PENV SIVAL	CPIGOPRECURSOR	SOUTH DEPOTE THE PARTY CONTINUES OF THE PARTY OF THE PART	2	!							
1	GP 140 PRECURSOR	7			-						
ı	CP160 PRECIENCIA	Т									
1			6		7						

PCGENE	PIICTLZIP	All Viruses (No Botercaphages)		П	П	1		\Box	П	Γ.	
1	PROTEIN	į	ţ	_;	7	A III CA	7	4814	1414	APLA 0	VIII V
ı	GP160 PRECURSOR	SEMIAN INDICINALIZERICE NOV VINUS (NINERS D) ISOLATE)		_							į
ı	GP 160 PRE CURSOR	SIMIAM INDIDINODE FICIENCY VIRUS (KOW ISOLATE)	130.154	765.792	177 603						
ì	CPIAOPRECINSOR	SIMILAN INDAMODE INCIENCY VIRUS (R70 ISOLATE)		_	101.134						
1		CINIA DAMAN CONTRACTOR NO VINCON AND AND AND AND AND AND AND AND AND AN	740.780		!	<u> </u>	 		!		; !
2	COLON PRECIONADA				!	-	İ	!		≃ ⊹	:
ł	CF160 PRECURSOR	SIMILAR MANUACOLITICAL TARASTATION TO SOLATE			!	-	İ	1			1
_	PISE PROTEIN	SINIAM SARCONIA VIRUS		:		!		i			!
	ENV POLYPROTEIN	SUGIAH RETROVIRUSSRV.	50.12								İ
PERBA AVIER	EABA ONCOCOM PROTI IN	AVIAN ERYTIROBLASTOSIS VIRUS (STRAIN ES4)	337.349								-
	EARLY TRANSCRIPTION FACTOR	FOWLPOX VIALIS (STRAIN FP.1)	17-12	19.61							
	EARLY PRANCESSION FACTOR	CHOPS SIBROMA VIBITORS RAIN KACZAN	1		i !					 : :	:
Т	EARLY VE ANGOSTONIA EACTOR	VACCINIA VIBILE JETRAIN CONTRIBACION	1	Ì	i	-	-	:	:		
1	EASE TRANSCILL HON FACIOR	AACLAIN VINOS (SIRAIN CO. LINIVILA)			1			;	!		!
	EARLY TRANSCRIPTION FACTOR	VACCINIA VIRUS (STRAIN WR)	7-12		-	7					
i	EARLY TRANSCRIPTION FACTOR 82 KD SUBLINIT	VACCINIA VIRUS (STRAIN COPE MIACIEN)	2.3	101.11	165.107	_	530.583				
ī	FARLY TRANSCRIPTION FACTOR IN ED SIGNAT	VACCINIA VALIS SERVINA	1		 						
T	The state of the s				1				i		1
	TOR 12 KD SL/B	VAUOLA VIRIUS		100		ī				į	i
	ALKALINE EXONUCLEASE	HERPES SIMPLEX VIRUS (TYPE 1/STRAIN 17)	5 : 8 8 : 8			•					
PEXON HSV3	ALKALINE EXCHICLEASE	LEDPES SINCTLEX VIAUS (TYPE 2)	23:18		-			:	:	_	
- 1 -	AS K AP BAC B KOSM WILL G A CR	FOUNDER SECOND CONTRACTOR AND ABAR.	134.301	-	!	ļ.				- 	!
			į	İ	!	1		-	:	:	1 i
	ALK ALINE EXUMUCLEASE	PSEUDOLOGIES VIRIS (STRAIN MA-1)	2	:		-					
	ALKALINE EXONUCLEASE	VARICELLA-70514 VIRIN (NIRAM HIMIAN)	;	11.7.1		•					
	41 4 KD 1:0ER PROTEIN	HUMAN ADENOVIEUS TYPE 40	1			:					
METERS APPEAL	ALA PORTINE PROTERL	INDIAN AMENDY SERVICE TYPE AT	114.555	-				Ī		İ	-
	STATE OF THE STATE				-		İ		:: !	::::	1::
- 1	FIBER PROTEIN	HUMAN ADENDVIRIS 1 VF. J	137-133			į					
ì	FIDER PROTEIN	IIIMAN ADEMOVIRITS I VITE 9	41.41			١			İ		
ł	Case parish	POVINE ADEMOVIBILE TYPE I MEACTADEMOVIBILE DOCT	10.00	175.801	İ		-	-	İ	İ	
ł					-		:	:		:	•
- 1	PIBER PROIEIN	CANINE ADEMOVIACE LITTE I CHIRAIN GLANIII			_	_	:				
	FIDER PROTEIN	MOUSE ADEMOVIRUS TYPE I	31.313	27:27		12.50	5 PT - 5-EL	_		_	
Γ	GAG POLYPROTEIN	AVIAN ENDOCENDINS VIRUS EV. I	25.38						:	_ :	
Ī	GAG POLYPROTEIN	AVIAN ENDOCEMBUS ROUS ASSOCIATED VIRIUS 0	13.					:	i 	<u> </u>	
ī	OAD SOLVED TEN	AVIAM LIVES OF VICALATORIS UIBLIS LATIO			!	!		1	!	:	:
ī	ONO POLITICAL DE LA COMPANION	A VIALE OF THE PARTY OF THE PARTY			-	-			1		
i	CAG FOR TEROIER	AVIAN MTELULY TURIATUSIS VIRUS HITI				Ţ.				-	
POAD AVISU	CORE PROTEIN P19	AVIAM SARCOMA VIRUS (STRAIN URZ)	33 76								
	CAG POLYPROTEIN	AVIAN SARCOMA VIRUS (STRAIN YT)	33.76								
1	GAG POLYPROTEIN	BABOON ENDOCENOUS VIRUS (STRAIN M?)	393.422	·							-
ŀ	GACIPOLYPROTEIN	BOVINE LEUK EAUA VIRUS LAUSTRALIAM ISOLATE							İ	-	İ
POAD BILVI	CAG POLYPHOTEIN	ROVINE I PUREMIA VIRUS (IAPANESE ISM ATF BLV.)	11.310						-		
	CAC POL VPROTEIN	CAPARATE AR PRINTING SAUCEDIALITIC VIRSIS (CIRAIN CORK)				Ì	Ī			-	į
1	CAC POL VEROTERA	CHINAL CAPCOLA SPICE			i	Ī		Ī		İ	
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Ī	CAC LIFE IN	MANAN STELL CONTINUE OF STREET STREET			1			Ì			
1	UAU TAKUELA	ILLIMAN I CELL LEURENIA VIRUS ITPE I (L'ARIBBEAN ISULATE)			İ						
1	CAUPOLEM	HIMAN I CELL LEURENIA VIRUS IYPE I (ISOLATE NIT.2)	2								
- 1	GAG POLYPROTEIN	THE I CARVIST ISOLATE)	65.91								
POAD IIVIBI	GAG POLYPROTEIN	INDIAN DONNODETICIENCY VIRUS TYPE I (BITTO ISOLATE)	14.59	i 							
- 1	GAG POLYPROTEIN	INDIAN DOMINODEFICIENCY VIRUS TYPE I (BIIS ISOLATE)	16.59								
	GAG POLYPROTEDA	INTIMAM INDIAMODES ICIENCY VIRUS TYPE I (BRU ISOLATE)	10.50	i	į				:		
	GAG POLYPROTEIN	HUMAN DOMINOUS INCIENCY VIRIUS TYPE I (CIX: 41) INILATE)	10.50	:	_			İ	i :	. :	i
1	GAG POLYPROTEDN	HUMAN BOREMONFINCIENCY VIRUS TYPE ((LLISOLATE)	16.59		:	-	:	:	!	:	i :
ī	GAG POLYPROTEDN	DAMAN DAMPHODE ICIENCY VIBIG TYPE LUIXIN ICIN ATTA			!	i			Ī		i
ī	CAD BOT VEROTERA	INDIAN INGENITIONS VIBIG TVBE LINE ICOLATES		İ		İ	Ī	Ī			
	CAC BOL VEROTE DA	TOTAL STREET STREET STREET STREET STREET STREET			İ	i		Ì		Ì	
•	CAC BOX VANCARION	Ì			-	1		İ	1	İ	į
•		INIMAN MANINOUS INCIDENCY VIRUS LYTE I (NIAL ISOLATE)		:	;	į		-	-	-	į
	STATE STATE	=:			;				-	-	<u> </u>
		HIMAN DUNINGUES IN TERM, Y VINUS 177E I (N.W. YORK, S ISON, A JE.)	-	-							-
DOM IN INC	GAG POLYFIOLEIN	INMAN BUMMODE (CIENCY VIRUS TYPE I (NDK ISOLATE)	68.91	137.373	_						
MOAD INTO	DAD POLYPROFEIN	HIDRAN BORINODE FICIENCY VIRUS TYPE I (DY1 ISOLATE)	16:59								
7	GAG POLYPROTEDI		16.59								
POAG IIVIRH	GAG POLYPROTED	FIRMAN BANDONF FICTENCY VIRUS TYPE I (REALAT ISOLATE)	16:69		<u>. </u>						
l								1			

PCCCME	PRICTLE	All Viruses (No Dattersophoges)	П					П	П		
Н	LAGILLIM		144	PER	SEE S	345	443	3864	1414	ABIA!	SAEA !
POAD INIO	GAG POLYPROTEIN	21		Ī	T	Ť	İ		T	Ī	
1	GAG POLYPROTEIN	HIGHAN IMMUNODEFICIENT Y VIRUS TYPE I (2)/CDC-214 (SOLATE)	5			1-	Ì				:
ı	RETROVIRUS-RELATED GAG FOLYPROTEIN	MOUSE INTRACISTIFINAL A.PARTICLE	111.111		<u>. </u>	<u>-</u> -		:	<u>.</u>	-	
9	GAO POLYPROTCIN ,	INAIN URA)	16:43	:			:				-
	GAO POL YPALIEIN		16.28								
	GAG POLYPROIEM		13.93								
1	GAÖ FOL YPROIGN		11.18								:
PGAO SCVLA	MAKIA COAT PROTEIN	VIRUS L.A	618-645	;							
POAD SIVI	DAG POLYFROTEIN		101.4	į			:				
POAG SFVJL	DAD POLVPROTEIN		10.101		-	-					
POAG SIVAL	GAG FOL YPROTEIN	SUMIAN DOMINOPERICIENCY VIRUS (ACALLYS ISD). A TE)	180.213		i						
POAD SIVAG	GAG POLYPROTEIN	SINGAN INDAMPORTETICIENCY VIAUS (AGA!) ISOLATE)	107:101								
PGAO SIVAT	DAG FOL YPROTEIN	SINIIAM MORNOHEFICIENCY VIRUS (TYO.) ISOLATE)	18:31			1			İ		İ
POAG SEVEZ	DAD POLYPROTEIN	CHIND ANZER IMMINIONEFICIENTY VINIS (SIV(CT.))	2	 : !	- : :						
POAG SIVOD	GAO POLYPROTEIN	SINGAR BENEINER I CHEN Y VINUS INCH. A 11. CHILD	20.2			_					
POAG SIVILI	GAG POR YPROTEIN	SIMILAN INMUNCIONAL FICTENCY VIRIS (MALIO ED ISOLATI)		;		:		i	:	:	:
POAD CLAN	GAG POLYPROTEIN	SCHURBEL MONREY RETROVINUS (SMRV.11)	186-107		!	j-		-			
TOUR AND THE	Social B CL (Tr ABERDAIN	TATION OF THE AIR TOTAL MINE AND AND AND AND TANK	1			1			-		
PCI EX VARV	POSCIBLE GLUTARE DOXIN	VARIOLA VIRUS	11.61	-		<u> </u>					:
PCBAN OVA	Caraca Da	ACROSIC CRESTINA CRAZING DAIR VIRING	201.234	:	:	: !	:	•			
200	N. Walter	ABELIAN LICIA MI CE ANIM DOLE VINING	300 313								
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NOW WALLY	CRUM IN TACTOR	VALCINIA VINUS (SIRAIN WA)		Ì		-	Ī				
TOWN VALL	CACWINITACION	ACCULA VAROS			-	1		T	İ	Ī	
1	FRINGE SELICAND	CARCOLLAND VINCO (SINCE)	Ī	ī		اً			1	į	
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	TRUBABLE INC. ICA SE	THE PERSON ALL THE TANK THE TA	T		İ	Ì	Ī	Ī	İ		
MEASURE THE SECOND	PROBABLE JULICASE	FEM. P. S. DOCLEA VICES (17 P. S.) MAIN MOST	T			Ī			-		
1	PROBABLE IN ICASE	INCOME TRACES AND THE LEGISLAND TO	1			Ť	1	Ī	Ì	Ī	
1	PRODUCE INC. IVA CH	VARICE LA POSTER VIBIG (STRAD) DOBARS	ī	7	!	1	Ī	Ī	Ī		
200	THE WAY OF THE WAY WELL AND A CE	CAUSE DISTRIBUTE CONTRACTOR OF THE CAUSE OF	ī	ï	Ť	Ì			Ì	ļ	!
THE PART COAD	HEALA COLLINIAN RECIES ARE DESCRIPTION	BANDE CORONA VIETE ACTE AND 111			Ì	Ī			Ì		
VIEW CVEN	HEMACON CONTRACTED ASE PRECINCOL	MOVING CORONA VIDITA AS IR ADM (V. 110)		Ī	Ì	-	Ī		Ī		
PIEMA CVIM	HEMAGGI LITIDION ESTERASE PRECITISOR	BOVDAR CORONA VIRUS (STRAIN MEBUS)	1		Ì			İ	Ì	Ī	
PIEMA CVBQ	HEMAGOLUTININ-ESTERASE PRECURSOR	BOVINE CORONAVIRUS (STRATH QUEBEC), AND (STRAIN L9)	\$1710		i i	Ī					
PIEMA CYNOC	-	IRUMAN CORONAVIRUS (STRAIN OC4))	391-413								
HEMA CWAS	_	MUTURE CORONAVIRUS MIN (STRAIN A19)	401-433								
PIEMA CYMS	-	INCHING CORONAVIRUS NOIV (STRAIN S)	40)-418								
PIEMA LANC	=	DIFLUENZA A VIRUS (STRAIN AVAICHIZARI)	17.5	3.33	j						
MENA MAN	=;	INFLIDICA A VIRUS (STRAIN ABANCKOK/179)	7	2	j						-
MENA INDICO	≕	INCLUDICA A VIRUS (STRAIN AMERICALIGAL/HORKAIDO (777)	310-313								
PIEMA IACKA		INPLUENCE A VIRUS (STRAIM ACTITIC REPORTABLEMENT)	330-337		<u> </u>					ļ	
NEW ACTO	HEMACKAL UTING PRECURSOR	INTUENCA A VINUS (SITIATIFIA ALTITLA ENVOETUMANT/PUMA)	101		16.333	1	Ī				
MENA IACK	I GMAGGLUT INTO PRECIMSOR	DOLUCKA A VIXUS (STANIN ACTUCK ENPERHISYL VANDAIN)	303.319								
MENA IACKO	IENAGGLUI IND PRECURSOR	INTILITY A VINUS (STRAIN ACTUER EMPENAS YLVAMA/I) TOTAL	102.316		Ì	Ì					
PIEMA IACKS	SEMAGOL UTINON PRECURSOR	DIRECTAL A VICES (STRAIN ACHIERENSCOTLAND/S9)	7			1					
PIENA IACKV	HEMAOGLUPON PRECURSOR	MATTERIAL A VISITS (STRAIN ACTUALEMY) (TOULNIS)	770-746		j						
NOW WATER	HEMALALUININ FRECURSON	CALUCALA VINES (SIEVIS AUGUNALEMINADO)			j	Ì					
PICHA IADA	HENACOLUINON PRECURSOR	THE LIEUTE A VIEWS (STEADY ADDICTOR AND ADDICTOR ADDICTOR AND ADDICTOR ADDICTOR ADDICTOR ADDICTOR AND ADDICTOR ADDICT			İ			Ī	İ		1
1	-#	THE LUMB A VISIT AT SAME AND AMERICAL AMERICAL	Т	1	Ì	Ì	Ì		Ì	Ī	
MENA IANII	-	INT. LENZA A VIRIS (STRAIN ADJUCKATORYATION)	T		İ				İ	İ	
PIEMA IADRU		DOT UNITA A VIRUS (STRAIN A/DUCKAIOKKAIDOGAD)	Ī	104-111		Ì		T	İ		
PIEMA LADIN	42	DOT UERZA A VIRUS (STRADY A/DUCKARORKAIDOO)3400)	T	104.33	İ	Ī	Ī	Ī	T		
PHEMA IADMIA	+-	INDITIONAL A VINUS (STRAIN ADIREKAIDORKAIDONAS)	Γ	100		Ī		Ì		Ī	
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PCCEME	Process	All Virour (No Berreriophoges)		П		$\boldsymbol{\sqcap}$	T	П	П	·	
THEHAME			4	,	7 7 V	- 2018 V	4 TO 10)-15/Hg	(- WIN	AMEA.	V
MEMA AADHIS		INTLIENZA A VIRLIS (STRAIN ACHICKAIOKKAIDOCHA)			!	1		Ì	Ì	1	į
PIEMA LADIG	-	A VIRUS (SIRAIN	-	2	!					Ì	1
PIENA IAMI		THE REAL A VIRIUS (STRAIN ANDUCKATION KAIDOVIOUS)	21.43	106.13	 	.]				İ	İ
	THE LANCE LITTING TO BE CLE CO.	INTITIENZA A VIRIUS (STRAIN ANDICKAGAPHIIS PRIMA)	17:30	123-110					İ	-	
		A A VIRUS (STRAIN	36.30	10:10							
	TO COLUMN THE COLUMN T	A A VIRUS (STRAIN ANDIKENEW ZEALANDVIVIE)	110.011		!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!						
THE WAY		CONTINUE AND A PARITY A RESIDENCE A DATE ALVA 11	95.5	133.110							
VENA LADO	PENALUL INTELLEDINOR	A C LOCA LOCA LOCA LOCA LOCA LOCA LOCA L	17.16	10, 101							i
	MENAGOL UTINALI I	VIEW COUNTY			1	ŀ			Ī	Ī	
	HENYOCE CLININ PRECUISOR	TRAIN AVENCE AND/021/77)	6	100						Ì	
PISMA LAPR	HEMACGLUTINGS PRECINSOR	Ŝ	30.74	113.332							
ł	SELVACOU INDIAN PRICIPETOR	INSTITUTAL A VIRUS IS IN A MAREY TEAL AUSTRALIA 2019)	310.337			-					
		120	116.111		İ						İ
MENA MOU	JENGAGGLUT MEN PRECURSOR						Ī	Ī		Ī	1
PIEDA LAGUA	HEMAGGLUTIMEN PRECURSOR	INTLUENZA A VIRUS (STRACH ANGULLIASTRAKHAM/11/114)	117.170			-			-		1
BIREAL LAUAT	INCLUSION THREE SECTION CO.	INTI (IENZA A VIBLIS (STRAIN A/EOUINE/ALGIERS/72)	321.338			•				_	
THE PARTY	ILEMANCE OF THE CONSUM	10 TO 10 TO	375 945			Ī		Ī		Ī	
PIER ME	HEMAGGLUT DROW PRECURSOR	A VINUS (SIRAIM ARQUINALAMBRIDGELIA)						1		-	1
PIEMA IAIK!	INMACCLUTOWN PRECURSOR	_	330 346	2.5		-	-		-	:	:
	4000100 mm - 100	SAME INCOME A VIBRACA CONTRACTOR AND INCOME AND INCOME.	310.244	115.332							
2	WENT COLUMN FILE CANON		777		Ī		ĺ	Ì	İ		
MEN MOE	HEMAGGLUTDON PRECURSOR	A VIAUS (STRAIN ACQUINDUCTROSTION)				•				ĺ	
PIGNA LANGO	HEMACOLLITION PRECURSOR	INTELENZA A VIRUS (STRAIN ACQUINERONTAINEBLEAUTS)	136-352	200							Ì
7417	STATE OF THE PARTY BEECH IN COR		31.33								
		1200	316.343	11.12	İ			İ			
TEM WAY		A VIAILS (3 PAAIN ACQUINCIA CALLAND			į	!		i	:		!
NEW MEE	HEMAGGLUTININ PRECURSOR	A VIRUS (STRAIN AN QUINTA EXINGIONING)	\$ 1		!			i	i	i	
MENA IAIRO			230.346	115.132						1000	
		BARTISTON A CORTE CORATA ACCURATE ALIANDA	216.392	121.121		j-	Ì	İ			
MOM WIND		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		-	-				!	İ	
MENT MOST	HEMAOGLUTININ PRECURSOR	INTLUENZA A VICUS (STRAIN ARQUINEMEN MARKETTO)			!	•				: !	
MISMA IAIDAN	INSTANCE UT DATA PRECURSOR	INTLUENZA A VIRUS (STRAIN ARQUINEMEN MARKETHITY)	315-332							!	
		A VSEUS ASTRAIN	315.332			آ ا					
THE WAY	HEMACOL ULIMIN PAECURSUR		100 310		Ī		ļ			i	
PIEMA MIBO	PERCENTION PRECIASOR	A VAICE COMPANY				L	İ	-	:	-	:
PIEMA MISA	HEMAOGLUTININ PRECINSOR	A VIDES (STRAIN	236-232					-			!
PIENA IAIRE	HEMACCI IN NIN PARCIA COR	INTLUENZA A VIRUS (STRAIN AFOUNE/SAO PAULOVING)	330-346	22:51							
	TANADO PROPERTINGO	INTELEBRITA A VIBILGESTRADA AFOLINE/SWITZERLAND/13/121	230.266	13:15		<u>-</u>					
	TIEMINACE OF INVITATION OF THE STATE OF THE	7 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	115.36						-	ĺ	
MEMA WHITE	IGMAGGLUTIND PRECURSOR				-				1		
MEDIA MITTO		VINUS (STRAIN ARQUINETOR YOUT)	100	2						1	
PIEMA LAKE		A A VIRIUS (STRAIN AS QUINEARUCUAY/1/6))	336-383	21.53							
PIEMA IAIAP	INSTANCE I PRINCIN PRECITESOR		117.134	İ							
*****		A A VIRUS (ST	100	316 316							
		MANUAL PROPERTY.	303.334		İ	Ī					
PICTOR INCHAR	SEPARATE STA	ALL ALL STREET	11.00	127.110					Ì		
	TICHACALO INTO THE COMPON	2	9						İ	İ	
MON ME	IEMAGGLUTOWN PRECURSOR	A VINCOS CONTRACTOR					Ī	Ì		İ	
MENA INES	IEMAGGLUTIND	A A VINUS ISTRAIN	2.5				Ī		Ì		
MEN WES	HEMADGLUTING PRECURSOR	A A VIRUS (SIBAIN	7	200				İ	j		
MEN SER	HEMAOGLUTININ PRECIPSOR	< 1	19-101	201.24	116-333						
PIEST ANTO	IEMAGGI CIENT	A VIRUS (SIBATH	37.59	133.330							
WIENA LAPIN		INFLUENZA A VIDIUS (SIBAIN APILOT WITALICATAINE/220/14)	110-311								
PHYSICAL IACUTA	HE MACCO INTERNA	, <	3	28.53	!						
		MARTITENTA A VIRILIS ISTRACIN AMERICAN TIMENSTONEMENT INSERVATION	1110.111	ĺ					Ī		-
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MENA MSE		A VIEW 13 13 15 15 15 15 15 15 15 15 15 15 15 15 15						Ì	Ī	Ì	
PIEMA CASH		VALLS (STRAIN	234-230								
PIEMA LASTA	HEMAGGLUTININ PRECIAISOR	VENUS (STRAIN	230-246	113 113						:	
PIEMA CAIKE		VIAUS (STAAIN	33-55	130 113						-	•
PIESAN IATKO		VIPUS (SIBAIN	233-249								
STELLY IN THE	HEMACOLITINE PRECIESOR	INT. LENZA A VIPLIS (SIRAIN AVIORKEY/ORFCONTI)	330-246		:			!	į	:	
1	• •	VINITS ISTRACT	270.244	ĺ						İ	
1		V 217 6137 31 612 4	1		100	-	-				
MENT INDO	IEMACE CITININ PRECIONALE				- : :	-			 	;	į
PIEMA IAMI	_		9	97.62	-	-		1		-	
PIEMA IAJOI	IEMACCLUTOWN PRECURSOR	SIKA	8.6		-		į				ļ
PIEMA IAZCO	_	INTLUENZA A VIRUS (TIPAIN ASWINFACOI ORADOVIA)	17.59	133-110						1	
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MILEGAL A VERIS (STANIA ASSUNDENCIONA) 11-14 10-15 10-												
EMACAZI THE PRICE IS IN THE CASE OF TH	THE WAME	WIND THE PROPERTY OF THE PROPE	VIRILA IN DALICIPATATA	AREAI	ARFA?	ARCAS	AREAG	AREAS	AREAG	AREA 7	AREA	ARTA 9
Execution 19 19 19 19 19 19 19 1	MENA IAZUI	HEMACOLUTION PRECUISOR	INTLUENZA A VIRUS ISTRAIN AJSWINEAIONG KONGALITAS)	1	100	1						
Extract times reflective	MEMA IAZII)	HEMAGGLUININ PRECURSOR	VIBIS	1.4	200				: i 	İ	:	!
E-MACKED THE PRECEDUAL T	FIEMA IAZUK	-	VIRUS	17-59	111.110	:		:	:	:	•••	:
STATE OF THE PROCESSION STATE OF THE PRO	MENA DUBAN	_	INTI ITELIZA B VIRIIS (SIRAIN BIANN ARBONING)	18:13	30.10		!					
ELECACOLINES FURLISCO FOLIATE FURLISCO FURLIS	PIEMA PABE		INGLIENZA B VIRIIS (SIBAIN BOFILINGIAN)	=======================================	101		İ				-	!
ELACOLUTION PLOTO	PIEAA INGBO		INTILIENZA B VIRIIS (SIRAIN B-BONNAS)	116-132	101							
ELMOGUTINEN PLECTOR		HEMAGGI UTININ PRECURSOR	INTI UENZA & VIRIIS SIRAIN BENCI. AND DIVIN	21.15	•			- - -				: : :
ELACOCUTION FILESCA		INEMAGOR UTINA	INSTITEMENT D VINUS (STRAIN INFUKUCIK AROBI)	100.124	26.50	<u>:</u> 	:	:				
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	MEMA DIBIO	HE MAGGI LITININ PRECIESOR			100.00	!					: i	:
SELECT THE PRECINCAL SELECT SEL	PICHA PAGE	HEMAGGI DIDNIN	INFILIENZA @ VIRUS (STRAIN BADARAKIUS)	108.134	6	i					. !	
EMACQLUINNE PECULÓN DELIBERA DE VIDERA DE	PIEMA MAID	HEMACOL UTININ PRECIASOR	INTLIFUZA B VIRUS (STRAIN BAD/16)	130.136								i i
BAUGGLINEN PRECINGON FILLERA & VING (FILLER PROPRIETION) 111-17 151	PIEMA INILE	=	DALLENZA D VIRUS (STRAIN BA F.E.40)	13.130	103							
EMECALTINEN PLEATER OF THE STATE A VINE STATE OF THE ST	PIEMA INBAD	:=	INSTITEMEN D VIRUS (STRAIN BAIARYLANIVS)	10:00	193 307							
EMACGUIDEN PRECISAGE PRINCES I VERSE VER	PIEMA PARE	=	INFLUENZA B VIRIIS (SIRAIN BAIEMPHIS/6/16)		E		-					
BALAGLUTINEN PRECINSOR PRILEGES VINES STATIN BONECONATO 11:119 11:	MENT CARRA		INGLUENZA B VIRUS (STRAIN BINAGASAKUIM)	108:124	101:101		-					
BALGOLUTION RECULSOR BALLERZ'S WING STAIN BESTANDENSYNNY 11111 11111 11111 BALGOLUTION RECULSOR BALLERZ'S WING STAIN BUSTANDON'S 11111 11111 11111 BALGOLUTION RECULSOR BALGOLUTIO	PIEMA MICA		VINIS (STAVIN	100	30:36	<u> </u> 	:					
PARTICUL TITRE PRECUESOR PARTICULAR A WIND STRAIN DELIVERATION 111-111 18-11	PIESCA MOSI	HEMAGGLUTDATH PRECURSOR	S VIRUS (STRAIN	10:130	301.316		-					
	PIEMA BASS	HEMADOLUTION PRECUASOR	VIRUS (STRAIN	118-135	100							
PRICE PRIC	PIEMA DIBUS	-	VIRUS (STRAIN	116-132	394.300		ţ.					
BALLOGAL UTBNI PRECINCOL	MEMA PON	-	POLITENZA B VIRUS (STRAIN BAICTORIA/1/1)	116-132	1							
EMACGUI INDER PRECINSOR PRELIGNAS & VIUTO (STAIN) (STAIN) (10-15) 16-15 16-	PIEMA DIBVE	-	INTELENZA B VIRUS (STRAIN BAICTONIANAT)	131.130	30.50							
EMAGGLUP DEP PRECIATOR ANI LUERZA C VINUS (STAMIN CRALL FORMIN) 410-414 410-41	FIEST MOY	-	INFLUENCA B VIRUS (STRAIN BY AMAGATA/16/81)	108-124	106-301							
EMAGGLUTION PRECISES INSTITUTE CONTROL GIALM CREGATILATE STILLING 196-414 196-	MICHAE INCOM	_	INTLUENZA C VIRUS (STRAIN OCALITORNIA/18)	402-666			-					ļ
PRINCELLINE PREFERENCE PREFERENCE PROPERTY PR	PIESTA DICEN	-	INSTITUTAL C VIETS (STEATH CANCEL AND TOUT)	416.4%			-					
EALOGOLUPRIN PLECUSOR POPLIGNAC VARIS STAND CONTOURS 1911	PIEMA DECOL	_		430-454			1					
EAL/GOLUPINE RECUSOR FIGERIA & VIRIS (STAIN CONDIANNESS DURCORA) 449-45 449-	PICEMA DICHY	_		429.453						-	-	!
EMACQUIDEN PECUSOR INSTITUTE OF VALUE (STAND CANSESSIEVE) 19431	PIEMA DICH	HENAGGI UT INDA PRECURSOR		107-07								
EMACQUITIENT PRECUSOR INFLIENTA C VIRIS (STAIN CAMESISSISTIPLY 0) 194-41) 194-	PICEMA DACKY	HEMAOGI LIT DATA		439-453			[.	Ī				
EMACQLITIBUR PETCHSON Not LEBYZ & VINUS (STAIN CRYANATS) 49-415 49-415 49-415 49-415 49-415 49-415 49-414 49-	MISMA DICK	HENAMACH HERAIN PRECINCOR	INTELLIFACE CVIRILE SCIBAIN CANCESCONDING	130.41								
EAAGGLUTER'S PRECINSOR FRELER'S C VIDES (STAND CPICTREMING) 10 a std	PITELYA DICHA	_	DELEGISTA CHELL CHEATH CALABARDI				-					
EALAGGLUT PRIN PRECINSOR FREUENCY CYBUS (STANIN CPROCEINGOLISM) 10 - 13	PITEMA DACE	-	INGILIENZA C VIBLIS (STRAIN CALCINETIIN CLORE)	1979			-					
EAAGGLUTBRN PRECINSOR NUTUENZA C VBUS (STAIN CPACAGLINGAINST) 419-434	PITEMA DACES	HEALACCI LIT ONTH PRECITES OF	INCLIENZA C VIBINS (SIBAIN CAIGHEIGHGAINS)	410 614							Ī	
BANGOLUTRIN PRECINSOR INTLUNES STRAIN CYANAGALAZION 104-14	TAY WILL	HENACOL HINNING BEST IN COR	CARL LEAVE A CORTA CARACTER CONTRACTOR CONTRACTOR	1							1	
EMAGGLUTRIN PRECUSOR INTLUENZA C VIRUS STAIN CYANAGATAVIOTI) 104-154 111-141	PIEMA INCTA	_	INFLUENZA C VIBUS (STRAIN C/TAYLOR/17)1/47)	257010							-	
EDAGGU UPGPR FEBALDEDIASE MAPPY VRUS STRAW SEL-I) 101-121 131-141 131-144 181-144	PIEMA DICYA	HEMADOL UTININ PRECURSOR	INTLUENZA C VIRUS (STRAIN CYAMAGATA/1941)	430-454								
EMACGLUT DRIVE (MAURIDA SE MAUR	HEM MODE	HEMAGGLUTININ-NEURAMINIDASE	MUMOS VIRUS (STRAIN SBL-1)	521-101	100	235-246	167.394	11111		-		
IEDAGGU UT DRIA WELLALDHIOLASE WARDS VILLES STATIN RW 10 11 11 11 11 11 11	PIEMA MARCH	A INTERACCLUTIONIN NEUTANIONIDASE	PRINCE VIRUS (STRAIN ANY ANIARA VACCINE)	101-125	12:12	225.246	167.194	197417				
IDANGOLUT DRAY MELIAJADHO ASE MARREY WALEST EDISEASE VIRUS (STRAIN AUSTRALIA VETORIANIS) 191-101 1	PIEMA MANGE	HEMAGGI UTININ-NEUTAMINIDASE	PARAS VIAUS (SIRAINAW)	101.133	3:5	22.24	161.194	197.411				
IEMAGOE UT DRIVE RELIAADRICA SE NEWCASTIE DISEASE VIRIS (STRAIN ALSTRALIA VYCTORIANI) 91-110	PIEMA MONUS	HEMACGLUTIONN-NEURANDHOASE	MUMOS VIRUS (STRAIM SBL)	101.135	1							
IEMAGGUITB@N-NEIRAABHOASE NEWCASTIE BISEASE VIRIG (STRAIN BEAUDE TIE CUSS) 9; 1:0	MEMA NOVA		NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/12)	93.110								
ILEMACGL UTDRIA PERIOADERASE PRESENTATION PROPERTY	PHEMA NOVE	IEMAOGLUT IMDA-NEI IRAMINIDA SE	MEWCASTLE DISEASE VIRIIS (STRAIN BEAUDETTE CAS)	93.110								
ILEGACGUI UPDRI-RELIALARMINASE NEWCASTIE EDISEASE VIRUS (STRAIN BI-INTOPERAT) 19-110	MEMA NOVO	HEMAGGE UTDEN HEI MAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN D76/16)	93.616								
	MEMA NOVI	IEMAOCI UTDVIN-NEURANDAIDASE	NEWCASTLE DISEASE VINUS (STRAIN BILITITIONE NAT)	93-110								
	MEMA NOV	IEMACCI LTDM-NEI MAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN ITALIEN/45)	91.0								
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r١	PROBABLE PROCESSING AND TRANSPORT PROTEIN	MURDIE CYTOREGALOVIRUS (STRAIN SKITTI)	Π	701.179	110-411					İ	
-1	टा	PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKITAUSER / DECKTR)	2	696.71E							
ICIS VZVD	PROBABLE PROCESSING AND TRANSPORT PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DURIAS)	П	619.619	33.104			ĺ			
Ī	MANAGEMENT FROIEN	TEACES SWOLEX VIRUS (17PE 1/STRAIN 19)	£1.424							İ	!
Ī	FARLY PROTEINS	ī	2	ļ							
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PKRS VARV	TO KD PROTEIN KINASE INMAN OG	VARIOLA VIRITS	166.314								
PKRF1 SFVICA	POSSIBLE PROTEIN MANASE C20	SHOPE FIDROMA VIRUS (STRAIN KASZA)	63.08			- 					-
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PKSEC RSVPA	TYR PROTEIN KINASE TRANSFORMING PROTEIN SE	ROUS SARCOMA VIRIUS (SIR.	151.374		:	. !		İ	:	!	j
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1200	LAMA CAPPACI ENPYACE LANCE SUBLINIE	SHOPE FIREDAIA VIRUS (STRAIN KASZA)	34.26	336.578	679 699	1			-	!	i :
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PLOVE PRINS	MOVEMENT PROTEIN	PEPPER MILD MOTTILE VIRUS IS I RAIN SPAIN	25.30	100 91					;	:	
PAROVE THESAN	MOVEMENT PROTEIN	TOBACCO MED GREEN MOSAIC VIRUS (TMV STRAIN U2)	186.201		İ			ļ	į	:	:
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ACAP FIRM	MIKEL FOCAPSED PROTEIN	FELINE INTECTIONS PERITORITIS VIRUS (STRAIN 79 1144)	11.74		: !	ĺ			: !	!	;
PICAP HUNTIV	MACLED CAPSID PROTEIN	ILANTAAN VIRUS (STRAIN 76.118)	117.34	:	!					!	:
PICK BAZVI	MUCI EOCAPSID PROTEIN	ILAZARA VIRUS (1501.ATE AC210)	428.446								
PNCAP BON	MIK'L FOCAPSID PROTFIN	INTETICIES HENALLIPERI LIC NI CRUSIS VIRUS ISTRAIN ROUND BILL	110.13	310 345							

MAY 645.1	PCCUT	יונוניי	AN Virgos (No Berreitophogen)									
			YIRUS	1 1		: 1	AMEA	ARGA	MIAE	181.A.	ARIAL	1111
Column C	-	ACLEOCAPSID PROTEIN	IMPATIENS MECROTIC SPOT VIAUS	3.0		İ	- 1					
MACHEGOLIE MACHINE M	_	AICLE OCAPSID PROTEIN	MEASTES CHAIS (STRAIN PUMONSTON)	\$0.50							İ	
	_	AUCLEOCAPSID PROTEIN	MEASI ES VIRUS (STRAIN II ALI 1)	40.50						: :		:
		AK LEOCAPSID PROJEIN	MEASILES VIRIIS (STRAIN YAMAGATA-1)	80.58	1	 	!	:	1	•	i.	
	- See - See	AICLEOCAPSID PROTEIN	MUNTS VIRUS ISTRAIN SUL-1]	36.178		!			:	:	1	:
	3	ACLEOCAPED PROTEIN	MONOS VIRUS (STRAIN MITTALIARA TACCINE)	36.176								
	ı,	OCLECAVID ROLEIN	PROSPECT HILL VIRUS	2	311-336	11.47	21.34					
MANA FOR THE PROPERTY AND STATES AND STATE	- 1	A CLEACASID PROTEIN	INDIAN PARAMELIENZA I VIRIIS (STRAIN C19)	2.2	107							
	ı	ACLEOCAPSID PROTEIN	HOMAN PARAINGLIIENZA I VIRIIS ISTRAIN WASHINGTON/1957)	42.50	16.102						<u>.</u>	:
MACHIGE CORP. MACHIGE CONT	4	NOCI EOCAPSID PROTEIN	BOVINE PAPAINT LIENZA I VIEUS	167.184						. !	:	
MACHIGOGRAPH MONTAL VARIAGE STATE AND TABL	ł	AKLEOCAPSID PROTEIN	INDIAN PARAINTI IN N.A. 1 VIRIUS (STRAIN NIII 47065)				-				İ	! !
MACRICATION PROTEIN		AKLEOCAPSID PROTEIN	PUDMALA VIRUS (SIRAIN HALLNAS RI)		331-346					ĺ		
MICHIGATOR MAINTAIN TO THE AND THE	7	AUCLEDCAPSID PROTEIN	PUUMALA VIRUS (STRATIN SOTIKANO)		20.276	2	ŀ			1		
MOCLEGATION PROFILES MARIES VALIG FILEMAN 1979 1979 1970 197		UCLEOCAPSOD PROTEIN	AABIES VIRUS (STRAIN AVOS)	299-332			-					İ
WALLEG CASID PROTEIN WITH VALLEY I LEVEL WALLES AND STATE WALLEG CASID PROTEIN WA		ACCLEOCAPSID PROTEIN	RABIES VIRUS (STRAIN PV)	199-111						İ	!	 -
MACLEGATION MILE NATION	- 1	OCCLEOCAPSID PROTEIN	RABIES VIRUS (STRAIN SAD BIT)	299.133		!	-				-	!
	2441	TUCLE OCAPSID PROTEIN	MIFT VALLEY ! EVER VIRISS (STRAIN 211.540 MIZ)	ī		i	-				!	!
MACLECATION FOR THE SEROAL VILLE (TALLAL ST.) 151 161		TUCLE OCAPSID PROTEIN	SEMDAI VIBUS (STRAIN Z / HOST MUTANTS)			:	j -	.	-		· :	:
MACHEGA JOSTON MACH		ACLEOCAPSID PROTEIN	SENDAL VIRUS (STRAIN ENDERS)								1	<u> </u>
MACIECA-JUSTICIAN MACIECA-JUSTICAN MACIECA-JU		ACLEDICAPSID PROTEIN	SEMDAI VIRUS (STRAIN HARRIS)		101-4							
MACE LOCA 2410 PROTECH MACE LOCA 2410 PROTECH MACE LOCA 2410 PROTECH MACE LOCA 2410 PROTECH MACE LOCA 3110 PROT		OCLEOCAPSID PROTEIN		15.62	16.102		-			:	· !	
MACLEGGATO PRODUCED MACRODA VULUE MACROA VULUE MACLEGGATO PRODUC	•	OCLEOCAPSID PROTEIN	SEOID, VIRUS (STRAIN SR.11)	3.13	1000			Ī		!	ļ	!
MACLICGANID ROTERN		MICLEOCAPSID PROTEIN	SANDELY I EVER SICILIAN VIRIS	20.00					[İ	i	!
MCCLOCAPID FOOTEN	PHCA TACV	CCLEOCAPSID PROTEIN	TACARIBE VIAUS	19.34		: !	!		1		!	!
MUCL DCANTO PROTECH VALA, HEADORANGIC STRICELLA VIRUS (STAIN HARATI) 240-244 MUCL DCANTO PROTECH VALA, HEADORANGIC STRICELLA VIRUS (STAIN HARATI) 240-244 MUCL DCANTO PROTECH VALA, HEADORANGIC STRICELA VIRUS (STAIN HARATI) 240-244 MUCL DCANTO PROTECH VALA, HEADORANGIC STRICELA VIRUS (STAIN HARATI) 240-244 MUCL DCANTO PROTECH	_	UCLEOCASID PROTEIN	UNKUNICHE VIAUS				ŀ			Ī		!
MACLEGGA 310 PROTEIN VELACLAM \$100ATHIS \$110ATH PARAMINES	_	UCLEOCAPSID PROTEIN	VIDAL HEMORAGIC SEPTICERIA VIRUS (STRAIN 07.71)		ĺ	<u> </u>					-	İ
MUCLECOASID PROTEIN VESSCULLA I TONAM DEGINERAL VIRUS 1972 150LATE BOD 110.139 110.139 110.130 110.13	_	UCLEOCAPSID PROTEIN	VIDAL HEMORNIAGIC STRTICEMIA VIRUS (STRAIN MAKANI)				-			 	:	
FORTING ACTION ILDAAN DOGING ITEMA VILLED ITE		UCLEOCAPSID PROTEIN	VESICULAR STONIATITIS VIRUS (SEROTYPE NEW IT RSEY / STRAIN OF	3	İ			İ		-	:	! !
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	آ	ECATIVE FACTOR		110.139			•				1	
FUNDAMENTAL FUNDAMENTAL		EGATIVE FACTOR	HUMAN BOALMODE! ICIENCY VIRUS IN PE 1 (150LATE ST)	106-130			-					-
MALENDA A. MAL	7	EULAKONDASE	INTLUENZA A VIRUS (STRAIN A/BLACK DUCK/AUSTRAL IA/702/78)	1.70							i -	!
Fig. 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	-	EULAMPRIDASE	INTLUENZA A VIRUS (STRAIN ACHILE/I/4))	7.1						i	!	
	_	E I LAMINED A SE	INTLUENZA A VIALIS (STRAIN AMACKIAL BERTAZIONO)	*							İ	
Section Sect	-	EIRALDINGASE	THE STREET AND COUNTY OF STREET		-						İ	
WELLERIZA A VIRIS (STANT A VIRIS) 139	-	EURAMONDASE	IRUS ISTRAIN ACOUNTACOMICAL	Ŀ		I					Ì	
INTLIENZA A VIRIS STAIN A A REWINSON 1-34	П	EI MAMINIDASE	INFLUENZA A VIRIS (SIRAIN ARQUINEAL NIUCKYINI)		İ				Ī			1
INTILIENZA A VINIS (STAND ASSESSMENT) 130	7	EURAMINIDASE	VIRUS (S	2:5					Ī	İ		
FOR LUCKARD AS FOR LUCKAR A VENUS (STRAIN AND PRINCIPALITY) 1.0	٠,	EIRAMMDASE	VIRUS (SIRA	2.		İ	ļ		İ			
FOR LUCKARD ASS FOR LUCKAR A VINC STANDARD AND ASSESSMENT 1.10	ī	EIRAMMDASE	VINCIS IS IRA	0.0					İ		!	
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	ī	E (ILAMNIDA SE	CHES (STRAIN APPLIEST CONTINUES OF STREET			!			1			! !
	Т	EIRANGNIDASE	VIETS (SIBACN ANGIE ABOVA TERVATICABALIANS)		Ī	1				-	İ	i
	T	EURAMINIDASE	VIRUS (SIRAIN	Ī		Ī						.
NOTICE AND ASSESSMENT NOTICE AS A VEGUS STRAND ASSESSMENT		EURAMINIDASE	14	Ī		!					į	
PATLEDAM A		EIRAMONDASE		2.					!		1	1
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		ETILAMINIDASE	5	2				İ	Ī	-	-	!
	▔	EIRAMINDASE	VIBITS (STRAIN BARING/1.67)	2							İ	
	_	ELIA AUTONIA SE	VINIS	2								
NEUTALADODA SE DOS LUENZA B VIBLIS SI BANDA SE B	-	TUCKURDASE	THE CONTRACTOR OF THE PRINCIPLE AND POTATE TO SERVICE AND POTATE T	2.5							i	
NEURAADHDASE INTERNATION OF LEACA B VIRUS (STRAIN BARANIES INTERNATION OF CONTINUE OF CONT		EURALONDASE	TRUS (STRAIN BATARYLANIYS)	2 2	j					i	i	
METITAL MANATASE		EURAMONDASE	THUS ISTRAIN BARAITISTING	2	Ī		1	T			Ì	
		IF URAMINIDA SE	CIRTIS (STRAIN & ORT CONTINUIS)	2	Ī		1	-			-	

- 1 1		All Virgas (Ne Racies of high)	П								
מור היאם	CAOLEIN	MANUAL ENTERING ACTEANN PACING APORE/22/292	3	Tories.	•	-	:	7		. L. T. L.	
		POLITICALE O VINUS (SIRAIN UNISSANCIONEI)	2			i	i	-	:	: ;	:
PKRAM IMBVI	MITALINIDASE	PRICE NET STREET STREET TO TO THE STREET	2			ī					: :
PNSI SEDEV	PROBABIE MONSTRUCTURAL PROTEIN PRECURSO	SOMEN DENSORIE LEGIS VIRUS	2			İ					!
NS SEC	PROBABIE STRINCTURAL PROTEIN PRECURSOR	BOXIBY K OF NORIK I FOSIS VIBILS	2		<u> </u>	-		į	:	•	;
PHSI SONEV	PRODABLE MONSTRUCTURAL PROTEIN FRECURSO	BOARDY A THE PACIFIED WITH THE STATE OF THE CONTINUE OF	2 2	111	į	İ	İ		:	i	: i
TASS ISAN	NON STRUCTURAL PROTEIN	MAN TO STOLLED WAT I VISITE AS IN THE	9	- 199	:	-	Ì	1	Ī	i	!
TANK ISAN	MAIN BOXING THE HOUSE IN THE I	VACCINIA VIRIS (STRAIN COFF MIAGEN)	12		:					į	
אליים ומציים	Mari Bosme Tarphospita LASE i	VACCINIA VIRUS (STRAIN WR)	\$70	107.01	1					İ	-
7877	MAIN EDGINE TREMINGENATAGE	VARION A VIRIES	901 104		i			İ		į	
100	MACCONTRACTOR CTRICCION AND AND AND AND AND AND AND AND AND AN	IN BOCK CIMIN ET VIETIK ITAFF AF KIE APZIEGANDA. 11021	107.704	150.330	15			Ì	İ	! !	}
2000	MANOR ANTICENCE STRUCTURE CONTROL OF STRUCTURE	TOWN BOX VIBILS	90.5			Ī		:			!
	THE PROPERTY OF THE PROPERTY O	AVVOLA VIEW AND A TE ADVITABLE AVVERGE BALL	1			1	-	-			-
NAV. MINA	POLITICAL PROPERTY AND ALLOW A SUBONIL	TOTAL STATE OF THE POST OF THE		: - 1	11:::	1				İ	
A A A CCC	POLY(A) POLYNELASE REGULATORY SHAUNI	VALCINIA VIACIO INTERIOR CANTINIA INTERIOR INTER		i							!
MAN WACCA	POLY(A) FOL TAGLASE REGILLATORY SUBLIMIT	VACCINIA VIAUS (STRAIN WE)		ĺ	1	- 					
TANS VARV	POLY(A) POLYMOLASE REGALATORY SUBLIMIT	VARIOUA VIRGIS		22. 744	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	·				İ	1
PPCPA MYVAL	PROCUEDING LELL NOCLEAN APPROLI	ACTUACION CALIFORNIA DE LA CALIFORNIA DE	-			İ			İ		
MAN IN AN	II I KD PROTEIN IN PR. S P. CION	CACTIA PRECIATI NOCALA MULLIA AFRICA CITA DECISIS VIALIS			::::				İ		
PPE39 HOVAC	2	AUTOCALITY CALIFORNIA MIKI BAR IN THE MONS VIRES		:	; ;	j		-			i
PPEJB NOVAC	TE EARLY PROTEIN	AUTOCA ATTA CALIT (IRMICA MINISTER THE THEORY) VIKINS						Ī		İ	į
PENS ADEOS		INDIAN ADENOVIBUS TYPE 2		j	:::			!	İ	i	!!!
PPENI ADEO	PENTON PROTEIN	HUMAN ADEMOVIRUS TAPE S		1	1 :: :	1		!	;	1	
PPEN) ADEGX	PENTON PROTEIN	AVIAN ADEMOVIRUS GALIO (STRAIN SAT)	-	2						İ	
PPIVE ADED!		INDRIAN ADEMOVIRUS TYPE ?	=			-	-	i	:	i	•
PPIV2 ADEMI		MONSE ADENOVIRUS TYPF I	50								
PPOLI BAYMC		DARI EY YELLOW MUSANC VIRUS (CLANIAN INDIA)	33.33	313.616		2			:	-	
PPOLI BATH	- 2	BARLEY YELLOW MOSAIC VIRUS HAPANESE STRAIN II 1)	24 75	2		5	1000-1-000		į	-	
PPOLI GOAV		HUNGARIAN GRAPEVINE CHRONE MOSAIC VIRIIS	11.	1040-1083	= 1	·	İ		:		
	AMA I POLYPROTEIN	CRAFEVINE FAM. EAF VIRUS	180.1%	Ē.	20.00	20.00	2	2	1,9:1,16:	= :	2070-7044
PPOLI TBRVS		TOMATO BLACK RING VIRUS (STRAIN S)	113:1159		_	-	:	:	;		
		ARABIS MOSAIC VIRUS	13.15	32	12.					ı	
PPOLI BATHO	~ 2	BARLEY YELLOW MUSAIC VIRIIS ICH RAIAM ISOLATLI		60.485						į	
PIOLI BATE		BARLEY YELLOW MOSAIC VIRUS (IAFANÍ SI, STRAIM IL.1)	335.330	\$ 5			į				ļ
11013 CILV	RNAJ POLYPROTEIN	GRAPEVINE PANLEAF VIRUS	20.00	201.00		į					ļ
PPOLI THRYS		TOMATO BLACK RING VIRUS (STRAIN S)	13.466	24.55	26.00	1201-1221		į		-	
PPOLJ TREVA		IOMATO RINGSPOT VIRUS (ISOLATE RASPBERRY)	316.360	:	2						
PROLO BOVEV		BOVING ENTEROVINGS (STRAIN VG. 9.27)	11.13		_		-÷				
POLO BYOY	GENONG POLYTROTEIN	BOVINE VIKAL DIARRILA VIRUS (ISULATE MADE)	11-11	6					1890 7481	101-101	100
2000		COUNTY COLOR DIABOTICA CIDATES (CIDADES CO. 1)			_		,	100		1001 0101	1911
	OCH CALL FOR LAND		3416.3416	74.	100		_				
PROF O COXAS		CONSACR EVIRUS AND ISTRAIN COED	190-067		-				İ	Ī	
VIOLO COXA	GENOME POLYPROTEIN	COXSACRIEVINUS A23 (ECHO 9 VIRUS)	16.19		!					Ī	
PPOLO COXA	GENOME POLYPROTEIN	CONSACKIEVIRUS AS (STRAIN CRICGS)	(1811)	100	1	Ì					
I COLUMN	CENOME BOLYPROTEIN	CONSACRIEVALISMI	1433.1494	19	Ī	ĺ		1			
POLO COXO)	~	COXSACKEVIRISBY	221-255	103-130	1315-1610						İ
PPOLO COXID		CONSACRETATION	37:16	53	109	Ì					
POLO COXOS	GENOME FOR YPROTEON	COXSACKLEVIRUS BS	103:1301	505.1610							
PROLO DENIS	GENOME POLYPROTEIN	DENGIE VIRUS 11PE I (STRAIN SINGAPORE S275/90)	3	E	1311-1316	021-120	1617-1678	1111.1140	100.2161	2401.2436	1010 106
PROLO DENIW	GENOME POLYPROTERY	DENGITE VIRUS TYPE I (STRAIN WESTERN PACIFIC)	919.016	1111111			_	_	-		!
POLO DENE	GENOME POLYPROTEIN	DENGUE VIRUS 1 YPE I (ISOLATE MALAYSIA MI)	136.150	į	_	_	_	_			
FOLG DENTE	GENOME POLYPROTEIN	DENGUE VIRUS IYPE 2 (STRAIN 16681)	20.05	76 61	13:13	1346-1281	101-101	1613.1670	30.01	1347.7364	1001.1032
		The state of the s	200			_	- -				
POCO DENS	GENOME FOLVEROIEIN	DERGOE VINUS LIVER (ALMAND INDICATIONS)	200, 2074	100.04	2	90	200	96.198			7.79
DENSO DENSO	PROLICIDENTO CENOAR POR VPROTEIN	DENGIF VIBUS 1 YET 2 ASTRAIN D. OAL									
	of myre remaining		ł					1	1]

	91616-7119										
	PROTIN	Cincia de poticionen de la companya		•	ı.	ļ					
PPUT O DENZI	1	ILINGIA VIRUS TYPE JISTINAIN JANIAICAL	32	7	3	7	CALA 2	O NEW	AREA?	ARA B	746.7.
			17 mm. 2 72 m.								
PPOLO DENZA	GENOME POLYPROTEIN	DENGINE VIRUS TYPE I (STRAIN IN CARRA A.C.)	001	981-16	1	-					
_	CENCIATE POLYPROTEIN	DENCINE VIRUS TYPE 7 (STRAINPRISO SI)	919.044	E	1-	100	136.138	1611.1620	116.00	1917	100
$\overline{}$			1667.1981	;	7		1	_	_	-	1
	GENDALE PORYTROLEIN	DENGIE: VIRTIS TYPE 3151P AIM TOME A 1934)	619 664	17.63		201.1319].
_		ים אנשים ביוונע ויינים	20.00	12 to 13 to	1217.124		C-1 1141	200 000	111:11:11	74.7 144.	1.1.1.1.1
	STATE OF A PARTY OF A		N. 11.74				_	_			
	CHAPTE TOLITABLE	DENGOE VIRUS 1 YFE 4	1309-1227	-	1611-1627	1120.2346	2342-2159	2400-3420	1045-1064		į
	CENORE FOR LESS IN	ECHOVILLS II (STRAIN GREGORY		72.79		.			İ		
	CENCER POLITICISM	EMCEPHAL DAIYOCARDITIS VIRUS		558-578	12.23	40-1767					i
	CENCER FOLLYROLEIN	ENCETIAL DIAYOCARDITIS VIRIUS (STRAIN TAIC IS NOMINARII TOCZINI		1001	114:11			i			_
The Court of the C		ENCEPTAL CALYOCARDITIS VIRUS (CHANIN TAR TELINAME CINE ART)		1130.1141	11% 1217						_
C E PORCO		MENGO ENCEPHAI OMYCICARIJI IIS VIRLIS (STRAIN 174)	\$60.500	<u> </u>	:		-	:	:	-	:
TO ENGO		MENGO ENCEMIAL ON YOCARDI (15 VIRUS	611.519	-		1				İ	İ
200		FOOT-AND MOUTH DISEASE VIRUS (STRAIN A10 &1)	1 1 1 1	1801-18	1019-1017	100.1911	465.1483	1764.1791	İ	Ī	
PPOLO FEDVS		FOOT AND MOUTH DISEASE VIRUS IS HAIN AS	163:113	_			_			1	1
POLO FADVA		FOUT AND MOUTH DISEASE, VIRUS (STRAIN ATT)	-		1016.1017		146.140	17.130	:	:	:
PPOLO FLEDVO		FOOT AND MOUTH DISEASE VIRIS (STRAINS OF AND DIDEST		100	1017	1			:::!	:	
PPOLO FAMOVS		FOOT-AND-MOUTH DISEASE VIRITS (STRAIN CL. SANTA PAU IC. SEI)			!		_				į
POLO FIGUR		FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C!)		930.00	İ	1		Ī	İ	Ī	1
POCO HCVI		IRPATITIS C VIRUS (ISOLATE 1)	-	ï			181	111.114	200,000	911111	
PPOLO BICVA	GENOME POLYPRO I EIN	HOO CHOLERA VINUS (SIRAIN AL FORT)	101.116	13	1267.130	1378.1802	-		_		141.1785
7			3677.3893	_			_	_	_		
Process	GENOAGE POLYPROTEIN	HOG CHOLERA VIAUS (STRAIN BRESCIA)	101.138	1143-1161	1001.000	1718-1165	1170.2107	111.25.11	10111111	100	147.1761
٠,			1177.160)	1	-				_	_	
	GENOME POLYPROTEIN	HEPATHIS C VINUS (ISOLATE BK)	10:31	101.169	019 619	1001.00	127.2147	3441.3446	1702.410	1000	
VPOLO SICVE	GENOME POLYPROTEIN	IEPATITIS C VINUS LISOLATE ECT	13.	:	,	7	_	_	_	i	İ
	GENOME FOLVITIONED	IEPATITIS C VIRUS (ISOLATE II)	10:21		010.010	M9-109	3	167.680	2042.2457	2817.7810	
TO THE PARTY OF TH	GENORGE POLYTROTEDA	HEPATHUS C VIAUS (1500. A 1E INC V. 476)	113:133	103.160	1	i	ī	ì	_		j
	CAMONE FOL THEOLETA	DEPATITIS C VIRUS (ISOLATE DICTOT)	175			-			Ì	İ	-
	DEPONDE POLYPROTEIN	INFPATITIS C VIRTIS (150) ATE LICTIO)	11.51			l	İ	Ì	Ī		İ
		HEPATITIS CVIRUS (ISOLATE HCV.RF)	113-113	10)-160				İ		i	
HALI O IOM		HEPATHIS CVIRIS (SOLATE HC-JI)	13:03		_			İ		_	1
	GENOAG POLYPROTEIN	HEALTH FURTHER AND	=	ī	- 1	(0, 70)	ī	-			
POLO JICVII		INDEATING VIEW AND AND IN THE	Ī	7	ī	ī	19:10	3	1127.2347	1017.701	1011.1010
		INDAMINE CYRUS INCH AIR AIR INC. IN			;	╗	╗	_		_	
PPOLO HCVIA		IGPATITIS C VIRUS (150) A IF TAPANT SET		i	101.101	107.101	ī	= :	_	_	010.1010
PPOLO HCVIT		IEPATITIS CVIRUS (150) A 1E (1C. 11)		•	Т	i		_		2 2 2	7618.1107
PPOLO HCVTH		INCPATITIS C VIRUS (ISON ATE TH)		Ī	ī	⋮	Ť			2	İ
PROLO HCVTW		IEPAILIS C VIRUS (ISTA ATE TAIWAN)	113.131	141 140	9 9 9 9 9	907 117		1	- 1		
•		IEPALITIS A VIALIS (SIBAIN ((M. 1)	103.333	-	,	7		_	-	_	_
	GENOME POLYPROTEIN	HEPATHES A VIRES (STRAIN 24A)	ī	19.01		101 - 101 -	_	1001.100	1	. !	:
	LENGTH FOR THROTEIN	5	100		-		_	1		<u>.</u>	: :
	CENTRAL FOLLYROIDE	ICPATITIS A VALUS (STRAIN 101)	Ī	101.10	1011.1101		2048.3002	İ		!	i
	MEMORY TOUR IN COLUMN	ILPATITIS A VIRUS (STRAIN CRISS)	199 610				<u>.</u>		İ	İ	:
	CENTRAL FOLITINGS	JEPATITIS A VIRUS (STRAIN (IA 16)			_		İ	<u> </u>		-	:
	CENORAL POLICE IN	PERMITTED A VINUS (STRAIN IN 17)		195.1210		ě	160,040	-	:	!	:
	Change for Velocities	ILLA IIII SA VIRUS (SIRAIN LA)			_		1002.000	<u>-</u> -	:	:	;
TAY OF DEATH	COLORA SOLVED IN THE	INCEPTIONS A VIALUS (STRAIN)		1103.1210	100 100	2009-1019-	1000.000	i		· :	
	2010 PO VENDER DE PROPERTO DE	SIMILAR RECALLES A VIRUS (STRAIN AGALT)	_		_		<u></u>	! !	İ	:	:
	CENTRE POLYPROTEIN	THE PART OF THE PA	•	197			!	i	: !	: :	
	GENOME FOL YPROTEON	l	Ī	,	7		_	_		_	!
	DENOME POLYPROTEDA		T	i	_			_	_	1961-1961	
I _	GENOME POLYPROTEIN	TO STAND BEING BOTTON OF THE PARTY OF THE PA	Ì	_	1033 1003		1610-1634	_		_	i
1			3.4.5	101 : 108 :	_	117.118	_	41). [A4	1831.1840	1948.194.8	

PCCINE	P13(T1.Z1P	All Virgos (Na Barredarbaces)									
CILE RADIK	CROILLE	KIRIX	AFF.	AIN'A 2	JHCA 2	AIIC H	Ain.A.	MILLY	AWA?	311131	AIO,A V
TANO INGIN	IIIN INTERNATION	HIMAN I'M I WOVERTO THE AND KNEET	111.14		:	-:					
March movo	STRUCTURAL POLYPROILIN	AVIAN INITECTIONS INTO A STATE OF THE STATE	Ī			11				ļ	!
A VOICE	ENGAGE FOLVEROIEIN	TATANESE PROPERTIES VIRES (STRAIN SALIA)	ī	9		2		1462 7461	1 :::		
	PARTY TO THE COLUMN	TAPANCE FROM PRINCIPLE STREET STREET						7.67		-	
	ENGAGE POLITICISM	MATANTE ENGLISHED VINIS (SIRAIN FAINANDE)			: :						٠
2	ENOME TOUR VALUE IN	TOTAL PARTY TO A THE PARTY OF T									
TOTAL MUMBER	EMONE FOLITHOLINE	AUNIN VIRUS (NIRA)M MINNERS (2	094		100	200	77.77	241	7	2
2000									_		
Т	CHOME FOR TERDIEIN	LANGAL VIRUS (SIRAIN IF71)				701.6		1312.144	101010		1370
╗				20.70	2.04.2	•			:		:
_ i	CENCHE POLYFIOTEN	LANGAT VIRUS (STRAIN VILLANISEV)	•	\$27.55	1	- !					
MOLO LIV	GENONG POLYPROTEIN	LOUPING ILL VIRUS (L1)	63.89	117.451	115.44.7						
	ENONE POLYPROTEIN	LOUPING ILL VIRUS (STRAIN SD 326)	161.331						i	İ	:
ī	GENOME FOLYPROJEIN	MOSQUITO CELL FUSING AGENT (CFA FLAVIVIRUS)	120.03	1134.1199	1402-1428	700.100	1032.1087	2017.2017	7110.0101		;
7-	ENOME POLYPROFEDI	MARZE DWARF MOSAIC VIRIIS	10.50			_				1	;
_	CENOME BOX YPROTEIN	AND AND AND ENGINEERING COURT		100	10000	101		1000	1000	Ì	
	The se and the second	MUNANT VALLET ENTERTIONS VINUS				6	2011	200	1001	İ	
	CENTRAL POLITICAL	URALI HUGAL UM MUSAIL VIRUS	9		94					i	
	LACKE FOLVFLOIEN	PEPPER MOTTLE VIRUS (CALIFORNIA ISOLATE)	680.717	126.046	1009-1034	1301-1310	1455-1482	148-1500	1676-1607	1921-1945	2003 2033
_	GENOME POLYPROTEIN	POLIOVIRUS TYPE I (STRAIN MAJIONEY)	1409-1433			-					
	GENTAE POLYPROTEIN	POLIOVIRUS TYPE I (STRAIN SABIN)	1410-1433			į.					1
_	GENOME POLYTHOTEIN	POLIOVILUS TYPE 2 (STRAIN LAWSING)	1608-1431						-	Ī	Ī
_	GENOME POLYPROTEIN	POLIDVINUS TYPE 2 (STRAIN W. 1)	1608-1631			Ī	-	-	İ		-
7	GENORAL POLYPROTEIN	POLICOVIETS TYPE 3 (STRAIN 3)1273	17.500	0101.1010		İ					į
_	CENTANT BOX VOR CITE IN	Section of the sectio			: !	-		1			İ
	The second second	The state of the s						ti ti ti ti			
i	UCACHE FOLLING	M. UM POLITVINOS (SIRAIM D)		2	į	3	1440-1495	1497.151	26/16 7674	2	
- 1	ENGINE FOL THROTEDI	FLUM POR POLYVIRIIS (STRAIN EL AMAR)	-	1461-1411							
_	POLYPROTEIN	PLIM POX POT YVIAUS (ISOLATE NAT)	133.178	113.740	1007-1516	1407.1994	-	2605-2623	1066 3090		ļ
PPOLO PPVRA CI		PLUM POX POLYVIRUS (STRAIN RANKOVIC)	2 2	111 140	1001	1467.1494	1446 1511	1601.2621	1011 1101	i	İ
PPOLO PRSVII		PAPAYA RINGSPOT VIRIS (STRAIN P. MITTANT IIA)	22.280		:	!!!!	_	:	-	:	:
		PAPAYA MINGSPOT VIBITS (STRAIN PANILLANT IIA S.1)	101.101	-				İ		:	:
и.		PAPAYA ROGSPOT VIRIIS (STRAIN W)			i				i		į
		PEA SPED BOONE MOSAIC VIRIES IS FRAIN DPDIE	Ī	- 146.346 -	110.00		1001		100	****	1
		POTATO VIBIR VISIBATIO	ĺ,		_		3		_	51	į
ła	CENOAGE POR VPROTECN	POSA PO VIDENCE VIDENCE A BRANCH A BRAN	T		1:						İ
			ŀ					100	10 / 1 C	47.	5
1	GENOME FOR YPROTEIN	POTATO VIRUS Y (SIBAIN M)	7		100	2				_	
OWN O TOTAL	PROME POR VERGIFOR	POTATO VIDE VICE AND CO.	T			_			10	2	2
	FACAGE POR YPROTEIN	PARCHIP VELL OV SCROK CIBIC LICON ATE B. 1311								Ī	
C TABLE	TACASE BOT VERDIEN	CT LANGEMENTALING CONTRACTOR AND ARCH.				-	÷		2	Ī	
STATE AND IN COLUMN	FLOOR FOR CHECKER	The state of the s									ĺ
	THOU IS NOT THE OWNER.	SUCKECKER MUSKIC VIPUS (STINKIN SL.)	2								
	ENOME FOLITACION	SWINE YEAR UNEAR COLASE VIRIS (STRAIN IV) TO	20.5	1505 1670							
	ULTONIA POLITICISM	SWINE VESA ULAR DISPASE VIRIIS (STRAIN (RQ23773)	13.190	1585-1610	_				_		
STATE OF THE PARTY	EMONIE POLYTROI EIN	i	•		=	310.134	1630-1651	1740-1761	1310 0111	1166 2183	3765.2761
MARIO DEL	ENONG FOL YPROTEIN				_	310.134	1630-1653				:
PPOLO TEV	EMONG POLYPROTEIN		827.053	931.980	1016-1042	114 1130	107.1120		1		!
POLO THENS G	ENONE POLYPROTEIN	3	920.941	1074-1095	0118.1110	1520.1544	1610.1477	Ī		İ	İ
PROLO TREEVO G	ENOME POLYPROTEIN	Ī		1117-1111		616.1635				Ī	
PPOLO THENO G	ENOME POLYPROTEIN	MEDENS MURINE EN FFIIA ONIVELITIS VIRUS (STRAIN GOVII)	Т			9	471.011	1446.1677			
Prot 0 TUNY	ENOME POLYPROTEIN	Ī	T	1		la	÷		Ì		İ
PHOLO TYNKY	ENOME POLYPROTEIN	TOBACCO VERN MOTITING VIBILS	2			_			1	İ	
ļ.,	ENONG POLYPROTEIN	WATERKE ON MATCHET	Ŧ			:	i		2	j	-
POLO WAY	ENONE POLYPROTEIN	WEST MILE VIRES	ī			_					
PHOLO YEAVI	GENOME POLYPROTEIN	VELLOW FEVER VIRILE AND THE		1	777		7260 7367			2636.263	2705.2811
POLO YESVI	ENDAGE POL YPROTEIN										
PHOLO YEAVE	ENONE POLYPROTEIN	YELLOW FEVTA VIRIS ISTRAIN 1000/11									
PPOLK POLIN G	ENONG POLYPROTEIN	POLIOVIRUS TYPE LISTRAIN MALIONS VI				Ī			j	j	1
TAN SE MICHAE	MONSTRIBLITIONAL POR YPROTEIN	VENEZIETAN FOLIDIO FUE FILE STATE ST		_						į	ļ
1					7	-	-		112 /114	1111 1111	

PCCENE	1	All Virgars (Ne Becteriophoges)	П		П		П	\Box	П	Г	
THANATOT	PROTEIN	YRUS	125	ARA.	3	7	45	2	CALLA.	ARTO !	AMI A
POLN JCVC	NON-STRUCTURAL POLYPROTEIN	FEINE CALICOVALIS (STRAIN)	ī	2	-		İ		!	i	:
MOLK ICVA	MON-STRUCTURAL POLYPROTEIN	PELINE LALATINIANS (STRAIN TATAN) SI, 1 4)			1			100	1	: 1	İ
POLY SCA	NON-STRICTIONAL POLYPROJEIN	FELIME CALICIVITY'S (STRAIN ! 9)		107-707	ī	_	-				!
DEVEN IS VID	NOW STRUCTURAL POLYPROTEIN	TETATION CONTROL TO THE STATE OF THE STATE O	2		1		1	1			:::
POLN IR VAC	MON-STRUCTURAL POLYPROTEIN	ILTAINIS CARDINIS (SIRAIN)	2	102	! :	!			İ	-	į
	NON-STRUCTURAL POLYPROTEIN	HEPAILLIS E VIRUS (STRAIN MY APPIAR)	١		· i	:		;		1	:
	NON-STRUCTURAL POLYPROTEIN	LEPATISTIS E VIRUS (FIRALS PARISTAN)		1233-13-0						-	
PPOLN MIDOV	MONSTRUCTURAL PALYPROTEIN	MIDDELITURG VIRUS	_	674.643			i	ļ			į
10	MONSTAUCTURAL POLYPROTERM	ONYONG-MYONG VIRUS (STRAIN GULU)		413.634	- 1	200	_				
PFOLK BUDY	NOW STRIKETURAL POLYPROTEIN	AADDIT HEMORAHAGIC DISEASE VIALIS	26.180	10.73	27.120	33.60	110.01	1100	1		
POCH BUDY!	NON-STRUCTURAL POLYPROTEIN	AABBIT IBJOANIACIC DISEASE VIRUS (STRAIN V.DS)	:_	:		!	<u>-</u>		:	:	:
TO BE IT IN	TOTAL CHIEF THE ALL BOX YOR CHIEF	BOSS BIVER VIBILS IS BAIN NI (02)	10.104	1 611	1111.1111	107.1305	Ī	Ī	i		İ
	MONTH OF THE PARTY						·	-: -	!	:	
	MUMS INCLINEAL POLYTROLEIM	AUSS RIVER VIRIS (SIRAIR 191)				Ţ	;			-	
PPOLN RUBYT	NOWSTRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN 110 RIP.N)	3		٦,	_			20.00	1	
PPOLN STV	NONSTRUCTURAL POLYPROTEIN	SEMLIKI FOREST VIRIS	-	617.641	2062-2017	_					
PPOLN SDADO	NOWSTRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYP) (K'KI I BO / SIRAIN I INCHYN I? 4)	!	1131	P.M. 1114						
VICTOR N 1044	MONSTREAT BAL POR VPROTEIN	SINDAIS VIRUS (STANIA LIEST)	L	9.1.21	744.076	1790.1812	_	2218 2218	!	:	i
7774	PLAN BERT LAKE BAN VODOTETA	ECCEL AND	Ī	!							i
	The state of the s		100	1	!	;	:	:			٠
	HAN MENTINASE POLITIKA	DIMONIS TELL UM MUSAIL, VIAI/S			ļ	1		Ī	1		
770	-	TURNITY TELLOW MOSAIC VIRUS				-		:			_
PICE TYPEVA		:	2		-	:		;	:		
PPOLE TYMVE	_		113-233	3	13.13		İ	İ			
POL 5 555V	STRUCTURAL POLYPROTEIN	EASTERN EQUINE ENCEPHALITIS VIRUS	33.50	113.239	401.303				i		
PPOL CEEVI	STRUCTURAL POLYPROTEIN	EASTERN FOLINE ENCEPHALITIS VIRIES	3.50	214-230	193 (61	-					:
PROLE ELEVA	STRIPTIMAL POLYPROTEIN	VENEZUELAN EGGINE ENCEPHALITIS VIRUS (STRAIN TC-13)	13.48	239.245	50.532	+					ļ
Part of Section	CIBICATION AT MAN VANDA COLO	VENEZIE AN FRING PACEPHALITIS VIBLE (SIBAIN TRINIDAD DON		230.345	100	ĺ	i	1		1	
	STATE OF THE STATE	A CALL MARKET TO A CALL				:					
	- STRUCTURAL FULTROOLEN	AVAN IN ELIBOR BURSAL DISSIPACION (SIRAIN 1879)		İ		-	i		!	:	İ
POLS ISDVA	STAUCTURAL POLYFROIEIN	AVIAN IN ECTIONS BUILDING THE STATE OF THE S			-	-	Ì	1		1	
POL BOYC	STRINCTURAL POLYPROTEIN	A VIAN INSECTIOUS BURSAL DISEASE VIRUS (STRAIN CU.1)			İ		· ·				
PPOLS HIDVE	STRUCTURAL POLYPROTEIN	AVIAN INTECTIOUS BLASAL DISEASE VIAUS (STRAIN PIRC. 94)		į							1
PPOLS MOVS	SIRUCTURAL POLYPROTEIN	AVIAN DEECTIOUS BURSAL INSEASE VIRIS (STRAIN STC)				▼.					
PPOLIS DNAVC	STRUCTURAL POLYPROTEIN	ONYONG-WYONG VIRUS (STRAIN GULU)	468.708								
PPOLS MAY		AOSS MVEA VIRIDS (STRAIN 148)	1216-1243							i	
PPOLS AUBVIL		RUBELLA VIRUS (VACCINE STRAIN HPV77)	101.102								
PPOLS RUBYM		AUBELLA VIRUS (STRAIN MIJ)	280 301		1						
PPOLS RUBYR	STRUCTURAL POLYPROTEIN	AtiBELLA VIAUS (VACCINE STAAIN RAIT.)	381-303								
PPOLS RUBYT	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (STRAIN THERIEM	281-303	2							
PPOLS SEV	STRUCTURAL POLYPROTEIN	SEMLIKI FOREST VIRUS	12.50	2 2	100						
PPOLS Shabo	STRUCTURAL POLYPROTEIN	SINDBIS VIRUS (SUBTYPE OCKLIBO / STRAIN EDSOYN B1:1)	13.52								
POLS SDOV	STRUCTURAL POLYPROTEIN	SINDRIS VIRUS (STRAINS IDSP AND HALP)	13.53		1						i i
PPOLS WEEV	STRUCTURAL POLYPROTEIN	WESTERN EQUINE EMCEPHALITIS VIRUS	36-51	308.93							
THOU AVOLE	POL POLYPROTEIN	AVIAN RETICULOENDOMIELIOSIS VIRUS	183-303								
POL BAENA	POL POL YPROTEIN	BABOON ENDOCEMOUS VIRUS (STRAIN M?)	226.344		9101.	90 · 106					
PPOL BIVOS	POL POLYPROTEIN	BOYDE BOADNOOFFICIENCY VIRUS (ISOLATE 106)	101-110	23.76	3		Ì				
FO. 21/17	POL POLYPROTEIN	BOYD'E DAMINON FICIENCY VIRUS (ISOLATE 177)	=	10.76	3			Ī			
PPOL BLVAU		BOVING LEUKEMIA VIRUS (AUSTRALIAN ISOLATE)	487.504								
PPOL BLVI	POL POLYPROTEIN (NEVEASE TRANSCRIPTASE	BOYINE LEUKEARA VIAUS (IAPANESE ISULATE BLY-1)	487.504								
PPOL CAEVC		CAPRIME ARTHRITIS ENCEPTIALITIS VIRUS (STRAIN CORK)	191-419	636-671							
PTOL CAMVC		CALL DECOVER MOSAIC VIRIS (STRAIN CM 1841)	184-704	380-407	471496						
POL CANVO	ENZYMATIC POLYPROTEIN	CALL DECOVER MOSAIC VIRUS (STRAIN ON!)	135.199	175.402	3						
PPOL CAMVE		CAIL IT LOWER MOSAIC VIAUS (STAAIN BBC)	184.204	180 407	3						
THE CANN		CAULIFLOWER MOSAIC VIRUS (STRAIN MYBISS)	70.97	107 581	5	173-405					
TO CARVS		CALL D'LOWER MOSAIC VIRUS (STRAIN STRASHOLMG)	Ī	100							ļ
POL CEN		CARNATION ETCITED RING VIRIES	1	3							
PPOL COYNY	$\overline{}$	COMMELINA YELLOW MOITH E VIRUS	Ī	186.1	20 16. 16. 16.	2		Ì			
MOLEAVY	POL POLYPROTEIN	EQUIPME IN ECTIONS ANEWLA VIRUS (CLOWE 1)69)	27.438	1	-						
POL FIAVO	POLYPROTEIN	I OTIME THAT CITIONS AND AND VIRES (CLONE CL.)	22.0				7				
										1	

PCGENE	Pricruzie	AM Viruses (Ne Becceriafibages)				П	П	П	П	T	
LILE HAPIE	PROTEIN	YIRUS	285	SECO.	AREAL	VEC I	ANTAL A	41541-1	DELGA-	APEA!	AREA
POL EIAW	POL POLYPROTEIN	EQUINT INFECTIOUS ANIMIA VIRUS (1501 ATE WYDNING)			!	-	1	:	i ::	:	
- 1	POL POLYPROTEIN	FELINE ENTRICENDUS VIRUS I CT.1			1		:	:	;		
TO TAPE	POLYPROTEIN	FELINE INCHINODIL TO II NEV VITAS (ISOI ATE TE I ALORIA)	1 1 1 1 1 1		!	1	1::1	į	i	;	
t	POL POL YEAR OLE IN	THE PARTY OF THE P	ī	064.69	1000	041.100	İ			. !	:
-	POLYTICIAN CHRONELL	PRODUCE TO CALC VILLE ACTION OF COMMENT	T	464.417			İ			.	
ı,	ENCYMAIL FOLTER	INTERIOR CONTRACTOR CO	Ĺ	768.788		Ì	Ì	Ì		-	
. 1	TOUR TOUR VIEW OF THE PARTY OF	GIBRON APE : FIREFAILS LIBITS	9	8	100		İ			İ	ĺ
THE IN	POLICE TO VEROLETA	BILDIAN I CELL LEINENIA VIRUS INTELISIRAIN ATKI	10.36			İ	Ì	İ	-	i	į
1	POL POL VPROTEIN	HIMMAN T-CELL I FIRE LAHA VIRIS TYPE I (CARMINIAN ISINATU)	330.346						: !	:	
1	POL POLYPROJEIN	HINMAN T CELL LEUKENHA VIRUS TYPE II	608 637		İ	F					!
1	POL POL YPROJEDN	INDIAN INDAINOBEFICIENCY VIRIS TYPE I (ARVZISTZ ISOLATE)	100		!			ĺ			
1	POL POL YPROJEDA	INDIAN DONNONEFICIENCY VIRIS TYPE I (BHID ISOLATE)	615-660	877.899		ŀ	İ				
ł	POL POL YPROJEN	INDICAM DOGRAMONE I CIENCY VIRUS TYPE I (BIIS ISOLATE)	13.19			•					
ì	POLYTROIEIN	INDMAN INDAUNODEFICIENCY VIRUS TYPE I (HAU ISOLATI:)	53.69			-				:	!
ı	POL POLYPROTEIN	HUDMAN DAMUNODE LICIENCY VIRUS TYPE I (1:1.1 (SOLATI)	633-643	910 010		-			- i	:	
ш	POL POLYPROJEIN	HUMAN INDITINODE ICIENCY VIRUS TYPE I (HXB2 ISOLATE)	200			j ·					
1	POL POLYPROTEIN	HIMAN MARINODEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)	160 140								
1	POL POLYMOTEIN	HUMAAN DIDITIMODEFICIENCY VIRUS TYPE I (MAL ISOLATE)	139 686								
PPOL HVINO	POL POLYPROTEIN	INDIAN DOGINODEFICIENCY VIRUS TYPE I (AIN ISOLATE)	163.690								
ı	POL POLYPROTEIN	INDIAN DOGMODEFICIENCY VIRUS TYPE I (NEW YORK S ISOLATE)	27.52	2	İ				ا	ļ	
PPOL INVIND	POL POLYPROTEIN	INDIAN INDIANODETICIENCY VIRUS TYPE I (NOK ISOLATE)	2	20 00					İ		
- 1	POL POLYTROTEIN	HUMAN INDIANDEFICIENCY VIRIS TYPE I (OVI ISOLATE)	100								
70 IVI	POL POLYPROTEIN	HUMAN INDAMEDINE FICIENCY VIRUS TYPE I (PV221SOLATE)	9	17		-		j		1	i
. 1	POL POL YPROTEIN	INDIAN DOCUMODEFICIENCY VIRUS TYPE I (AFAIAT ISOCATE)			:	-					!
70.7	POL POLYPROTEIN	1									i
- 1	POL POL YPROTEIN	HARIAN BOARNODEFICIENCY VIRIS 197E I (22/COC.2341/OLATE)	3	910 618	j	7	Ì	-		i	
TOTAL BINITS	POL POL VEDOLETIN	2 2	20,00	18	İ	İ	İ	i	-	1	1
i	POL POL VPROTEIN	HAMAN BEANDOEFICIENCY VIRIS TYPE 2 (150) ATE CANZI			İ	-	İ	:	i	-	!
1	POL POLYPROTEIN	INMAN MONODEFICIENCY VIRUS TYPE 3 (150). A TE D194)	197.424	210-520	-	-	İ	Ì		i !	!
PPOL HYDDS	POL POLYPROTEIN	INDIAN DAG BODEFICIENCY VIRUS TYPE 1 (1501.ATE D205.1)	903.934			-					
t I	POL POLYPROTEIN	INDIAN DEGNODE HOLENCY VINUS TYTE 2 (150), ATE GHANA. 1)	38.95	10.61	_						
H	POL POLYMOTEIN	INDIAN DERUNONE MIENCY VIRUS TYPE 1 (150). ATE NITI. 2)	3.5	261.16	10.00						
1	POL POLYPROTEIN	HIBAAN DAGONOPETICIENCY VIRUS 177E 2 (ISOLATE ROD)	2			İ	Ì				
PPOL IIVISB	POLYPROTEIN	HIDLAN DORMMODE HEIRNCY VINUS TYTE 3 (ISOLATE SELISY)	31.00	001			1	Ì	Ī	Ī	
1	PUTATIVE POL POLYPROTEIN	ILANSTEA INTRACESTERNAL A PARTICILE	3	101.133	460 417	İ	Ì		Ī		
PPOL EMA	PUTATIVE POL POLYPROTEIN	MOUSE INTRACISTERMAL A.PARTICLE	183-701	200-236	200	531.552	96.30	Ì			
PPOL UNAL	PROBABLE FOL POLYPROTEIN	MOUSE INTRACISTERMAL A.PARTICLE	102-130	126-155	10	435.042					
770, 131,	POL POL VARATERIA	MANY CELL FOCHING SORVING MINERAL FUNCTION VIEWS (1804 AVE 7)		200	Ş		Ì	Ī		Ī	
PPOL MEVAK	POLYPROTEDY	AKA MADAE I EUKEMIA VIRIS		726.744	1						:
PPOL ME.VAV	PUL POLYPROTEIN	AKV MITTELEUKEMA VIRUS		971.998	1004-1024	(MI.109)	_	!	;	: :	:
PPOL NO.VCB	POL POLYPROTEIN	CAS-BR E MURINE LEIREMIA VIRUS	3	0110	2						
	TAL POLITACION	FRENCH MANAGER UNIVERSITY (1904 A 19 27)			60.00	98		Ì			
	TOTAL TOTAL STATE OF THE PARTY	FOREST LA MINE LEVEL A VINITE AND A COLOR			200		İ	j	İ	i	
1	NI DE CONTRACTOR	AND ONE VALIDAME IN FIRE FAIR VIBILE			\$ \$!	201		-	-	:	:
PPOL NATO	POL PULYPROTEIN	RADIATION MATURE LETTER FATTA VIRUS	-		1004.1024	1001		İ	İ	:	!
PPOL MLVIK	POL POLYPROTEIN	RADIATION MITTINE LEUKTANA VIRUS (STRAIN KAPLAN)	10.10	189.400	- 89 949		İ	Ī		i	
PPOL MATIVIB	POL POLYPRUIEIN	MOUSE MANDMARY TIRKIN VIRIIS (STRAIN BRE)	10.38	131.751	!	<u> </u>	_	Ì			
PPOL HOMY	POL POLYPROTEIN	SOUGH MASON-PILLER VIRUS	20.20								
PO ONS	POL POL VAROIERA	OVINE LEMITIVIAUS (STRAIN SA OMVV.)	368.303	467 411	3	8				ĺ	!
700	FOL PARTIEN	RUCE DARCINA VINOS (STRAIN PRACUE C.)	7	100	Ì			Ì	Ì		
The state	Marine Marine	RICE HOUSE BATTE IN COM VIBILE AND SPINES	ī			1	İ	1	Ì	İ	
	POLITICALIA:	ANT DESCRIPTION OF THE PROPERTY OF THE PROPERT				-	1	1	1		

PCCFAE	10110011011							•			
FILENAME	PROTEIN	All Virues (No Becteriophoges)									ſ
PPOL SFVI	POL POLYPROTERY	SDGAN FOAMY VIRING ITYPE II	3	3	3	ABEAS	BEA	4864	ABIA	AREAL	ARCAS
POL SFVIL	POL POLYPROTEIN	SOUGH FOAKY VIBILS IT VE 17 STEAM 1 P. 1.	Ť								
POL SIVAL	POL POLYPROJEIN	KINIAN MANDONICE CONTRACTOR CONTR	7			20.00					
DAVE SOM	200 No. 100 No	SECTION OF THE PLANT OF THE PROPERTY ISONATE)	=								
200		SIMILATE INTERPRETATION OF THE STATE (ACMI) ISON ATE)	_	700.930						į.	::::
	rut rut ren in 1	SIMIAN INDITINODE I ICIENCY VIRIS (ISOLATE AGM / CLONE GAL I)	23.6%							1	
NA STATE	FOL FOL YPEDIEIN	SIMILAN INDAMPORT PICIENCY VIRIS (TYO.) INMIATE)		110.516					1		1
200	POL POLYPROTEIN	CHBO'ANZEE MANIMUNEFICIENCY VIRIUS	Ť		!						
POL SIVEB	POL POLYPROTISM	SINGAN MANAMORI I PUBLIC VIEWS MENT ATE CHAIR	ī		: !	İ				_	
POC SIVE	POL POLYPROTEIN	CIMIAN INDICATE OF THE PARTY OF			:	:					:
PPO SIVE	POL POL VPB CIENT	SIMPLE STATE OF COME A VINIS (KINIS) IN THE STATE OF THE	100.40	100.00							
27/12 8044		SIMULATE INTERPRETATION AND INTERPRETATION OF THE PROPERTY OF	100 403	111111	109.90	: 		-	İ	; !	İ
	TOTAL PROJECT	SIMILAR INSTITUTOR FIG TENCY VIRUS (F 216/SAGIA ISON ATE)	143.370	100 149	<u> </u>	i i			į		
300	FOL POLYPROTEIN	SIMIAN BORONDELICIENCY VIRING I'RIMCI I ISOLATED	146.371	18	-						
POL SOM	POL POLYPROTEIN	SOCIALEL MONEY PETENCHEIN			: : : : :	-					
PPOL SMSAV	POL POLYPROTEIN	CIVIAN CARCINAL CARLO		:							:
AND SOL	SAZVALATIC BOLVERONES	THE PARTY AND TH	2	I							
	LINE INVITED IN	CARDINE VIRUS	=======================================								
2	FOL POLYPROTEIN	SINGAN RETROVARIS	141 741	1		1	1				
70, 41,	POL POLYMOTEIN	VISNA I BRISMBIR ACTOR AND ACTOR			-						
PPOL VILVI	POL POLYPROTEIN	VICINA BENTALINA SERVICE SERVI	200	9	18						İ
POL VII VI	POLINI YPROTEIN	STATE STATE OF THE	41.507	45 - 664	97.00	٠.					
A 100 A 100		VISHA LEMINIMUS (STRAIN 1914 / CLONE L'VI (KS2)	418.307	651 666	3					Ī	
	LANDS STRUCTURAL PROSPRIOPROSEIN PPING	HUMAN CYTOMEGAI OVIRIS (SIRAIN ADIG)		11.210	:	!	-	<u> </u>	!!	i	1
TELEVANA	HOSPHUPRUTEIN	HUMAN CYTOMEGAL UVIRUS (STRAIN AD169)	114.141			İ					
PFF HSV60		HEAPES SOOT EX VIRUS LIYPE A LYTEAIN CO.		1	}	Ī					
PPMS HOAVA	65 KD LOWER HAT TAX PHOSPHOPROTEIN	HERITAN CYTOME CALOVERILE ACTION IN ALLICON		è							j
PPES BOAT										i	İ
AVACAL ITEMA		MANAGE TOPECAL OVINIO (SIRAIN TOWNE)	20:32			!		:			-
	ALMA FIGSTRUFACIES	HUMLAN CYTCHEGALOVIRUS (STRAIN ADISS)	79.102		-	<u>:</u>	İ	Ī	i I	1	
	TOTE IN TRU	MOUSE MANONARY TIMEDR VIRUS (STRAIN BR6)	19.60	-						i	
PART MORTING		MOUSE MANAGARY TIBLION VIRITE ACTIONS CO.			1	-					
PPRIL MOUTING	PROTEIN PRIS	MONICE MANAGEM TITAGE CONTINUES CONT	•								i i
PPRT MOUTVO	PROTEDIPATO	Walles Mandale Comment of Salada Oct.	•								
PRASH LISTHA	TRANSFORMENT PROTECUS BY: AND BYE	MOUSE MUMBER THAT THE STRAIN CR.	19.00					İ		İ	
PRACE BRACK	TO THE CONTROL OF THE PARTY OF	HAMAET MUTURE SARCONIA VIRUS	49.35		İ		Ī				
THE COLUMN	PANSICAL PROTEINS P.11 AND P.19	RASILED RAT SARCOMA VIRUS	12:51			-			İ		
	ACTAN ELEMENT PROTEIN	CAMPOLETIS SONORENSIS VIRIIS	1		-	1					
WENT VACCV	HIT AMPICIN RESISTANCE PROTEIN	VACCINIA VIRUS (STRAIN WR), AND IS IRAIN COFFINIACEM	1								
PREFIT VARV	AUS ANDICIN PESISTANCE PROTEIN	VARUOR A VIRUS									
PREV SIVAG	PEV PROTEIN	SINDAN DANDRESCIENCY VIBILE ACAD SOLVE	1		317.515						
PREV SIVOR	REV PROTEIN	SIMIAN MANIPARTIENCY VIBILE MOST AND PART									
PRIRI ASFM3	RIBONACLEOSIDE DIPHOSTITATE REDICTASE	ABBICAN CWINE FLATE VIOLE 1601 157	2		ļ						
PRIR! EDV	RIBONARI EOTIDE BENNETANE	CASTERN STATE WALLE VINCE (ISULATE MALAWILLE, 70/1)	130 164	189.310	101.10		ĺ		Ī	ĺ	
PRINT HOLVA	PROPERTY CO. THE SCHOOL SET	L'SIEIN-BACK VIXUS (SIKAIN 1195.E)	39.112		!	Ī	Ì		İ	i	
MAN INCHIL	TO THE POST OF THE PERSON NAMED IN CO.	HUMAN CTIONE GALOVIRUS (STRAIN AD169)	102-312	717-699				Ī	İ	İ	İ
TO THE PERSON	AUDOM POPULE REDUCTIVASE		415-110	207-613			İ	Ī	İ	i	
	ALIBORACLE DI LIDE II EDUC I ASE	(AIN ABAP)	56.55	266.248	707 149		İ	Ī	Ì		j
VEACUAL IN 18	ALBOMOCLE DI ILIZE IL EDUCTASE		18.131				Ì				
ZERI VACC	RIBONIACLEOTIDE REDUCTASE		-		:::					-	
TRIK! VACEV	RESOMUCT. EOTEDE RECONCTASE	VACCONIA VIRUS (STRAIN WR)			1:::		-				
PKIR! VARV	RIBONUCLEOTEDE REDIXCTASE	VANOLA VIRUS		İ							
PRIRI VZVO	RIBONIXCLEOTIDE REDUCTASE	VAUCELLA-ZOSTER VIRUS (STRAIN INILIAE)									
PRIRE EBV	ANDONUCL EDITOE A EDUCTASE	FPCTERL DARB VIBIL ACTO ALL DOLD	26.50	27.70	258.210						1
PEGEZ HSVII		THE STATE OF THE S	309-236						Ī		İ
Ĺ	BIRONGIC: Entire BENICA ACE	HEATER SUMPLEX VIPIUS (TYPE I / STRAIN 17)	3.2	175.202			İ	İ	İ	İ	i
1			50-02	245.261	174.29	İ	İ	İ		-	
			19:10	333.200				İ	İ	İ	
	DIBONAL COUNTY BELLEVILLE		144.366			İ	İ	İ	i	İ	-
			19:19	31.33	-	i	İ	İ			
			313.310		-			j	-	_	į
PRINT SPAKA			2		1	!		j			
PRING VACCO											
Π.		4	2	T				Ì			
PRING VACCV	AUROMICLEOTIDE REDUCTASE		30.						İ		

PCGENE	417	All Virone I'ne Buirelefhegen)	AREAL	ABGAS	V TVINV	PALAS	LANG	ARCAS	AREAT	Vade	AMEA 9
7000	DESCRIPTION OF DEPOSIT ASS					1		•			
The same		TER VIAUS (STRAIN INIAIAS)	117.258		:						
ALAN AVEVE	SALL SERVICE BROTEIN STANS OF TRANSPORT	IAN ROUS ASSOCIATION VINITS TVPT			:	-				•	
MAGIL AVOVE	MAIL SENTIMENT AND THE PROPERTY OF THE PARTY	CONTA VIBILIA CONTACTO AND SCHALL CONTACTOR	20110	365 390	100	361.37	:				
A AVEC	ENA-POLISIES INAISCENTING SECTION	STATE A VIBILIA	21.15	200	1.34	361.578	i !		- 		!
1	MAA MEASSOCIATED INCASSING STOCKED	CODA VINE CONTRACTOR MILECTON	20.00	62.18	100	1003-1012					
HOI VACCC	DNA-DOLECTED KNA POL. 147 K.D POL. 1727 IDE		Ī	104 150							
	DNA DDECTED RNA POLYMENASE 147 KD POLYTE VA	CCIMICA VINICALIA WINI	1	-		100	Ī		:	!	:
PRPOI VARV	DNA. DIRECTED INA POLYMERASE 147 KD POLYPE	MOLA VIRUS	2		•	-	i				
PEPOS CAPVIC	DNA-DIRECTED ANA POLYMERASE 133 KD POLYPE	PRIPOXVIAUS (STAAIN KS-1)	-			!					
PRINCI COWPY	DNA-DIRECTED RNA POLYNERASE 112 KD POLYPE	WPOX VIALIS	2	20 324	50.00		-	:	:	:	:
PRINT VACEV	THE THE CITY BANK HOW YAVE ASE 117 RD POLYPE	VACCOMA VIBUS ISTRAIN WAT AND ISTRAIN CONTINUALLIN	2 3	30.37	505 08				:	-	
	2007 100 100 100 100 100 100 100 100 100	ABITA VIRGI	2	2.0	20.00	-		!			
	DAA-DIRECTED KAN POLITIKE AASE 114 AUTOLITIES	CANCELLA COMPANY COMPA	1		:	!	!	:		:	:
NO VACE	DNA DIRECTED HAN POLYNCHASE DIRECTOR	THE STATE OF THE S		!	:	:		:			
	DNA-DIRECTED RNA POLYMERASE 35 KD POLYFIF	VACCIMIA VIRUS (STRAIN WR)			_	•					
ALPOS VARV	DNA DIRECTED RNA POLYMERASE 19 KD FOLYFIF	VARIOLA VIRUS		-							
	DAY DURECTED BINA POLYNERASE 19 KD FOLVETP	VACCINIA VIBLIS (STRAIN WE) AND (STRAIN CONTINIACION)	:		_						
VATA INST	THE PRINCIPLE AND VALENAGE IS NO PORTO	COMIN VIBIOS ISTRAIN WITH AND ISTRAIN CONTINUACION	*								
	THE PARTY OF THE P	CABINE A VIDER									
	UPA-UNEC IED IMA POLITICASE IVAD POLITICA				!	-	1	!	:	:	: {
78706 7087	DNA-DIRECTED RNA POLYMERASE IS ND POLYTER	POWILOS (STRAIN FF. 1)							101.1		1.4,
PEPON LELV	ANA DIRECTED RNA POLYMICANSE	LYSTAD VIRUS		3:	_	_				_	
			30.00	_	٠.	;		i	!		
200	ALLA PARECTER DIVA BOY VALERAGE	COUNCE AND FEBRUARY	97:11	603-617	134 774	150-520	3510-2551	1011			
3	APA WALL ILM MAY TOL I PILMASE		341.764	15		133.114	100.000			_	
	ANA DIRECTED RAN POLYMERASE SUBLIMITY	JINDRI VIRUS (SIRAIP III) III III III III III III III III	ı		_	•					
PRESI LANN	ANA DIRECTED RNA POLYMERASE SUBUNIT PI	MELLENZA A VIRUS (SIRAIN ANNY AKHORAFIZI)	74.75		!		-	1	:	,	1
PARE LABSI	THAT DIRECTED BNA POLYMERASE SUBUNIT PI	MILUENZA A VIBUS (STRAIN ARCHING/11/34)	744.762			•••					1
13	SELA PUBLICATE BALA BOI VACEBAGE SITHING PI	NOT LIENZA A VIBING ISTRAIN ACTUM DIMM/7)	244.363		!	!					
		1214	100	i	<u>:</u>			-	İ	İ	i !
THE LACE	The Official Car Port Presents Street 1				1			1			:
RED'I LAIREO	ANA DURECTED RNA POLYMERASE SUBLINITY	-		:				:			•
	ANA DIRECTED ANA POLYMERASE SUBUMIT PI			i	-				-	:	
	RMA.DIRECTED RNA POLYNERASE SUBLINII PI	VIRUS (STRAIN	70.00	İ	-	-) ! ! !	:
PREDI LAKOR	ANA DIRECTED ANA POLYNGRASE SUBLIMIT PI	MILLENZA A VIRUS (STRAIN ARORE A 1266)	144-162			-					
	ANA DIRECTED BNA POLYNORASE SCIBITUIT PI	TO LIENZA A VIRIUS (STRAIM AN EMINGRAD/134/37)	344.363			•					
٠.	BNA DIEFCTED BNA POLYMERASE SUBINIT PI	MILLERZA A VIRUS (STRAIN AN ENINGRALVIDALIVE)	204.262								
	PAR STREET BANK BOX VACEBACE CITIZENINE P.	VIETS (STRAIN	244.262		<u>.</u>	į	<u> </u>		i		-
	THE CHANGE OF THE CONTRACT OF		244.262	i							-
	AND DESCRIPTION OF THE PARTY OF	A VIDIO CETO AIN	244.767	İ			Ī				
MAC MAC	MA DOECTED INA TOLIMERASE SUBURILL					Ī					
	MANUFECTED INVA PULTMERASE SUBURILLE			Ī						-	
P	RAA-DOLECTED MAA POLTMERASE SUBLINII FI	THE STATE OF THE S		İ	İ				İ	i	
rate (ASD)	ANA DIRECTED ANA POLYNGRASE SUBLINIT PI	2	797	j	-				İ	!	
•	ANA DIRECTED ANA POLYNCERASE SIBILNIT PI	2	266.762							İ	
	RNA DIRECTED RNA FOL WIERASE SUBUNIT PI	VIRUS (STRAIN AVICTORIA/1/15)	9	14.36	-						
ι.	RNA-DIRECTED RNA POLYNGRASE SUBUNIT PI		244.162						į	į	į
	RNA-DIRECTED RNA POLYMERASE SUBINIT PI	VIRIUS (SIRAIN ACWISCOMSIN/1527/11)	244.262		-				:	-	
PAUL LAZIU	ANA DOLECTED ANA POLYNGRASE SIBIRIT PI	INFLUENZA A VIRUS (STRAIN A/SWINE/JUNG KONG/126/12)	244.762			į			i		
PRED LAZON	RNA DIRECTED RNA POLYMERASE SUBLIMIT PI	MELLENZA A VIRUS (STRAIM ASWINE/ONTARIO/UTI)	144.262								
HAY IGER	ENA DIRECTED ENA POLYNGRASE SUBINIT PI	Z	244.362							İ	
SEED PARK	BMA PUBLICATED BMA POR VACEBAGE STRING PI	STRAIN BVANN ARBONING ICOLD ADAPTEDIN	201.172	-	. !						!
4	DAY NOR CHENT BUY BOY WAS BACK CITAINED BY	B VERT CARACHET BLAND ABBORTOM INTO BUT PET	204.222							İ	
	ANA-DIMENTED MAN COLUMNATE SUSSIES			Ī	-	İ		Ī			Ī
MAN DATE	MAN-DIALCIEU MAN FOLTPMANSE SUBURITY			1		Ī	1			1	!
•	TANA DIRECTED ANA POLITICE AND SUBJECT OF	TOTAL STREET STREET				-		-	:	:	•
_1	MAA DRECTED RAA POLTALERASE SINGUAL 71	A VIACO ISTRAIN MANY ANTONOMINO			•	-	:				
_1	RNA DIRECTED RNA POLYNERASE SUBLINITY	A A VIRUS (SIRAIN ANYCRAIIONRAIN MOS)		i	:	i	!	;	:	:	•
- 1	ANA DIRECTED ANA POLYNIERASE SUBINITY	A VIRIS (STRAIN AFOWL FLAGUE VIRUSROSTOCKA)			-	-	1		:	i	-
PRACT IAGUS	ANA DIRECTED ANA POLYMERASE STRING PE	A A VIRUS (SIRAIN ACIOLI) AIAR VI ANIV 10477)	200	i	i	ļ	1	İ	i	-	
יות עווי	ANA DURCTED ANA POLYNERASE SUBLIMITY	A VIRUS (STRAIN AT QUINEA DADON/416/71)			<u>-</u>		Ī	Ī	Ī	Ī	Ī
TREE MEI	ANA-DIRECTED RNA POLYNGRASE SUBLINIT PI	A VIRUS (STRAIN AL EMINGRADY) 4057)	334-333				1			-	
PURP IALES	RMA.DIRECTED RNA POLYMERASE STIBLINIT PT	INTELERNMENT AND THE CONTRACT OF THE CONTRACT	\$14.337		_						

PCGINE	PITCTLZIP	All Virune (No Batteriophages)				г		ſ			
LILEBAME	INDICIN	VIRUS	6716	0 MI A 1	A COLUMN	12	41.45	A8124	411.1	MEAS	1
PART IAPITE	ANA DIRECTED ANA POLYMERASE SUBJECT FOR	INSTITUTION A VIRIS (STRAIN AFINITALIZATION AFINITALIZATION)	1				-	-	!	:	
PALES TARUE	ANA DIRECTED ANA POLYNICASSE SUBINIT PT	A A VIRUS (STRAIN	_	:	:			:	!	:	1
PRRF1 IASON	ANA DIRECTED ANA POLYNERA SE SUBIRALI PI	A A VIRIJS (SIRA	314.557								
TANK TANK	BNA DIRECTED RNA POLITICEASE SIGNINI P.	A A VIRUS (STRA	25.5					i			
יייייייייייייייייייייייייייייייייייייי	ANA DIRECTED ANA POLYMERASE SUBMINI PA	INTELLECTOR A VIRIS (PIRAIN AVAILAGE SALITIVITY)				-		1	!		!
וווצאן ניחזא	ANA DIRECTED MAPOLYNIERASE SIBILINIT PI	A A VIRUS (ST	123	1			:	!	:	-	
PRINT IAZEE	ANA DIRECTED RIVA POLYMERASE STIBLINIT PT	VIRUS ISTRAIN	115.55	į	:		• •	; 	; !	:	!
MRN INETT	RMA DIRECTED RNA POLYMERASE SUBLIMIT PT	Y	\$30.539							1	i
Name of the last	RMA DIRECTED RMA POLYMERASE SUBINITY PI		*	i							
Dan Cant	DAY DURE TED AND FOL THERASE SUBINITY	DELIEPZA B VIRUS (STRAIN BIANN ARBOROING [WILD: TYPE])									İ
PRESS DECIS	THE DOMESTED AND POLYACEDA OF STIRLING BY	ENGLISHED CHILD STRAIN CHINGS				i		:	:	!	
PRUD IAANH	BNA-DORECTED BNA POLVMERASE SUBLINIT PI	INCLUSIVE A VIETS (STRAIN ANN ARROPANA)	310.314	199		+		İ			1
PALLET ASUD	MA-DIRECTED RIVA FOLYMERASE SURINGERS	N.K. AUNIVITA	76			1	i		!		1
PRATE IACIE	HNA-DIRECTED RNA POLYMERASE SIJUUNIT PJ		Z Z	542.560		. : .			-		
PRED) LASTR	ANA-DIRECTED ANA POLYMERASE SUBLINIT PI	AFOWL PLAGUE VIRUSAIOSTOCKING	316.334					İ		I	
PRED LATEN	RNA-DIRECTED RNA POLYMERASE SUBURIT PI	DELLENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSAN EYBRIDGE)	319-234	2	ĺ	1	Ī	Ī		İ	
PARPI IAOUS	AMA-DARECTED AMA POLYMERASE SUBUNIT PI	INTLUENZA A VIRUS (STRAIN A/GULL/A/ARVLAND/704/17)	39.334	25.56		Ţ. 		-	:		I
PILLO IAGUA	AMA-DIRECTED RIMA POLYMERASE SUBUNIT PI	INFLUENZA A VIRUS (STRAIN A/GULL/ASTRAKITAW127/44)	219.234	242.560							
Paul Mare	MA-DIRECTED THA POLYAGAASE SUBUNIT P)	5	19:334	300							<u>'</u>
THE PARTY	MAN DIRECTED ANA POLYNDRASE SUBUNIT P)	INTLUENZA A VIRUS (STRAIN ACQUINEA ONDONITATION))	7.	3							
	MAN DURECTED RIVA FOR THE RASE SUBLING FO	INTUENZA A VIRUS (STRAIN AEQUINE/FRACIII /1/56)	2	36.5		-					j
	AMA. DURCTED BUA POL VALEDA CE CITATINI PI	DATIFIED A VIBIL COMEN AND AND SAME	36.7.	227	Ī	-	Ī	Ì			
PRED INCE	RNA DIRECTED BNA POLYNGBASE SIGNIANI PI	INCLUENZA A VIENZA INTERANA AR EMINICIA ANTICALIA		8 5		İ		İ			
-	ANA-DIRECTED ANA POLYNGRASE SUBUNIT PI	DRIUENZA A VIRUS (STRAIN AA ENINGRADVIJUTIST)	16.51	3	-	1		Ī		-	1
PRE) IMES	RNA-DIRECTED RNA POLYNGRASE SIBUNIT PI	DELLENZA A VIRUS (STRAIN AL ENDICAADV) (447/5))	319.314	35.55		ŀ		Ī		İ	
AND INVE	RNA-DIRECTED ANA POLYMERASE SUBINIT PI	INTLUENZA A VIRUS (STRAIN ARIAL LARINGE V CORNATIONS)	219-334	343.500			Ī			Ī	
	THE PARTY OF THE PARTY WAS ASSESSED.		2	3		7					
	ANA DIRECTED ANA POLYMORASE SUBJECT DE	INSTITUTE A VINCE IN THAT ANY ADDRESS		3							! !
10	RNA-DIRECTED RNA POLYNGRASE SIBILINI PI	STRATE ARUDOV TURNSTONENEW ILRST Y/47		95	-	İ		1	-		-
1 1	RNA DIRECTED RNA POLYNGRASE SUBINIT PI	A WAUS (STRAIN ASEALMIASSACIUSETTS/11/47)		- 3	İ		1		İ	ĺ	-
MAN TO THE	ANA COLECTED ANA POLYNORASE SUBLINIT PI	A VIRUS		342 540				Ī			İ
	RAN-LARE LIED AND PULTING ASE SHELINITY	INTEREST A VIRUS (STRAIN A/TURKEY-SIRMI (OTANS)) 40)	19.214	25.500							
ZW7	ANA-DIRECTED ANA POLYMERASE SUBLINIT PI	NAME		9			İ				
	RNA-DIRECTED RNA POLYNGRASE SUBLINIT PI	VIAUS (STRAIN	30.5	35.5	İ	Ī	Ì	Ī			
PRUS INZTE	RNA-DIRECTED RNA POLYNGRASE SUBUNIT PI		315.334	505.50		Ī	Ť	Ī	Ī	İ	
PRES DARK	- iı	ISTRAIN DVANN ARBORUMA ICOLD ABAPTERIN	98-1	119.561			İ	Ī			
Т	NA DIRECTED ANA PARTMENASE SUBLINITED	DATURNZA B VIRUS (STACIN BLANN AABONING (WILD: TYPE))	\$	\$15.561							İ
PRRET DACIT		212				T	Ì				
L	RNA-DIRECTED ANA POL SUBURIT PI	THOCOTO VALUS	10.5		İ	Ī	T	Ī	Ī		
ī	RNA-DIRECTED RNA POL YNGRASE	HUMAN CORONAVIRUS (STRAIN 27ºE)	8	410.436	12.03	10(1:0)	33.130	1561.1560	23.2169	7074.3003	111.1116
	RNA-DIRECTED RNA POLYMERASE	MENTING HEPATITES VIRUS (STRAIN DEFECTIVE HIN)	Π	Т	i	-	Ť	-	_		
FRUTA CVIOLI	MANDELECTED RIMA POLYNERASE			1100-1215	1-1	413-1449	41.1480	-	1783-1806	2016.2015	117.2354
PARPE BEV	RNA DIRECTED RNA POLYNGRASE	BE BNE VIBIL	2	2640.7676		5	405-3435	700			
PRIATE CYMAS	RNA-DIRECTED RNA POLYNERASE	DNA VIBITS MITO IS THE FIN A 191				2	Ì			i	
	ANA DIRECTED RNA POLYNGRASE	MURUME CORONAVIRUS MILIV (STRADY DIA)	_		_	200		İ	İ	i	
PRIME CVPFS	NHA-DIRECTED ANA POLYNGRASE	_			i i	_	-	İ	1	:	1
	RNA-DIMECTED RNA POLYMERASE		901-00	,	ī	Ī	İ	İ		Ī	-
PART BY	THA DIRECTED RIVA FOLYNG RASE	AVIAN INFECTIOUS INFONCTIFTS YINUS (STRAIN BEAUDETTE)	H 00	330.165	110.11	1105-1155	16 M-1674		Ī		İ
1		PLOCHAMINE VIKUS (STRUDENT, 107 ISCILATE USA)		146-16							

PCGUNE	אונדונזוו	All Viceses (Ne Barteriophoges)									
THE WAST	PROTEIN	YIRUS	AFEA I	AHES J	C VINO	ARCAN	ANTA	4 1 1 V	411.17	A 1 1 1	
PERM BUNYW	ANA POLYNIERASE	BONYAMWERA LIRIS	20.00	2.12	4 40. 46. 9	10%.1116	1117.1114	37.0	1111.111	Mary cent.	201 303
PRINT EBOV	RNA DIRECTED RNA POLYNIFRASE	CDOLA VIRUS	2.5						 -		!
	ANA POLYNGRASE	ILANGAAN VIRUS (STRAIN 16 110)	151.160	2 6	110 46,	361.138	1011.1105		i L	 	! :
-	ANA POLYPERASE BETA SUBLINIT	PRINAM RESPIRATORY SYNCYTIAL VIRUS	1 :		!					ļ.	-
PRINT HOUSE	RNA POLYMERASE BETA SUBUMI	HUMAN RESPIRATIONY SYNCYTIAL VIRUS (STRAIN AZI	9	1111.1206	1033.1643	_	10.9.101	2018.3017			
	RNA-DIRECTED BNA POLYNIFBASE	MARRIAG VIRIS STRAIN MISORE	9,5	1	-	17.71	-	146.160	911 946	100	1
7			11.031	1000.3017	_		_				
PRESE MARVE	PMA.DIBETTED BMA POLVACE A CF	MARRIAG VIDIN (CITATIVATION)	15		_	100	- 47	1	10.00		
7	WATER ICE PART OF INCASE	THE PROPERTY OF THE PROPERTY O		\$	_		≃≝	•			
7					= :				_		
PRIN NEAS	RMA POLYNGRASE BETA SIMINIT	MEASLES VIRIIS (STRAIN EINENNSTON)	205-313	?	120:02	1160 1183	_	1930-1940	_		
Į	ANA POLYNGRASE BETA SUBIRGI	MARA'S VIRIIS (STRAIN MIYALIARA VACCINE)	34.5	110-115	-		100	113.1150	1601.163	1130.314	
PRINT, NOVE	ANA POLYMERASE BETA STRUMIT	WEWCASTILE DISEASE VINUS (STRATM BEALDETTE CAS)	304.724	1571.1592	41.192		_	-		!	i
Į.	ENA POLYNGRASE BETA SIMINIT	IN BLAN PARAMETTENZA S VIBIG (CTRAIN TOCLINA)	75.	180.080	÷		100	9	1		İ
L	100 May 100 Ma						-				
- 1	ANA PULTMERASE BEIA SUBURII	HUMAN PARAINILLIENTA I VIRUS (STRAIN MIL +1685)	135.69)	94.5	101.10		_	1068 2084	=======================================		
	AMA-DIRECTED RINA POLYNERASE	PURDALLA VIRUS (STRAIN HAI LNAS hi)	131.184	3	1561-1565	1677.150	_				
Г	RNA POLYNERASE BETA SUBUNIT	RABIES VAUS ISTRADAPVI	344.384	102.561	741.162	446.144	_			İ	İ
Г	RMA POLYMERASE BETA SUBUMIT	RABIES VIRIS (SIBAIN SAI) DIO	344.304	100	121.151	144		1744 1741		-	
Value and	BMA DIRECTED BMA POR VACORACE	BLCE DWARE VIOLE			1						
	Man Supplied and the Party of	ARE DWAR VINO			1						
	MANDIRECTED MAY FOLT PERASE	ALL VALLEY I EVER VIRIS (STRATM ZH-548 M12)	200	000	-	1			_		
	RMA FOR YMERAST BETA SUBUNIT	SENDAL VIBUS (STRAIN 2 / HOST MUTANTS)	2	104.20	194.218	397.77	98.58	1405.1430	1844.18h4	2107.7138	
MIN SENDE	ANA POLYMERASE BETA SUBUMT	SENDAJ VIRUS (STRAIN ENTIFIES)	===	3	201.130	1225-1240	1664-1684	1927-1948	_		
ī	RNA POLYNERASE BETA SUBUNIT	SENDAL VIRUS (STRAIN Z)	19.59	2	194.218	•	900	1651.1636	1144.1164	100	
PRINT SECUS	ANA DIRECTED ANA POLYNGRASE	SEOUR VARIUS ISTRATIN BO. 191	161.168	1	917.76	3	100		-		
PRIN SVINS	BMA PON VACEDACE BEYA CIRCLAS	CILATAN WHITE GARING AND SINGE WALL									
7000	THE PARTY OF THE PERTY PROPERTY.	CONTRACT OF STREET	•					331			
٦	MAN FOLT MELASE BE IN SUBURI	SUPPLIED FELLOW RE! VIALUS	20-146	100	=	704-73	167.88)	116-911	1484-1510	1776-1792	
9	ANA-DORECTED RINA POLYNCENASE	TOMATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPINI I/BR-01)	958-974	1385-1410	1778-1800	1609-1617	16 18 2 370 3				
	RMA POLYNŒRASE	UNIX CONTENS VIR. 115	214.149	11.04	-	1570-15	2046-2012				
PILLY VSVIH	RNA POLYMERASE BETA SUBINIT	VESICULAR STOMASTITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN ILA	136-103	111111	901.93	1056.1913	1040.3063		İ	į	İ
Г	RNA POLYNGRASE BETA SLIBUNIT	VESICIALAR STOMATITIS VIRUS ISEROTYPE NEW JERSEY / STRATH OF		112.110	100	2010.3101	_				
Т	RNA POLYNGAASE BETA SUBURIT	VESICUE AR STOMATITIS VIRUS ISTRAIN SAN RIAM	1014-1007								
PRILITO ACL SV	ANA-DURECTED ANA POLYMERASE	APPLE CHUMOTIC LEAF SPOT VIRUS		200	100	1400					
1	PUTATIVE BNA DIRECTED RNA POL	BEST WESTERN VELLOWS VIBILS ASSET IN	1		_	-					
+	PUTATIVE DIA SUBCIED BUY DO	BABI EV CELLOW DEVADE CONTRACTOR ATE CALL									
т	BOTATION AND AND AND AND AND AND AND AND AND AN	TANK TO THE COMPANY VENDS (SOUTH FIRE PLANTS)	23.45		200						
7	TOTALITY MANASTACK TO MANA POL	BAALET TELLOW DWARP VIRUS (1501.A.1.E.P.AV)	2	2	201.05						
100000	FULLITY WAS DUCK IED MA FOR		139-716	2	505-512						
3	PROBABLE MANDUCETED HAS FOL		2	43-103	127.150	_					
2	PUTATIVE RNA-DIRECTED RNA POL	INSAIC VIRUS (WATERNIELON STRAIN	44).466	35.55	1017-1012	1337.1530					Ī
1	PROBABLE RMA-DIRECTED RMA POL	CUCUMBER NECROSIS VIRUS	37.100	<u>=</u>	470.494						
	PROBABLE INVA-DIRECTED RNA POL	CYMERIDADA RINGSPOT VIRUS	3	36.331	170.00		Ī				
	PUTATIVE RNA-DIRECTED RWA POL	INFECTIOUS PANCALATIC NECROSIS VIRUS (SEROTYPE JASPER)	221.258								
	RNA POLYNŒRASE	LYNCHOCYTIC CHORIOMENINGITIS VIRUS (STRAJN ARAISTRONG)	13.50	19.61	659 612	988.1004	1314.1346	1370.4.104	1033 3006	Ī	
	RMA POLYMERASE	LYNDHOCYTIC CHORIOMENINGITIS VIRUS (STRAIN WE)	13:52								
PRUMO MOAV	PROBABLE RNA-DOLECTED RNA POL	MAZE CHLOROTIC MOTTLE VIRUS	1	100	100						
L	RNA-DOLECTED RNA POLYNERASE	PEA ENATION MOSAIC VIRUS	177	1		***					
۳	PUTATIVE RMA-DIRECTED RMA POL.						Ī				
WALL PASSO	PUTATIVE BNA DESCRED BNA POL	POTATO I FARENT MADIS ACTOR WASHINGTON						İ	į		
PATING DESIGN	MITATIVE BUY, PREFIES BUY, BOT	PERSON NATIONAL CONTRACTOR OF THE PERSON OF		3	Ì						
Ţ,	SETTING THE PROPERTY OF THE PARTY AND	PER CLAIM HOLLE VINCS (SI MAIN SPAIN)	2	2	1069.1046	1491-1503					
T	TOTALITYE MAN CHACLICU MAN TOL	ALL LLOVEN RECHIFF, MOSAN, VIRUS	3.78								
ī	MAN-DIRECTED RIMA MOLTMERASE		161.176					ļ		i İ	İ !
7	KINA DARECTED KINA MOLTANEZASE	REOVING (TYPE I / STRAIN (ANG)	941.191						!	:	
7	KWA-DERECTED RWA POL SUBLIMIT VP		2:-	30.75	1	204.93	190.00	1077.1044		<u> </u>	
_ [RNA-DOLECTED RNA POL SUBIDITI VPI		117-156	20.20	101	100	L	1023-1046			
٦	RNA-DOLECTED RNA POL SUBLOVIT VPI	PORCONE ROTAVIRUS (GROUP CASTRAIN COWDEN)	10.30	356.374	111.111	769.784	ī	036.035			
	RMA-DURECTED RMA POL SUBLIMIT VPI	PORCINE ROTAVIRUS (STRAIN COTTINIED)	13:1	33.72	100	247 269	Ĺ		100	401.1101	
	RWA-DOLECTED RWA POL SUBLINIT VP.		11:136	247.269		ī	T		ī	:	;
Г	PROBABLE RNA-DIRECTED RNA PUL		1	12	1	Т	Τ			-	1
PRIMO TACY	RNA POLYMERASE			1		i	Ţ	Т			!
						_	1014: 4144 T			-	7

	10.10-0.10									•	
THE HAMP	Photography	All Virgins (no Betlemphages)		7	7	П	П			Ī	Γ
PARPO TOSVC	_	TOWATO BUSHY STUNE VIBILS ISTRAIN CHEBRY		4	7	3	ARIOL	7998	ANTA	TVIIV	ARIAS
PRING TCV	PUTATIVE RVA-DURECTED RNA	TURNIP CRIMAL E VIRILS		T		7	1	Ì			
PRILITO THICHY		TOBACCO MULD CREEN MOSAIC VIRISCIALLY STRADE 173		1	İ	1	Ť	Ť			
		TOBACCO MOSAIC VIRUS IVIN GARES		÷	1	†	1				
		TOBACCO MOSAIC VIBUS IS IRAIN KOREAN	70.73	-	4171	Ť	Ì	Ì		Ī	
PRING THATO	PUTATIVE RNA DIRECTED RNA POL	TOBACCO MOSAIC VIBUS (STRAIN TONIATOR)	200,334	÷	-	4171	†	Ť			-
	ENA-DIRECTED PNA/POLYACRASE	TOBACCO MECROSIS MIRITS (STRAIN A)	1		•	İ	İ	Ì		-	
П	ANA-DIRECTED ENA FOLYMERASE	TODACCO NECROSIS VIRIS (STRAIN IS)		:	•	:	·			=	
П	RMA POLYMERASE ALPIIA SUBUNIT	CHANDIPURA VIRUS (STRAIN 165) 5141	100	İ	!	Ì	İ	İ	-	1	
г	RMA POLYMERASE ALPHA SUBLIMIT	MUNOS VIRUS (STRADA SDI. 1)				İ	j	Ì			
_	ANA POLYNGRASE ALMIA SUBURIT	MUNUS VIEUS (STEAM) EMPCES				İ	Ì	Ì			
2	ANA POLYNERASE ALPHIA SUBURIT	MUMOS VINUS ISTRAIN MITABLE VACCIME.				1	Ì			Ì	
PRUP NOVA	RIVA POLYNERASE ALPHA SURIDAR	NEWCASTLE DISEASS VIBIR CORACE ANGUIA CONTRACTA				1	1	İ			
200	RNA POLYMERACE ALPHIA CIMINAL	MENTANTE MICHAEL VIEWS (STRAIN AUSTRALIA VALIMIANI)	27.4	j	-	•	-	_			
T	The box of the Alex Alexander	INCACASILE MISCASE VIRUS (STRATE REALIZE) 11. (741)	156-276			7		•	:		
Ī.	MAY FOR THE WAS ALVIN SUBURIL	HUMAN PALAINE LUENZA 2 VIRUS	216-243			•		İ		Ì	
T	MAY TUE THE KASS ALT IN SUBURI	TOPAN PARAING LUENZA I VIRUS (STRATH TOSIIIIIA)	216-243			-	ļ	İ	Ì		İ
7	DA FOLVELASE ALTRIA SUBUNIT	HEMAN PARAINGLUENZA 14 VIAUS (STRAIN TOSHINA)	230.245			<u>.</u> -		Ť			
٦	RMA POLYMERASE ALPHIA SUBIDIT	HIGHAN PARAINTLUENZA 48 VIRUS (STRAIN 68.333)	230.347			<u> </u>	Ì	Ì			
Ī	RVA POLYMERASE ALPHA SUBURIT	PLRY VIRUS	14.141	Ī	İ	1	İ				
	RNA POLYNERASE ALMIA SUBUNII	PARIES VIRUS (STRAIN AVOI)	1		İ	†	1	Ì		İ	
	ANA POLYMERASE ALPIGA SUBURIT	RABUES VIRIUS (STRAIN CVC.11)					1				
Г	RNA POLYMERASE ALPICA SUBLINIT	BARIES VILLICATED AND AND ACTED AND ACTED AND				İ	İ				
Г	ANA POLYNGRASE ALPHA SUBURGE	BARITS VIBING CETRAIN P.V.			1	1					
PROPERTY.	ANA POLYMERASE ALPHA SUBINGT	BABIS VIBIL (STBAM SAN BIS)					1				
PLEAT SVI	ANA POLYMERASE AL PILA SUBLIMIT	CINIAN CORNE (1619 API WIT		7.00		•					
PRESTY VAVO	ANA POLYMERASE ALPHA SUBLINIT	VESTINA AN AT ALCOHATING UMBIT REPORTING THE WAY THE PARTY OF THE PART	_	9	-	•					
-	S1718 PROTEIN	AND CALCULATION OF MACHINES AND SERVICE OF THE SERV				1					
7	COPERNITOR DISCORDANCE INC. BACTERS	CANCACA WALLE TO VERY VIRUS (STRAIN BATIV)	2.50			•		İ			
PSCOC VAPEV	Was an interest and a second econd and a second a second and	9.4									
_	TOPE TO XING DECAME A CE I HE PROTEIN	VALCUMA VIAUS (STRAIM WR.)	9								Ī
Τ	SPERCIDEN	AMILE AMORE I ENTONOMO UMINE	9.40			-				Ī	
۲	CHES A CHICAL PAS CHARLES	Charletoning and Charleton	25.73	93.646		.,					Ī
Ť	TABOUT I		17.70					İ		ĺ	
PANTA COMA	(WATA BEATER)	MY AUMA VIIIUS (STRADE LAUSAPPE)	63-60	317.343			İ		İ	İ	Ī
i	LABORT ANTIGEM		1					İ		Ī	l
-	LANGE LANDICEN	POLYGENOVA TELEVACING DISEASE VIRUS	354-169							İ	
	LARGE T ANTIGEN	POLYGALANDS BY (STRAIN AS)	203-334	139.444					Ī	İ	
7	LARGE T ANTICEN	POVING POR COLUMN	207.174	429.444					İ	İ	
-	LANGE T ANTICEN	MANAGER POR VONA VIEW	187-400							İ	
f	LANGE T ANTIGEN	POLYNOLIS IN	97.0	3.00							
F	LANGE T ANTIGEN	I WOMOTENEY POR VOLA UTBILE	2	428-443	_						
f	LANGE T ANTIGEN		43.48	516-547					-		
T	LANCE T ANTIGEN		576-591								
1 –	LANGE TANTIGEN	A WEST STATE OF THE PARTY OF TH									
8	LAIGE T ANTICEN	Ī	200	ī		1					
	LARGE T ANTIGEN	SUGAN VIRUS 40 (5V40)	100.00	177.167	7/0-9	†			Ì	j	
-	MIDDLE # AMTIGEN		77.17		1	1				İ	
Ë	MALL 1 AMIGEN					1			İ		
=	SHALL 1 ANTIGEN				1	1		j		j	
	SMALL T ANTIGEN	Ī				1	1			j	
┪	FRAMS. ACTIVATING TRAMS REG PROTEIN	WEDROSIS VIAUS	17		1	1	1	1	†		
	PLANS. ACTIVATORO TRANS REG PROTEIN	T	717	Ì	+	1		Ì			
8	MAMS-ACTIVATOR TRANS REG PROTEIN		110-414			\dagger	1		1		
	BANS. ACTIVATONG TRANS BEG PROTEIN	T	5.3	İ	+	\dagger		1	1		
VIAL MV2	TRAMS-ACTIVATING TRANS REGISTROTEIN	Γ	65.50				t	\dagger	\dagger	\dagger	1
Т	HAMP ACTIVATING TRANS REG PROTEIN		93.310			\dagger	T	\dagger	\dagger	1	Ī
7	INMS-ALTIVATING TRAPS REGIEN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (CANBBEAN ISOLATE)	102.216		+	t	1	t	t	t	Ī
		l				1			1	1	1

PCCDAE	Pricellin	All Virues (No Bacterioghages)		П	\Box	П	П	П	П	\Box	
Π	regiene	VIRUS		3	7520	OREGE	2824	DATA	10116	1	SEAL.
PTAT HVICE	TATPROTEIN	PIDMAM INMUDE FICIENCY VIRUS 17PE I (STRAIN UCANDAM ISO				1				j	Ī
MG /LV	FCELL RECEPTOR BETA CHAIN PRECURSOR	I EL DIE LEUKEMIA VIRUS	77.4			Ì					
PHO MINE	PROPAGATION TECHNOLINE PROSTANTALINE	EQUINE REACTORING TYPE I (STRAIM ABAY)				1				1	Ī
YANG SALE	I COMMENT PROTEIN	CONTROL MADE VIBILITATION OF THE TANKS THE TAN	7	363.380		1013.1034	1164.1330	1448,1484	1044-1363	1041.101	107.11.24
VAN COLUMN	PROBABLE LABOR TECHNOLOGICAL	INDIAM CYTOMEGAL OVIETE STRADI ADIAM	142.350	77777	1041.1077	107.1123	1331.114	410.1446	_		11.00.1771
PROJECTION OF THE	MACHINA TECHNOLOGY	HERPES SOUPLEX VIRUS (TYPE 1 / STRAD) (2)	2	23.646	33.039					-	
PTFOIL HAVAO	LABOR TECRNOSTI MOTEIN	HERPES SINCE EX VIRUS (TYPE 67 STRAIN GS)	11:133	345.365	919519	1037-1043	1308-1328	143.1570		Ī	
THEOL HIS WES	LARGE TECHNENT PROTEIN	EQUINE HEILPES YIKUS TYPE I (STRAIN ARAP)	27.10	Г	1013-1099	1107-1133	1618-1640	1961-991	3263-3389		
PTECO HISVEA	PROBABLE LARGE TEGINENT PROTEIN	HERPESVIRUS SAIMIN (STRAIN II)	163-481	714.117	919-1003	1121-1177	1155-1174	1177.1193	1503-1525	1607-1633	101-1015
			3421-2439			П				_	
MEGU VEVD	LARCE TECUNENT PROTEIN	VALICELLA-ZOSTER VIRUS (STRAIN DUMAS)	× 7	Ξ.	= =	60.63	267.620	101)-1034	160-174	1037-1657	
			100	200	200	·					
PTEMM ADEOL	DNA TERMONAL PROTEIN	HUMAN ADENOVIAUS TYPE 1	8-6	39.61		1					
PTERM ADEM	DNA TERMANAL PROTEIN	INDIAN ADENOVIRUS TYPE S	3	39) 616							
	DNA TERMONAL PROTEIN	INDIAN ADEMOVIBUS TYPE 1	61.60	3							
TERM ADE:	DNA TELLAPIAL PROTEIN	HISMAN ADEMOVIRUS TYPE 12	3	334-330	36.00	-				Ì	Ī
MON AND!	DNA TOPOISONERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)		. O.		-					
71077 ASTNO	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 10/1)	19.14	5		1				1	
PTRIM HONA	MYPOTHETICAL PROTEIN TRL 14	MOMEN CYTOME DALOVIAUS (STRAIN AD169)	139-163			••				Ī	Ī
PTREL AVINE	MEL TRANSFORMONO PROTEIN	AVIAN RETICULOENDOTICILIOSIS VIRUS	2.3								
PTYSY VEVO	THYNADYLATE SYNTHASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	=		Ì						
PUISE HEVEU	POSSBILE GANCICLOVIA KIPASE	HERPES SOULEX VIRUS (TYPE 47 STRAIN UCANDA-1102)	400-415								-
PUZI, HSV6U	PROTEIN 2L	HERPES SINDLEX VIRUS (TYPE 67STRAIN UGANDA-1103)	4-11								
PUDPE HOVAC	UDF-GLUCOSYL FRANSFERA SE PRECURSOR	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	452-479							į	:
	HYPOTHETICAL PROTEIN LA.1	HUMAN CYTOMEGALOVIAUS (STRAIN ADIGS)	•			-			-	;	-:-
PULOS HOMYA	HYPOTICETICAL PROTEIN ULS	HUMAN CYTOMEGALOVIRUS (STRAIN ADICT)	=			-		Ì			1
PLE CE V	VINION PROTEIN BEILT	EPSTERN DAUM VIRUS (STRAIN BYS 0)	20.76								
PULOS MONA	HYPOTHETICAL PROTEIN ID.6	HUMAN CYTOMEGALOVINUS (STRAIN AD169)	2								
Т	VILLON PROTEIN U.A	PERPESSION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PERSON				+				Ī	
Т	VILLON GENE SA PROTECIA	EQUIPM REJULTS TITE () INAIM ABAT)				-				Ì	
A	VILLAM GENE 4) FRUIEIN	PEDCES VICES SAFARIO (STRAIN 11)			1						
_	SECOND TROUBLE	LABORA POPULATION (STRAIN BY):)	100	200, 740	Ī					1	
V. 100	MYPOTHE BLAL PROTEIN OL	MUNICIPAL CONTRACTOR OF THE CONTRACTOR AND THE CONTRACTOR OF THE C	3	57-46						1	
AL ST LEVER	CALC (COO) TEN	FORTING DESPECYTENC TYPE 1.478 AIN ABAD.	11.11							Ī	Ī
ANAL COLOR	CENT 43 PROTEIN	HEAPESVALIS SANIRI (STRABI II)	17							Ì	Ī
PULAT VZVD	GENEL SS PROTEIN	VALCELLA-20STER VAUS (STAAM DURAS)	136-136	301.134							
PULM HEVIL	PROTEIN U.	HEAD'ES SOULEX YORUS (TYPE 1/STILADN 17)	\$14.530	365.536							
PULM VIVD	CENE SI PROTEIN	VALICELLA-ZOSTER VINUS (STRAIN DERIAS)	28-255	393.616							
PULSE HEVIL	ORIGIN OF REPLICATION BINDING PROTEIN	HEADES SOULEX VOIUS (TVPE I / STRADA 11)	564-580								
PLEON HEAVES	CRUCEN OF REPLICATION BENDONG PROTEDI	EQUING HERPESVIRUS TYPE I (STILAIN ABAP)	31-15	127-619							
74.60	CANCEN OF REPLECATION BINDING PROTEIN	VARICELLA. POSTER YTHUS (STRAIN DUMAS)	60.03	8	25. SE						
ME HOW	HATFORNE TICAL PROTEIN ULTI	HERALA CATIONE GALOVILLIS (STRAIN AD169)	2								
	MITOTRETERAL PROJECT UC.17	INCHASE CONTRACTOR OF STRAIN AD 187								Ì	
THE PARTY OF	WYSOTHER SET AT 18 14 PROTESTA	MORPES STUDIES OF VINES (2) STEATH AND 12)							Ì	1	Ī
PLE 14 HSVER	HYPOTHETICAL CENE AS PROTEIN	EOGENE PERPESVIRUS TYPE 1 (STRAIN ABAP)	161.00			T			Ì	1	
HE IS HEVEL	PROTECULA 14	MERPES COAPLEX VINITE IT STRAIN 131							Ī	Ì	
PUL 16 HISVED	GENE 44 PEDIEDA	EQUING HELPESYDAUS TYPE I (STILATIV AB 4P)	10.00	97110	134.110	T			1	T	
PULIS HEVEA	CENE 35 PROTEIN	HERPESYTHUS SAMIN (STRAIN II)		141 111		T	T	Ī	Ī	T	T
PULIS YZYD	CENE A PROTEIN	VAUCELLA-ZOSTER VIRUS (STRAIN DURIAS)	63.50	117.513						İ	Ī
PULLY EBY	PROTEIN BOLL!	EPSTERY BARR VIRUS (STRAIN 899-0)	111-101							ĺ	-
PULLI HCMVA	INTOTHETICAL PROTEIN UL!?	HEDRAN CYTOMEGALOVIRUS (STRAIN AD149)	10.63							Ī	
PLL13 HSVII	PROTEIN UL 17	IERPES SOCREX VIXUS (TYPE I / STRAIM IT)	134-181								
MEIN MONTA	GENE 33 PROTEIN	HEAVES VALUS SALIKIDU (STRADA I.I.)	=	24.378							
PULIT HOMYA	MYPOTHETICAL PROTEIN ULIV	HUMAN CYTOMEGALOVIRUS (STRAIN AD149)									7

	Pitchilip	All Virginia de la faction de la constante de									
THERMA	PROTEIN	Name of the last o									I
TULY PAYED	ULJO MENNIKANE PROTEIN HOMOLOG	PSEUDORABLE VIRIA (4 TRAININA II	7	AREA	ANA	ABEAS	AREA S	AREA	AREAS	1 1 1 1 V	. 7447
2424	_	VANICELIA POSTER VIBILE ASTA STRATES				1			Г	Τ	
PULLI HONYA		IGHAN CYCOKE OF CHAIR COMAS)	301-224			-					
PULJI HSVII		INCHES AND THE CALL OF HEALTH AD LESS	911-110							1	
PLE 31 HSV18	PROTEDVIRJI	PROVES SUPPLEA VIRUS (TYPE I / STRAIN 17)	98-114	130.146							
PULSI MANES	CEDE 40 PROTEDA	COLORS SUPLEX VIAUS (TYPE I / STRAIN ICEM)	911.96	20.145 145						Ī	
ML1 V2VD	OEAC 14 PAOTEIN	CHOINE MENTED VILLO I THE I (STRAIN ABAP)	110-143	184-331	179.403	613.433					1
PULLY HOLVA	HYPOTHETICAL PROFESSION 12 33	WALLA-ZOSTENIVRUS (STRAIN DUMAS)	130-191	186.337							Ī
PULSI EBV	PROTESN BOOF	HUMAN CT I UNE GALL DVIRUS (STRADY AD169)	19-99	L							
PULJE HOUVA	HYPOTHE TICAL PROTECTION	EVELLIN-BANK VIRUS (STRAM BOS-1)	124-135								
PULSE HSVII	PROTEIN 18 34	HUMLAN CYTOMEGALOVIRUS (STRATN AD169)	704-722				\int				
PULL OF THE	PROTEIN IN SCINISM CO.	PEUPES SUPLEX VIRUS (TYPE 1/ STRAIN 17)	47.166								
PURTY JECKNA	MANUAL DESCRIPTION OF THE PROPERTY OF THE PROP	INFECTIOUS LARYNCOTRACIEITIS VIRUS (STRAIN THORNE VEEZ)	20.05			-					
10000	SECOND TO SECOND	HUMAN CYTOMEGALOVIRUS (STRATH AD 169)	484.000								
1	VIOLET PROTECT ULTS	HEAPES SOULEX VIAUS (TYPE 1/STRAIN 17)		1	i 	.		į		Ī	
	VIRION PROTEIN UL 25	GOUNE IN A MISVINITY IN THE LAND AND THE				-			:		
NE SYS	VILLON GENE 19 PROTEIN	INCRESSIVING CANADA I CE A AND INCREMENTAL OFFICE AND INCREMENTAL OF	2	10.143					_	_	
MAN BITM	MIKD VILLON PROTEIN	DAR CHIOLIE AS SOCIETY	244-365	144.360		<u> </u>			İ	İ	
PULITY HOWA	HYPOTHETICAL PROTEIN IN 33	MARCHIOUS LANTINGOTHACTIETTS VIRUS (STRAIN THORNE VERT)	370,387	316.336		[1	j	
PULTS HOUSE	HYPOTHETICAL PROFESSION IN 18	PRIMARA CYTOMEGALOVINUS (STRAIN AD169)	307.324	416.507		ŀ					
PULLS HOLVA	HVPOTAKTICAL PROTESTING	HUMAN CYTOMEGAL OVINUS (STRAIN AD160)	290.264								
11 500	PROFESSION FOR THE PROFESSION OF 10	HUMAN CYTOMEGAL OVIRUS (STRAIN AD167)	-			1					
	TRUSTELL BFLF3	EPSTEIN-DARG VIRUS (STRAIN UPS.E)									
Y S	MYPOTHETICAL PROTEIN U. 11	HABAN CYTOMEGAL OVIETE CTRAIN SELECT	2				1	i !	-	-	
E MAN	PROTECT ULJ	MERPER CINE EX COLOR CONTRACTOR CONTRACTOR	410-437	\$63-602				Ī	T	\dagger	Ī
PULLI HSVED	CENE 29 PROTEIN	FORMS DESIGNATION OF THE PARTY	19-116					Ì	\dagger		Ī
PULDI HEYEA	OENE 69 PROTEIN	LESSON REPORT TO THE I (STRAIN ABAP)	104-135	280.309				T	İ		
PULJ 1270	GENE 19 PROTEIN	MEATES VINUS SABARU (STRADA III)	145-161	91.19							
PLEAS HEVIL	PROBABILIS MAINS THAT OF VOCASO SEE	VAUCELLA-ZUSTER VIRUS (STRAIN DURAS)	111.111	70.116							
PALL 33 MOVED	MANO BIONE OF CHANGE	MENTES SEALEX VIRUS (TYPE I / STRAIN 17)	137.141	79		1					
	POOR EN PLUTE OF TURKOTEIN 300	EQUING HEADES VIRUS TYPE I (STRAIN ABAP)				-			-		
100	PACES PACE ENVIOR ENVIOLED TO THE PACE OF	VAUCELLA TOSTER VINUS (STRAIN DURAS)									Ī
1	CHRU ELIY COUPLED REC HOMOLOG (4.1)	HUMAN CYTOMEGAL OVINUS (STRAIN AD148)	200				-				Ī
	MANUFACTURAL PROTEIN U.S.)4	HENCH CYTCHEGAL OVINUS (STRAIN ADIAN)	2						ŀ	\mid	
200.00	VINOR PROTEIN ULDA	HEADES SIMPLEX VINUS (1YPE / STRAIN 15)		12(-12)							
Т	VICTOR UENE 26 PROTEIN	EQUING MERPESVINUS TYPE I (STRAIN ABAP)	201-103						-		
T	UCAS 8/ FRUIEIN	HELPESVIRUS SABAIN (STRAIN !!)							-		Ī
Ţ,	VILLON CIEVE 24 PROTEDA	VANCELLA-ZOSTER VRUS ISTRAIN THINARE								1	Ī
╗	HYPOTHETICAL PROTEIN ULUS	HIDEAN CYTOMEGAL OVINCE ASTRAINS ANIAM	٦					İ			
YANG MENA	HYPOTHERICAL PROTECH UL36	HIGADI CYTOLEGAL OVINIS ISTRAMA ANIAM	٦		331.346			T		1	T
	PROTEIN BOLL!	EPSTERN BARB VINIK ALTBAND BOLD								1	Ī
٦	MOTERN (L.)?	HERPES SUPLEX VIRUS (TYPE 1/STRAIN 19)	7			_		l	-	t	T
-1	CENE DIFFORD	EQUING HEAVES VIRUS TYPE I ISTRAIN ABARA				1 197 599	118.777 02	629.859	1009.1078	1	-
- 1	CENE 43 PROTEIN	HEADESVIRUS SADARI (STRAIN III)	0.77	91.310	064-690	78.805	916.106	Ť			
1	GENE 21 PROTEIN	- Pilbase	2					T		\dagger	Ī
•				124	140-165	161-191	194-212	270.244	248.349	470.464	100
A MARCHAN			804-933				ī	Т	Т	Ť	
			27.4							+	Ī
Ť	17.			_				<u> </u>	-	1	
A			7	П				t	+	\dagger	1
۳			7		163.363	167-751		t		1	T
7	RANE PROTEIN		٦	103					+	1	
T				27.146	011.09	211.199 17	174-600	+	1	+	1
7	PROTEDY ULAS		25.48			Т	\dagger	1	<u> </u>	1	Ī
_	PROTER (A.4)		7				+	+	1	+	Ī
	PROJECT LA OT		٦					 	<u> </u>	1	Ī
_	VALUEN PROTEIN UL 49		Ì	3	313.5%	614-640 74	341.766	\dagger	1	1	Ī
T				j				<u> </u>		1	Ī
Т	STATE OF THE STATE	(STAATO PG.3)	527					\mid	H	1	1
1	٦		197.00	1						1	Ι
				1	1	1			-	L	Ī
											7

П	PIICTLE	All Virants (No Bactering Anges)		П	П	П	П	П	П	П	
TIL HAME	PROTEIN	YIN	3	1	2000	3	TVIV		3	GREAL	ARIA
MAC HOVE	WED ALMA TRANS-DOUCING PROFESS	EQUINE HEAVES VIAUS TYPE I (STIANIN ADAT)				†				Ì	1
7	ALMA TRAMS INDUCING FACTOR VI & KU PROTEIN	VAUCELLA (STEAM VIRUS (STRAIM DUMAS)	222			Ť	Ī				İ
╗	HYPOTHE TICAL BUILD PROTEIN	FFSTEIN-BALL VIRUS (STRAIN BOS-B)			İ	-	Ì			1	
آړ	HYPOTHETICAL PROTEIN 12.49	HUMAN CYTOMEGAL OVIRUS (STRAIN ADISS)		100	i	1	1			Ī	
٦	TEGUNENT PROTEIN ULA	HERPES SIMPLEX VIRUS (TYPE I / STRAIN IT)	738-327		1	Ì		Ì		•	
Т	HYPOTHE TICAL GENE 64 FRUTEIN	IGENESSVIRUS SAUMUU (STRAIN II)	137-353		†	1					
₹	PROTEIN ULSO	HUMAN CTIONE GALOVINOS (STRAIN ADIBS)				İ	1	Ī	Ì	Ī	Ī
HSV	PROTEIN ULS!	ICLUSES SUPPLEX VIRUS (TYPE I / STRAIN 17)		_						•	_
BVE	CENE 6 PROTEIN	EQUINE TERMENT VIEW TYPE A (STRAIN 1942)	20.00								
	(IENE BPROTEIN	EQUINDEDURANSVIRUS LYPE I (STRAPEART)	100	- :	-	-					
_	CENE PROTEIN	VAUCELLA-ZOSTER VIRUS (STRAIN DUMAS)	**		<u>'-</u>						İ
Г	PROBABLE DNA REPLICATION PROTEIN BSLFI	EPSTEIN-BARR VIRUS (STRAIN BIS-8)	64.59								
	DNA REPLICATION PROTEIN UR.33	HERPES SIMPLEX VIRUS (TYPE I / STRAIN IT)	11:11	16:50	<u> </u>	Ţ.					
L	DNA REPLICATION PROTEIN ULS	EQUINE IERPESVIRUS TYPE 4 (STRAIN 1942)	6.33	Г		İ				Ī	
Т	DNA REPLICATION PROTEIN ULS	EQUINE (IERPESVIR) STYPE I (STRAIN ARIAP)	1	110 69 119	110-111	ŀ			į		
Ī	PROMINAL MEMARITHMENT AND CHINE Co. PROFILIN	THEPS VIETS SAINING STRAIN 111	APP. VAR			•				_	
Ī	PROBABILE DNA BEPRICATION CENE A PROTEIN	VARICELLA 205TER VIRIUS (STRAIN DUMAS)	1	6.45.470	İ	Ì	Ī			İ	
+		HOWAN CYTOMEGAI OVIETS STEADY AD IAS	173.188		t	T				Ì	
PIE ST PECKEL	SE ST PERSTENDING AND	ITERES INCHES VIEW VIEW AT STRAIN (KIANDA 1102)	9.73	Ī	 	t				Ī	Ī
-	AVPOTOGRACIO PROTEDI LA AO	TO BARN CYTOMORIA OVIEWS STRAIN AD INC.	130.101		+	Ť	Ī			Ì	
10000	INVOLUENCE AND THE ASSESSMENT OF ASSESSMENT	INTANTO-COLONIA PORTO		100	T	1	Ī			1	
-	HYDOTHETICAL PROTEIN IS AS	WELLAN CYTOLEGAL OVER CITATA ADIAN				Ì	Ì			Ì	
Т	PROBABLE DAY BEEN IN PROTECULAR IN	IN BARM PATCALEGAL OVIDER CATE AND ANICON	334.345	017 000	410 410	436.446	100.001		Ī		1
	WOOTHET AT BOTTOM IN 11	AND AND COLORED OF THE AND AD LESS	91,716	i	Т	Т				Ī	
۳	UNANTHER TO BE DESCRIPTION	CONTROL DATE CONTROL AND BOLD			Ť	Ť	Ì			1	
]	Chante to All Carle is sent the	INCOMESSION OF A PROPERTY OF THE			l	i	Ì			Ì	1
T	MITUTE INC. 20 TAULEIN	SCATS VINOS SAMINA (SIRAIN II)		1	i	Ì	Ì				
7	CHANGE BECALE THOSE IN CLASS	TOPICAL CONTROL OF THE STRAIN ADDRESS			1	1				Ì	
Т	CONTRACTOR OF THE SECOND SECOND	INTERNATIONAL CONTRACTOR AND ADDRESS		100		İ	1	Ī		İ	
_	MATCHER LACE TROJEIN UL 18	HUNGAR CYTURE GALLOVIEWS (STEAM ADIES)		607.00	1	· 	Ì	Ī	ĺ		
1300	A THE PAST OF LOCATED WITH A SPACE BLANCH	TOTAL AND			1	İ	Ì				Ī
-	AT PER PARTY INVESTIGATION OF THE ACTION	MILEN CYTOLEGAL BUSINESS AND TOWNS	1		Ì	7	Ī				
T	TO SOUTH MAN INCOME TO SELECT	CONTRACT CONTRACT CONTRACT CONTRACT		100 000		•				Ì	
7	DIVINO HIGH AND THE STATE OF S	A PART POTO A PAGE A CONTINUE AND A PAGE A P	2	Т	***						
TIPO NE	Wybotherical profess sin	HERBES SECRET VERILS (TYPE 4 / STEAR) HEADING	191.13	Т	Т	Ť				1	
_	HYPOTHETHCAL GENE 24 PROTEIN	IEDZPESVORUS SADAGO (STIKADI II)		Т	170-101	T	Ī			T	T
L	HYPOTHETICAL PROTEIN U. 13	HERAM CYTOMEGALOVINUS (STRAIN ADISS)	133-190	Ŧ		T					
-	HYPOTHETHEAL PROTEIN AR	HEAPES SINGH EX VIRUS (TYPE 4/ STRAIN UCANDA-1102)	11.00		-	T	Ī				
PULM HOWA	HYPOTHETICAL PROTEDY ULFO	HUMAN CYTOMEGAL OVEUS (STRAIN AD149)	37.50			T					
-	HYPOTHE FICAL PROTEDY BA	HEAPES SAPLEX VIRUS (TYPE 6/STILAIN UCANDA-1102)	945	_						ľ	Ī
	HAMOTHER TICAL PROTEIN ULS	HEMAN CYTOMEGALOVIRUS (STRAIN AD149)	76.95		-			Ī			
PULST HSYGU	HYPOTHETICAL PROTEIN 98.	HERDES SOULEX VIRUS (TYPE 6/STRADA LIGANDA-1101)	36-55	411-001	-						
PULM HONA	PROTEIN ULY	HEREAN CYTOMEGAL OVERUS (STRAIN AD169)	2.4								
┑	HYPOTHETICAL PROTEIN BGLF)	EPSTED-BARA VIRUS (STRAIN 1995-1)	201-223								
7	HYPOTHETICAL PROTEIN UL91	HUMAN CYTOMEGALOVIRUS (STRAIN AD189)	\$56-\$26		H					ĺ	
PULES HIS VED	HYPOTHETICAL PROTED 138	HERPES SOURLEX VIRUS (TYPE 6 / STRAIN UGANDA-1102)	9.10	118-146	_						İ
MES HSVA	HYPOTHETICAL GENE 34 PROTEIN	HERPESVRUS SABAIDI (STRABA II)	107-309								
PULST HONA	DANCICLOVITI KIBLASE	INDIAN CYTOMEGALOVIRUS (STRAIN AD169)	206-328	19611967					Ī	İ	
╗	HYPOTHETICAL PROTEIN ULIDI	IRDAAN CYTONGOALOVIRUS (STRAIN AD169)	164-193								
╗	PROTEIN ULID	INDIAN CYTOMEGALOVIRUS (STRAIN AD166)	18-47								
┱	VILLON PROTEDY UT. 104	HURAH CYTCHEGALOVIBUS (STRAIN ADIM)	215.235	433-450							
MEAS HOWA	HYPOTIETICAL PROTEIN UL 106	HUBLAN CYTOMEGAL OVINUS (STRAD) AD169)	111-66								
ME HOW	HYPOTHETICAL PROTEIN ULTIT	HUMAN CYTOMEGALOVIRUS (STRAIN AD149)	3								
	ANYONE INCAL PROJECT USE IN	HOPEN CT ONE GALOVIAUS (STRAIN AD 169)	200-319					1			
1000		MUTAN CATOMERAL OVER 18 18 AND ADDRESS			+	1	j				
		MUTAN CONTOUR ON THE STAND AND AND AND AND AND AND AND AND AND			+	Ì		1			
		RUPAN CTIUMEUALUTINUS (STRAIN ADIET)	13 × 13		1	1	1	1	1	1]

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FILE HAME	PROTEIN	Viele				-	Т	Т	Т	ī	
PULDY HOMYA	-	INDIANA CYTOMEGALOVIRUS (STRAIN ADISS)	Т	т	т	Т	3	1	4	3	3
PUNO FOWP	ı	FOWLPOX VIRUS (STRAIN FP. 1)	100		I	-	T			T	Ī
PUNG HSVED	URACIL DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP)	24.330				Ī		T	Ť	Ī
	URACIL-DNA GLYCOSYLASE	VACCINIA VIRUS (STRAIN COPENIAGEM)	13.103			Ī		Î		Ī	Ī
Ы	URACIL-DNA OLYCOSYLASE	VACCINIA VIRUS (STRAIN WR)	13.103								
- 1	ULACEL-DNA GLYCOSYLASE	VARIOLA VIRUS	83-103							Ī	1
DAZA DAZA	URACIL DWA GLYCKS YLASE	VARICELLA-ZOSTER PIRUS (STRAIN DUMAS)	317-343							-	
	CENE CA PROTEIN I	EQUING HEILPESVIRUS TYPE I (STRAIN ABAP)	49.63								
AND ROVE	USI PROTEIN	EQUINE HERPESVINUS TYPE I (STRAIN KINTINCKY A)	19-97	i		-				:	:
NAME OF STREET	PROTEIN UST HOMOLOG	PSEUDONABLES VIRUS (STRAIM MIA.3)	120-136						į Į		Ī
1000 PC	MOLE I PROTEIN	JIGMAN CYTOMEGALOVIRUS (STRAIN AD169)	34.39			•					
MOSON HEAVI	PUTATIVE GLYCOPROTEIN USS	PERPES SOUTHER VIRUS (TYPE I / STRAIN 17)	53.78							Ì	
ACSO HSV2	PUTATIVE CL. VCOPROTEDA USS	HERPES SIMPLEX VIRUS (TYPE 2)	53.70						Ī		
TUSO HOWA	HYPOTHETICAL PROTEIN HOLF)	INDIANA CYTOMEGALOVINUS (STRAIN AD149)	29.30			T .				Ì	
PUBLI HOWA	HYPOTHETICAL PROTEIN HIGH!	HALBALM CYTOMEGAL OVIRUS (STRAIN AD169)	11:3			Ī					
PUSIS HONA	HYPOTHETICAL PROTEIN INLIA	HEBLAN CYTONEGALOVIRUS (STRADA ADIAS)	9.5	10:01	277	-				Ī	
PUSIT HOLVA	HYPOTHETICAL PROTEIN HYLTS	HUBLAN CYTOREGALOVIAUS (STRAIN AD169)	1	Ę		1				T	
MUSIC HOUNT	HYPOTHETICAL PROTEIN HYLFA	HEBYAN CYTOMOGOLI OVIRING (STRAIN ADIAN)	316.160							1	
PUSIS HOWA	INPOTHETICAL PROTEIN INLES	INDIAN CYTOMEGAL DVIRUS (STRAIN AD) 49)	Ī	441.444	Ī	1					
PUSIG HOAVA	HYPOTHETICAL PROTEIN HVLF1	DRIBANI CYTOMEGALOVIRUS (STRAIN AD142)	Ī	- 171	!	ij	1	-	: :	i	::::
PUBLIS HOMYA	HYPOTIUITICAL PROTEIN HYLF!	INDAM CYTOMEGALOVINUS (STRAIN ADISS)	10.1%			1					
PUBIO HOLVA	MEMBRANE PROTEIN HWLF1	HABAAN CYTOMEGAL OVIRUS (STRAIN AD169)	Τ	18.30	314.313	Ī					
PUSTI HOWA	HYPOTHETICAL PROTEIN HWLF2	INDIAN CYTOMEGAL OVERIS ISTRAIN ADIAN	Τ	Т							
PUSIZ HOMYA	EALLY MUCLEAR PROTEIN INVLF!	ISTACAN CYTOMEGAL OVINIS (STRAIN AD 149)	200			ŀ					
PUSID HICKAY	HYPOTHETICAL PROTEIN 100.57	DABLAN CHOOLE DAT DWELF (CHAIN AD LES)			1						
PUSSE HOSEVA	DITTOTHETICAL PROTEIN 1843 5	SALLAN CYTOACCAL OVER STRAIN ADJAN			Ì	•		Ī		Ì	
PUSZE BOAVA	GARDTEIN COUPLED REC HOMOLOG USH	HORAN CYTOMEGAL DVIRITY (STRAIN ADIAN)	1	47.47	1	7				1	
PUSTS BICKAT	O-PROTEIN COUPLED REC HOMOLOG US28	BRIBAAN CYTOMOROAL OVIRIUS (STRAPH TOWNE)	T		1		Ī				
PUSTS HOSIVA	HYPOTHETICAL PROTEIN HOUSE	HUBAN CYTOMEGALOVINIS (STRAIN ABIAN)	ļ,		Ī	1				İ	
PUSIO HOMYA	HYPOTHETICAL PROTEIN HOW!	HUMANN CYTOME DALL OVIRUE (STRAD) ADIAN	T	110		Ī		1		Ì	1
PUSD HOMVA	HYPOTHETICAL PROTEIN HILL!	HUMAN CYTOMEGALOVIAUS (STRAIN ADISS)	T		T	-				1	İ
PVBTK_LSV	7 KD PROTEIN	LELY SYNOTONGESS VINUS	7	T	T	1			1	1	
PVOTE NATV	FKD MOTER	POTATÓ VIRUS S (STRAIN PERUVIAM)	5	Ì					T	İ	
PVBTK PVSP	P KD PROTEIN	POTATO VIRUS X (PVX)	3	Ì	Ì	T				Ì	Ī
PVOTE PVX	7 KD PROTEIN	POTATO VIBUS X (STRAIN XX)	1	İ		T				1	Ī
PV01K PVXXI	I KD PROTEIN	POTATO VINUS X (STRAIN XC) (STRAIN CP)	77	Ì	T	T	Ī	T	1	T	
PVIII) ASSLS	LIS (16-1 PROTEIN	APRICAN SWINE FEVER VIRUS (STRAIN LISSS)	75.2	İ	T			T	T	T	Ī
PVIII ASPLS	135 KD PROTEIN	ALFALFA MOSAJC VIRUS (STRAIN 429 / ISOLATE LEIDEN)	26.78				T		T	Ì	Ī
VIII PAG	IND MOTEON	POTATO VIRUS M (STRAIN PLUSSIAN)	3.5			Ī			İ	T	
VUX TAYE	IS KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN PLB)	14.51		İ					T	
PVIO ROVAC	IFELICASE	AUTOCRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	79.102	146-863	1013-1037					T	
200	TALL TROUBLE	BALLEY STRPE MOSAIC VINUS (BSMV)		64-01						T	Ī
VACTO	PROTECTION	VANATA GERMAN IN THE STATE OF T	٦	2							
PVIA BELLY	A PROTECULA	BELLEVILLE STANDER WED	Т	2							
PVIA BLCV	I DECITED	DECEMBER OF STATES		127.25							
AVOD VIA	7 ± C44 ¥	COMPANDACY VINOS	747.767								
NAVY VIVE	IA PROTEIN	CONTRACTOR MOTILE VIEWS	744-763								Ī
NAT AIVE	A PROJECT	CULTIMER MUSAL VIKUS (STRAIN PAY)	775-800								
TVIA CANO	IA PROTEDI	CHAMBER MOSAL VINOS (STRAIN U)	77.500					_			
PVIA PSVI	1A PROTEIN	PEANET STIPL SMILE (STRAIN C)									
PV21X HSVTH	23 4 KD PROTEIN	TIENTS IN PRESIDENT AND		2							
PV20X MAV	29 KD PROTEIN	POTATO FARENCE VIOLETANDE	_								
PYZIK PLAW	18 KD PROTEDI	POTATO I RATEON I VIDING (STRAIN) WAS ENHANCED	2 3								
PVZME BUTVE	29 KD PROTEIN	BEET WESTEAN YELLOWS VIRUS (ISOLATE FL.)	T		1	1		1			
PV39K PEBV	29 6 KD PROTEDI	PRA EARLY BROWNING VIRUS	-		†	Ť	Ť	Ť	1	†	T
PVZA BLEV	1A PROTEIN	BROWE MOSAIC VIRUS	Т	746.177	1	Ť	1	1	1	1	1
			1		1	1		1	1	1]

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PCCENE			AREAL	AREA! AREA?	AREAD	AREA S	AREAS	AREA	AREAI	AREAS
V200 AVV	12A PROTEIN	COWPEA CHO. CAGTIC MOTTLE VIRUS		ī				1		
VAT ALV	PA PROPER	TOWATO ASPERMY VINITS	1000		! - 	<u>:</u>	· ·			
PVIOR TRVIC	TEIN	INBACCO RATTIE VIKITS (SI IKAIN TCM)	10:19	:	<u> </u> :	!		:	ĺ	
PVIIK TOBSY		OBACCO STREAK VIRUS (STRAIN WC)	226-350							
PVIG ASFB!	K'363 PROTEIN	SAICAN SWINE FEVER VIRUS (STRAIN BATIV)	11.164							
PV175 ASPLS		AFRICAN SWINE SEVER VIRUS (STRAIN LISSY)	6		<u> </u>	1			1	
PVIST ASPLS	LIS 312 PROTEIN	JACKAN SWINE, FEVER VIRUS (STRAIN LISSY)		1	<u>!</u>	<u> </u> 	:			
ı	CANTILLE VIACS	NAME OF THE PROPERTY OF THE PAR		<u> </u>	<u> </u> 	 			İ	
- 1	JA FROI ELIN	COUNTRY OF A CONTRACT OF A CON		<u> </u>	 					Ī
NA CAN		OCCUPATION AND ALL COMPANY OF THE PROPERTY OF		1			 		İ	Ī
1		CHICAGO MOSALC VINUS (STRAIN O)		-	$\frac{1}{1}$		-		†	Ī
200	MANGALE VIRUS (CTRADA Y)		317.332		<u> </u>				T	Ī
WILL ALIVE		VIAN INFECTIOUS BROWCHITTS VIRUS (STRAIN BEAUDETTE)	2.5		<u> </u> 		-			
AND ANY		AVIAN DEFECTIOUS BRONCHITIS VIRUS (STRADI MAI)	2		<u> </u> 	<u> </u>				ĺ
TANK AIVE		VIAN DE ECTIOUS BROWCHETS VIRUS (STRAIN PORTUGAL) 120/21	-						İ	
PVIA BIVUS		AVIAN DIFECTIOUS BRONCHITIS VIRUS (STRAIN UTCHESSES)	2						İ	
PVÍA TAV	1A PROPER	TOMATO ASPERMY VIRUS	147-166		<u> </u>	-				
PVSEK BEACY	18 KD PROTEIN	BARLEY STRIPE MOSAIC VIRUS	\$1.00°		 -	<u> </u>				
PV66K BWTVF	PROTEIN 48	CANINE ENTERIC CORONAVIRUS (STRAIN K178)	97-116							
PVPK TYMVA	69 KD PROTEIN	TURMIP YELLOW MOSAIC VIRUS (AUSTRALIAN ISOLATE)	13.39							
PVICE ALVILLE	19 KD PROTEIN	ALFALFA MOSAIC VIRUS (STRAIN 425 / ISOLATE LEIDEN)	44.59							
PVAM VACCE	PROTEDN A4	VACCINIA VIRUS (STRAIN COPEMIAGEN)	217.344							
PVADA VACCV	PROTEIN A4	VACCINIA VIAUS (STRAIN WA)	217.344			•				
PVACE VARV	PROTEIN A4	VARIOLA VIRUS	101.234	_		-				
PVAM VÁCCO	PROTECN AS	VACCINIA VIRUS (STRAIN COPENHAGEN)	3	-						
PVAM VARV	PROTEIN A9	VARIOLAVIRUS	Ī	٦						
PVAII VACCC	PROTEGRAII	VACCINIA VIRUS (STRATH COPCINIAGEN)		100		<u> </u>				
PVAIL VAKY	THOUSEN ALL	VACUULA VINUS	Ī	1	<u> </u>	 	1			Ī
VALUE VALUE	PEOTEN ALA	VARIOLA VIRUS	17.	<u> </u>	<u> </u> 	1	1		1	Ī
PVAIL VACCC	PROTEBLAIG	VACCINIA VIRUS (STRAIM COPEMIAGEM)	141.363			Ļ			İ	
PVAIS VARV		VARIOLA VIRUS	140 361		<u> </u>					
PVAIL VACCE	56 KD ABORTIVE LATE PROTEIN	VACCIMIA MINUS (STRAIN COPEMIAGEM)	429.443							
PVAIL VACEV		ACCIPITA VIBUS (STRAIN WR)	429-443							
PVAIS VAILV	SOUR ABOATIVE LATE PROTEIN	VALUELA VILLE AND VALUE AN		13	1	1	-			Ì
VAN VAN	PROTEIN AND	VALIDIA VIRUS	Т	10.00	+	1	1		1	Ī
PVALI VARV	PROTEIN ALL	VAZIOLA VIRUS	Т		<u> </u>	 -	<u> </u>		T	
PVASH VACCV	PROTEIN A28	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPEMIAGEN)	27.78							
PVAZI VARV	Photem Asi	VARIOLA VIRUS	13.70							
PVAJ2 VAČEV	PROFEIN AJS	VACCIMIA YIRUS (STRAIN WR), AND (STRAIN COPEMIAGEN)	267.70							
VALI VARV	PROTEIN A33	VARIOLA VIDUS	135.180	İ						
NAUS VACO	PROTECT AND PRECINATION	VACCIDA VIRUS (STRAIN CUPENICACEN)			<u> </u>	1	1		j	
TAXA LIVAN	PROTEIN A19	VACCIDIA VIBUS ISTRAIN COPENIACEM	T		<u> </u>	+	1			
PVAJI VACEV	PROTECNAJT	VACCINGA VIRUS (STRAIN WR)	8 4			<u> </u>	-			Ī
PVAM VACCE	PROTEIN A 40	VACCINIA VIAUS (STRAIN COPENSIAGEN)	6.30		<u> </u>					
PVA41 VACCC	PROTEIN ALI PRECURSOR	VACCINIA VIRUS (STRAIN COPENITAGEN)	47.71				_			
PVA41 VACEV	PROTEIN A41 PRECUASOR	VACCOMA VIRUS (STRAIN WA)	47.71							
PVA41 VARV	PROTEDIAN PRECURSOR	VARIOLA VIRUS	П		H	Ц				
PVA45 VACCC	PROTEGN A1)	VACCIDIA VIDUS (STRAIN COPENIAGEN)		301-336						
PVA01 VACEV	PROTEIN A41	VACCORIA VIDIOS (STRAIN WR.)	20.00	201-226	+			Ì		
	PACIFIC ALL	VACCIBAL VIEWS	Ţ,	201-228	<u> </u>	1	1		İ	
VALL VACEV	PROTEIN ASS	VACCING VINUS ISTRAIN WAS	Τ	10.5	$\frac{1}{1}$	-			İ	
PVALI BCIV	ALI PROTEIN	BEET CURLY TOP VIRUS	Τ		1	+	1		Ť	Ī

	916-14-14-14-14-14-14-14-14-14-14-14-14-14-										
	1110 1411	All Virtues (No Batteriophages)					_			Ī	
			1418	DIES.	V YOUV	VERV	AREA 3	AREAS	ABIA 1	AREAT	ABLA 9
1	AL TROPER	CASSAVA LATENT VIRUS (STRAIN WEST RENYAN 841)	55.74			1		_		_	-
	ALI PROJEIN	CASSAVA LATENT VIRITS (NIRAIN NICHERAN)	24.74		:	:					
אלבו אין	AL) PROTEIN	DEET CURLY TOP VINUS	13.181		:	<u>.</u> 	•				
אאם שאא		CASSAVA LATENT VIRUS (STRAIN WEST KENYAN 144)	10.00	<u> </u>	Ť	Ť		1			
PVAL) CLVV	,	CASSAVA LAIENT VIRUS (STRADY NIGERIAN)	19:11	-	İ	İ	1			Ī	
PVALJ TATON		TOMATO YELLOW LEAF CURL VIRUS (STRAIN MARMANDE)	19.15		ļ	T	Ì				-
PVALL TACV		TOMATO YELLOW LEAP CURL VIRUS	11.63			İ	İ				.
PVAT CAMVC		CALLIFLOWER MOSAIC VIRUS ISTRAIN CM. 11411	1	<u> </u> 	-	İ	Ī	i	:	:	
PVAT CAMIND		CAULTICOWER MOSAIC VIBINS (STRAIN DAY)				1	Ì				
PVAT CLIMIT		CALE DLOWER MOSANT VIRING 1978 AND BROCK			+						
PVA! CALMY		CALE IN COURT ADSAUC VIBER AND ADSAUCE AND		1		•					
DVAT CALMS		CONTRACTOR AND AND AND AND AND AND AND AND AND AND				_					
		CALLIFICATER MOSAIC VIRUS (STRAIN PVIAT)	134-157		-				Ī		
	ATHE HANNESSEEN PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN STRASDOURG)	134-153		-	-	ĺ	Ī	T		
VAT CABOY	APHED TRANSLESSION PROTEIN	CALALIFLOWER MOSAIC VIRUS (STRAIN W260)	24.46		t	†	1	Ì		Ì	
PVAT CERV	ANIED TRANSPERSION PROTEIN	CADVATION ETCHED BING VIRIN			1	1					
PVAT FAND	APHIED TRANSLOSSION PROTEIN	PERSONAL VALUE SEES SEES SEES SEES SEES SEES SEES S									
PURCH VARAL		CONT. MOSAC. VIEWS (STEAM DAS)	132-139			-					
		VALLEMA VEIUS (STRAIN COPEMIAGEN)	22:52		r	-	İ				
A A A A A A A A A A A A A A A A A A A		VACCING VINUS (STRAIN WR)	22:39	<u> </u> 	\dagger			Ì		1	Ī
VEG VACCC		VACCINTA VIDUS (STRAIN COPENIAGEN)			1	1	1		Ī		
PUBOR VACCV	PROTECUE	VACCINIA WHIRE ISSUED AND WAS		1	1	1					
PVROV VARV		UNESCHI AMERICA	40.5								
2000		ANGLE VIKUS	40.51							Ť	l
		VACCINEA VIRUS (STRAIN LC 16440)	181-231				t	T		1	
LABOY VACCC	ASOS.	VACCINGA VIRUS (STRAIN COPENHAGEN)	311.331					†		1	
PVBB VACC	MSOA	VACCINEA VIBING STRAIN LIGHTER				İ	1				
PVBOS VACEV	•	VACCIDATA UNBITE (ETTA APL UNBIT			-	-					
PVBOK VACCV		PRODUCTION OF STRUCTURE WELL	1/1/1/2			-					
PVB14 VAPER		VALLEMAN VIKUS (SIRAIM WR.), AND (STRAIN COPENDACEN)	59-63				İ				
		VACCEDA VILLE (STRAIN COPENIAGEN)	131-143		-	_				İ	
7417		VACCIPILA VIDIUS (STRAIN WA)	131-143			-			Ì		Ī
100		VALUE A VAUS	131-143		-	ŀ		T		Ì	
1		VACCINIA VIDUS (STILAIN COPENIAGEN)	31.18		-	l		Ì		Ì	
A A A C C A	MOTEON	VACCIMIA VIRUS (STRAIN WR)			+	-	İ	1			
WE CAN	BLI PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST RENY AN 144)	2	l		1	1		Ì		
N C	BL! PROTEIN	ASSAVA LATENT VIRUS (STRAM MICENIAM)	1 2 2	1		1		1	1	j	
	BCI PROTEDA	IQUASH LEAF CURL VINUS	344.344			1		†	ĺ		
PVBRI ABLOV	BRI PROTECT	ABUTE ON MOSAIC VIRUS (ISOLATE WEST INDIA)		1		+	1	Ì			
TVBA! BOMY	BEI PROTEIN	BEAN COLDEN MOSAIC VIRUS	1	1	1	1	1	j			
PUBLI PRIMI	PROTEIN	POTATO YELLOW MOSAIC VIRILY AND ATE VENEZIELAL					1				
PVBA! SLCV	BRI PROTEIN	SOUASH I EAS CITIL VIBILS			_						
PVCDI VACCC	PROTEDICE	VACCEMA VIDIG 1819 AND CODEMA CEM	212	-	-						
PVOII VACEV		ACCESS OF THE PERSON CONTRACTOR	0.0	_				l	İ	T	Ī
PVCSI VARV		VALLINIA VIAIS (STRAIN W.R.)	73.45		_	<u> </u>		İ	İ	Ī	Ī
PUTOS COURS	PART LANGE CO.	ACULA VICES	21.70				-	ļ	T	İ	
PWCBI ISWA	100000000000000000000000000000000000000	STOOTE FEBRUARA VIII (STRAIN KASZA)		L			+	T	ĺ	T	
200	,	SHUPE FERICIALA VICUS (STILAIN KASZA)	Г	18.19	-	t		T		T	
200		VACCIDITA VIEUS (STILADI COPENILAGEN)	183.20				l		İ	İ	
		VACCORA VILUS (STRAIN WR)	107.68		1		+	t	Ì	İ	
1		SHOPE FIBROMA VINUS (STRAIN RASZA)	į		ļ	1		Ť	İ	İ	
A A A A A	CAL PROTEIN CI	SHOPE PIDROMIA VIRUS (STRAIN RASZA)	9.5	1				1	Ì	Ì	
TVCU VACC				1	1	1					
FVCD VACEV					+	+	1	1	Ì	j	
PVC10 STVIKA	AL PROTEIN CIO	N KASZA1	100	+	+	+	1				
PVCIB VACCE				+	$\frac{1}{1}$	1	1				
PVCIO VACCY					1						
PVCIO VARV				1	+	1		1			
PVCI6 VACCC				1	1	1	1	1			
PVCIT VACCE					+	1					
PVCII VACOC		VACCIBITA VIRUS (STILAIN COPEMHACIEN)			1	1	1	1			
PVCA EBV	MAJOR CAPSID PROTEIN		1	101 771	1000	+	1	1			
			1	7	65	1	1	1			

PCGENE	PDCTL2IP	All Virginia (No Maries and Annas)									
TRVETTI		XIMUS.	7		33.6	- NIA	AILA?	AREA	C VINE	Y I VIMV	AMITA 9
VACA ICOAA		HUMAN CYTOMEGALOVINUS (SIRAIN ADIM)		П		: :		t	!	1	
E PAR	MAJOR CAPSID PROTEIN	HEAVES SIMPLEX VIRUS (1 VPC 1 / STRAIN 17)	207	1	1137.1153						
PVCAD HSVEB	MAJOR CAPSID PROTEIN	EQUINE HERPCSVIRUS TYPE I (STRAIN ARILY)	137-303	П							
VCA HSVSA	MAJOR CAPSID PROTEIN	ICENTES VIRUS SAIMIRI (STRAIN 11)	166-168	_	20.00	063.1019					
ŀ	MAJOR CAPSID PROTEIN	PSEUDORABIES VIRUS (STRAIN INDIANA S)	115.162								.
	MAJOR CAPED PROTEIN	VAUCELLA-ZIISTER VIRUS (STRAIN DURIAS)	311.401	010-100	1156.1176						
PVCOD NAVAC	DNA-BINDING PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POL VHEDROSIS VIRUS	10.09							<u> </u>	ĺ
VAUD VACEC	MOTERNEY	VACCINIA VIAUS (STRAIN COPEMIAGEN)	<u> </u>								1
VOS) VACCV	PROTEINO	VACCINIA VIRUS (STRAIN WR)	2.2							İ	!
PVD03 VARV	PROTEINDS	VARIOLA VIRUS	3.30		!					i	İ
PVD05 FOWP!	91 6 KD PROTEIN	FOWLPOX VIRIS (STRAIN #P.1)	346.765	115.137							İ
PVD05 SFWCA	PROTECUDS	SHOPE FUBRICALA VARUS (STRATH KACZA)	1	100			Ī				
PVD05 VACCC	PROTERVOS	VACCINIA VIBIR (CIBADA COMENIACEN)	97. 41	T	- 22						
PVTOK VACTV		The state of the s	2	7							
7 17 19 19		VALLINGA VIAUS (STRAIN WR)	100	894.7	2	1					
100	TROI EIN DA	VAUCULA VIRUS	376-340		13.33						
	DMA-BINDING PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN CM: 1941)	3.2			ì					
PVDB7 CANNO		CAULIFLOWER MOSAIC VIRUS (STRAIN DAI)	3.1								
PVDBP CAMVE		CAURIFLOWER MOSAIC VIRUS (STRAIN BRC)	17.56			ŀ				Ī	
PVDBP CALVA		CALL DI OWER MOSAIC VIRILS (STRAMANALS)				1					
PYDEP CALVS		CALB IN CORE MORAL VIBILS AND STRANGED IN			Ť	1					
PVEM VACCE	-	VACCINA MALIA 1978 IN PORTALL COM		T		•					
200	-	TACCING VACUS (STRAIN COPENIACEN)	P	Ti	340-538						
		VALLIMIA VINUS (STANIM WA)	70-07	335-380	540-558						
	TO LEW EZ	VALIOLA VIIUS	70-03		840 888	Ī	Γ				
VVEDS VACCE	PROTEINES	VACCOMA VIRUS (STRADI COPENHAGEN)	314.379			-					
PVESS VACCO	PROTED ES	VACCINGA VISUS (STRAIN DADLEN 1)	134.339			-	Ī				Ī
PVEOS VACCV	PROTECH ES	VACCINIA VIRUS (STRAIN WIL)	124-339		İ					Ì	
PVESS VARV	PROTEINES	VARIOLA VIRUS	124.330		İ	Ť					
PVEDS VACCC	PROTEIN EG	VACCORA VIRUS (STRAIN COPENHAGEN)	100		T					Ī	Ī
PVEDS VACCV	PROTEIN EG	VACCINGA VIRUS (STRADY WR.)	410-451		Ť				Ī		Ī
PVECS VARV	PROTENTA	VARIOLA VIRUS	251.243	157-019	Ì	T	Ī				
_	PROTED ED	VACCIMIA VIRUS ISTRAIN COPENIAGEM	256.370		Ť	†				Ī	
PVEON VACCV	PROTEDUES	VACCIPILA VIRUS (STRAIN WR)	354.370		İ	İ		Ī	Ì		Ī
PVEOD VARV	PROTECNES	VARIOLA VIRUS	314.336		İ	İ	İ			Ì	Ī
PVEIS HEVIG	PROBABLE (I) PROTEDN 2	HIMAAN PAPILLOMAVIRUS TYPE 16	103.483			Ť	1	1		Ì	
PVEIL NEVAC	EARLY IS S AD PROTEIN	AUTOGRAPHA CALIFORNICA MICLIFAR POLIVIEDBOGIS VIDILE			1	Ì		1	Ì		
PVEL BIVI	EI PROTEIN	BOVDE PAPELOMAVIRUS TYPE I	366.363	*****	1	1				1	
	EI PROTEIN	BOVINE PAPILLONAVIRUS TYPE 2	185.34	110	ĺ	Ì	Ì	1	Ī	Ì	
PWEL CLEVK	EI PROTED	COTTONTAL MABRIT (SHOPE) PAPILL ONIA VIRUS (STRAIN KANSAS)			Ì	Ť			1	1	
ı	EI PROTEO	HERITAN PAPEL COLLA VIELLE TYPE 11			İ		Ī	1	Ì	1	
L	EI PROTED	MEDIAN PAPEL CALAVILLE TYPE 13	711.04		+		1	Ì		İ	
L	EI PROTEIN	PROGNA PAPELCOMA VINUS TYPE 10	100	-	1,1,1		1				
	EI PROTEIN		25.25	T		Ť	Ì			İ	
	EI PROTEIN		318.366		1	Ì	Ì	Ì	Ì	İ	
PVEL 10V39	ELPROTEIN	PROJECT PAPELONIA VINUS 1 TPE 19			Ť	İ	İ		Ì	Ì	
	EIPROPEN	HOMEAN PAPILLONIA VIBLIS TYPE 41				1				-	
PVEL 10V43	EI PAOTEIN	HUBLAN PAPULOMA VIBUS 177E 42			1		Ì		Ì	İ	
	El PROFED	MANAN PAPEL COMA VIBING TYPE SE			1	1	Ì	Ì	Ì	Ì	
PVEI JOVED	EI PROTEIN		315.031	7.1	İ		Ì	Ì	Ì	İ	
Γ	EI PROFED	2015 F VPF 1		-		1	İ			-	
Г	EI PROTEIN	RICESUS PAPILLONIA (IRUS TYPE)	100		-	İ	Ì	1	İ	-	:
	PROBABLE EXPROTEIN	COTTONIAR RABBIT (SHOPE) PAPILL CALAVIALIS ISTRAIN KANSASI		i	İ	İ			-	i	i
	El PROTEIN	PRINCIAN PAPRIL CANAVIRUS TYPE !!	301.100	Ì	1	t	İ	Ť	İ	İ	
П	E. PROFED	INDIAN PAPEL GALA VIRUS TYPE 1)	2	İ		1	Ť			İ	Ī
	E2 PROTEDA		366.904	İ		t	T		İ	İ	
	EJ PROTEIN		286.300		İ	ĺ	İ	İ	İ	1	Ī
	EJPROTEIN	INDIAN PAPELONA VINUS TYPE 3A	311.334		İ			Ì	İ	İ	
PVEJ 19VJ	EJ PROFEIN		200-312		<u> </u>	T	T	T	-	t	Ī
									1		7

Service Service	10.0000									
FILENAME	PROTEIN	Vieus		Т	7	Т		П		
IVEJ (BV)	E3 PROTEIN	HERMAN PAPILL ON AVINUS TYPE))	197.52	5		2028	4	o vono	444	ABEA
PVEJ MPVIJ	EDPROTEIN	HUDMAN PAPILLOMAVIRUS IYPE 15	110.103	<u> </u>	 				Ì	
PVEJ HEVIS	E2 PAOTEIN	HUMAN PAPEL CONTAVINUS I YPE 19	303.510	<u> </u>	† T				i	İ
PVE2 IDV43	EJ PROTEIN	INDIAN PAPIL CONAVINUS TYPE 41	10.10	<u> </u> 	<u> </u> -	-			j	
PVEJ POUT	E3 PROTEIN	THEN TANKE TOKING TAPE IT	18.18	<u> </u>	 -	-				
PVE3 HPV46	EZ PROTEIN,	HUDIAN PAPILLOMAVIRUS TYPE AD	100	<u> </u>	 -				i	Ī
PVEJ PAPVD	PROBABLEEZPROTEN	DEER PAPILLONIAVIBUS	1 1 1 1		<u> </u>			-		
PVED PCV	EDFROITEN	PYGMY CHIMPANZI PAPITI DALINI WHIS INTE	2.18	· :		:			=	_
PVES BUPY	STORES.	BIS ANTALONIA VIEW INTO INTO	Par 101							-
PVE4 INVIE	PRUBABILE EN PRUTEIN	IMMIAN PAPULLMAVINUS INFL IS	**		•					_
PVE4 HDV41	PROBABLE E4 PROTECN	HEBITAM PAPILLONIAVIRUS TYPE 41	1	<u> </u>	†				j	
PVEA HEVSI	PROBABLE E4 PROTEIN	MAKAN PAPIL COMA VIRUS TYPE SI	20.03	<u> </u>	1				j	Ī
IVEN NAV	PROBABLE EX PROTEIN	INESUS PAPULOMAVIRUS 19PE I		<u> </u>					j	
PVESA HPVII	PROBABLE ESA PROTECIA	BENIAN PAPEL LONIA VIDIN 15 P. I.		<u>i</u>	1			•		
PVESA IPVAC	PROMABLE ESA PROPERTY	THE PART LINE AND THE PARTY OF			•					
PVE3 EPVI	E3 PROTEIN	POVINCE DARKS CARDS CARDS A CA			•					-
PVES HOVE	PACE AND E BE DECISION	MAINTENANCE CONTROL OF THE CONTROL O	2	<u> </u>	-				-	
PVE LOVE	PROBABLE BLOGOTERA		3	_ <u> </u> -						!
1000	PROBABILE BL PROFERM		<u> </u>	- - -					<u>-</u>	!
1000	100 100 100 100 100 100 100 100 100 100	MUMOUR PARTICIPATION INTO	45.65						<u> </u> 	
40.40	TOTAL STREET	FIGHER FAMILIANIA VIEWS	2.2					-	!	•
	LINGUE EN LUCIEN	INDIAN PART ON AVIATION TYPE VII	3.5						_	_
1	PROGRABLE ES PROTEIN	DIESUS PAPILLONIAVINUS TVPL I	11.5	:		:::	:		:	! :
	EA PROTEIN	BOYDAE PAPIL COLAVIRUS TYPE I	1					İ	İ	
	EA PROTEIN	COTTORTAL RABBIT (SHOPE) PAPILLONIAVIRUS (STRAIN KANSAS)	1	 	ŀ			-		i
2	EA PROTEIN	PROMON PAPELLONIA VIRUS TYPE 8	13)-131					İ	1	Ī
PVES IPVIA	64 PROTEIN	HARAN PAPILI ON A VIRUS TYPE IA	1	<u> </u>					i	
PVEA HPV1)	EA PROTEIN	INMAN PAPILLONIA VIRUS 1 VFF. 13	1	<u> </u>			1	:	<u>-</u> :	
PVEA HEVIS	Es PROTEIN	INDIAN PARLICHAVIRUS TYPE 35		<u> </u> 	7	-	-	:	<u> </u>	:
PVEA HEVSI	EA PROTECT	MINAM PAPEL CONAVIRUS TYPE SI	1	 	ŀ					-
PVEA HOVES	EL PROTEIN	PRINCIAL PAPEL COMA VIRUS 1 YPE 59	1.5	<u> </u>						Ī
PVE 10VE	ES PROTEIN	HUMAN PANTLOMAVIRUS 1YPE SO		<u> </u> 	ļ	Ī			+	İ
1 NEW 1904	Es PROTEIN	MACROMYS MINUTUS PAPILLONIAVIRUS	1.3	 	-	I		-	 	[
M C	ETPROTECN	COTTONIAL MABBIT (SHOPE) PAFILL UNIAVIRUS (STRAIN KANSAS)		<u> </u> -	İ		Ī	 	-	
	42 PAOTED4	HUDAAN PAPIL LOWA VIRUS TYPE 13	1	 	1			-	1	-
PVET IOVE	EPROTEIN	FREAL PAPEL CRIAVIALIS TYPE SI	10.3					-	ļ	j
PVE! IOVED	El PROTEIN	HIDAAN PAPILLIDAANIAUS TYPE (B	150	_				1	1	
LAGA PAGA	E7 PAOTED ⁴	MESUS PAPELOMAVIEUS TYPE I	79.105	<u> </u>					<u> </u>	
PVEM MVAC	EARLY ON KD PROTEIN	AUTOCRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	78.99				Ì		1	
VE GVIN	VIDLAL ENHANCING FACTOR	TRICHOPLUSIA NI GRANULOSIS VIRUS	154.135 237.346	100	-			1	İ	
ANTA STA	ENVELORE PROTEIN	BEANE VALUS	63.06 03.114	Т	<u> </u>		T		İ	Ī
TYEN DAM	ENVELOPE GLYCOPROTEDY PRECUMSOR	PHORY YIRUS (STRAIN INDIANULLING)		-				1	İ	Ī
	PROBABLE ENVELOPE PROTEIN	EQUIPME AATERUTIS VIRUS	Γ						1	
	PROBABLE ENVELOPE PROJECT	LELYSTAD VINUS	21-10		-		T	+	\dagger	
1	-	MOLLUSCUM CONTAGOSUM VIRUS SUBTYPE I			L			-	t	
A PART	4	MULLUSCUM CUMTAGIOSOMI VIRUS SUBTYPE 2								Ī
PVETN NOVAC	-	INCOLO VILUS	196-221 336-383	43).481					İ	
PVIEW VACOU	14 KD MAINS LATING AND BROTEIN BESTER OF	AUTOCACATION CALLO OUTICA NUCLEAR POLYTEEDROSIS VIAUS	12.103						t	Ī
PVIET VACO	M KO WATER MEMBER AND BECTERN AS ECTINGOR	VALLEND VIEWS (STRAIN COPENHAGEN)	100.303						l	Ī
PVF VACCV	N KD MAJOR MEMBRANG PROTEIN PRECTINGOS	VACCINA VINIC (CITALINA)	280-305						T	
PUTOS VARV	14 KO MAJOR MEMBRANE PROTEIN PRECURSOR	VARIOLA VIRUS	201-100	<u> </u>						_
PVIO VACCE	PROTEINE	VACCOUR VIBUS (STRAEN COPENHACEN) AND CERAIN LINES	60.00	_						
PVF09 VACCV	PROTEDIFF	VACCENTA VIRUS (STRAIN WR)	74.700	1						
PVT09 VARV	PROTEINFO	VARIOLA VIRUS	75.70	1	-		Ť			
TWIE VACE	PROTEDIFIE	VACCINIA VIRUS (STRAIN COPENTAGEN)	161-184	<u> </u>	-			Ī	1	Ì
A 11 A	PROTECULAR PLI	VANICLA VIRUS	161-180	-	-		T	-	\dagger	
יייייייייייייייייייייייייייייייייייייי	PROJECT PT3	VACCINGA VIRUS (STRATH COFEMIAGEM)	17-52		\mid		T	+	+	T
								1	1	7

							ľ	L	-	ŀ	Γ
3332	PHICHZIP	AB VINDER (No Becterophages)	1 4 1 0 4	ARFA?	ABEAT	ABFAS	ARTAS	ARFA & ANFA ! ANFA !	17.1	ī	O V IN V
THE REPORT	CROTTER	VACCINI VISITE AND THE	ī		4					,	;
WIS VACE	7	VALLINIA VIAUS (SIRAIR I. 1917)		:		<u>-</u>				_	
PVF IS VARV		VARIULA VIRUS				1		1	1	•	:
PUTPI FORDY		TOWLPOX VIRUS			1	1	Ì	1		1	1
PVEPS BOWDY	PROTEIN PP	FOWLPOX VIRUS	2					-	1	1	
PATE CANA	т	CAPRIDOXVIAUS (STRAIN KS-1)	11.6		i					1	1
Very frame	۲	FOWLPOX VIRUS	63:80								
MOVE CANA	CSEA PROTEON	CAPRIPOXVIRUS (STILATM KS.1)	31.76							_	
PVEIN CAPTUT	IN THE STREET PROTIEM	ORF VIAUS (STRAIN NZ2)	2.4		i	-				-	
	+	VACCINIA VIRUS ISTRAIN WR 65-161	1		i			_			
1	_	COLINE LEADE CURISTYPE LISTRAIN ARAPI	18:181					-		<u> </u> 	Ī
	Ŧ	LA ALL TERROR AND LAKE OF CAMERIA A	L	111.339	319-685	F				<u> </u> 	
	7	ALCOHOL TENERS IN CONTROL	T	124 564			İ				
A VOIC	_	VALCEMA VIRUS (STRAIN COTEMINALE)	T				Ì	Ī	1	t	Ī
PVGBI VACCV	-	VACCIPALA VIRUS (STRAIM WR)	T				Ī	1	<u> </u>		:
DVCB! VARV	PROTEIN GI	VARIOLA VIRUS		176.795		1	!	- 		!	!
DVGS VIVO	INVPOTMETICAL GENE I PROTEIN	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	20-62					-		1	
PWGM VACOC	PROTEINGS	VACCINIA VIRUS (STRAIN COPENHAGEN)	24.2			-	_		_		
2010	Phorein (1)	VARIOTA VIRIN	2					-	L		Ī
	Panetal Cu	VACCEMA VIRES (STRAIN COPERCIAGEN)	1					-		- 	
	-1	DARKET WELL						-		-	
	7	VANCEA VILLE				Ŧ	Ì			†	Ī
MON AVC	7	VALLINIA VIIIUS (3) MAIN CUTEMIAGEN				·		+		İ	
VOS VALV	PROTECTION	VAUCLA VOLUS						1			
PVCOS ICENTI	INTROTHETICAL ODAE I MEMBALANE PROTEIN	KETALJAND KERPESVINUS I	134-149	159-185				1			
PVGN BEVIL	INVOLUCTION CENT IS LOUGHAND PROTECT	ICTALIFIED NEWPESVINUS I	Г								
A CONTRACTOR	т	MEDIFICATION CALMINISTATICATION	22.65	155-379						r	
	۳	M-FATTBED LEED FOUNDER	Т	150-136		F					
	CHICAGO IN THE PROPERTY OF THE	CTALLE EN LES BAR CABINE A	T	3 30. 366			ļ		-		ĺ
	MINDING THE PROPERTY OF THE PR		Τ				Ī		╁	ł	Ī
PVOIS HBYSA	HYPOTHETICAL CENT 13 PROTEIN	MELLYES VOICES SAMOND (STRAIN III)				1	Ì	1	+	+	
PVGIP HEVI		ICTALIJIJD PERPESVIKUS I								+	
ACTIVITY TIONAL	_	AMSACTA MODREI ENTOMOPOXVIRUS						1		1	
MIAS IDA		SPEROPLASMA VIALUS SPVI-REAZ B	7	2		1				+	
PVG23 HSVII	-	ICTALUND HERPESVIRUS 1	108-111			7				1	
PVGID KBVII	HYPOTHETICAL OESE 33 PROTEIN	ictal Units Heathesvinus i	114-115							_	
PVOST HEVEL	HYPOTHETICAL GENE 17 PROTEIN	ICTALURIS HEAPESVIRUS I	2								
PVQ29 HSVSA	HYPOTHETICAL CENE 29 PROTEIN	HEAPESYTHUS SADAIRS (STRAIN 11)						-	,		
PVQ28 HBVII	HYPOTHETICAL GENETS PROTEIN	ICTALUNID HEAPES WIRUS I	į	401.511							
PVG25 HSVSA	HYPOTHETICAL GENE 28 PROTEIN	HEAPESVIRUS SABAINĮ (STRAIN 11)	10-40								
PVOM HEWI	INTOTAL CEMENT PROTEIN	ICTALUNID KEAPESVIRUS I	10-01						_		
PVOIS TRIVI	HYPOTHETICAL GENE SO PROTEIN	ICTALUMO MENPESVIRUS I	161-161					_			
PVO) VZVO	۳	VAUCELLA-LOSTER VIRUS (STRAIN DURIAS)	10.101				-				
PVOM NOVA	т	HERPESVRUS SADARU (STRAIN II)	100-133	144.363				L	<u> </u>		
PVG35 HBVII	т	ICTALUMEN HEAPES YIAUS I	114.78							-	
PVOIS HISMI	т	ICTALUND HERPESYINUS I	519-879	976.900	1038-1065				-	-	
PVD46 HSVII	Т	ICTAL UNID MEADES VIAUS I	3.5				İ			l	
PVG41 KKVII	WAYONE HEAL COM 41 MOTEN	ICTALIA DE REPESVAUS I	11:11	10.20	744.780					_	
IN M. SPZAG	INVIONMENTAL CASOL AS PROTEIN	ICTAL UNIO HE EPESVIAUS I	100-133	137.178	Γ	\$21.518			-		Ī
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IN IN TOUR	SAMPOTHETICAL CENT 45 PROTECT	ICTAL UNIO HE DESVIAUS I	Τ		T	I	Ī				
AVOIS HAVE	PROB TRANSCRIPTION ACTIVATOR EDRU	HELDESVILLE SABIITA (STRATIV !!)	9	===			Ī		-	\dagger	
PVOST HEVE	HYP CEDE 11 MEMBRANG PROTEEN	KCTALUMD (EINTS WILLS)	*	107	T	Ī	T	-	+	+	Ī
PVOST REVIEW	SIMPOTIETICAL CENTESS PROTEIN	ICTALUMD NEWPES VINUS I	239-252			Ī	İ			1	
PVOA HAVE	SECTION STATES CANAL SEPTIONS	ICTALIBIDIO NO REPESYRUS I	23.33	10.151	111.100	ĺ		-		l	
PWOM DRIVEN	HYPOTHETICAL CENT IS PROFEIN	ACAPESVINUS SABATAL (STRATA 11)	181.5							t	
פערער אנעוו	т	ICTAL UNID HERPESYINUS I	1135-1136		Ī	Ī	Ī	\mid		l	Ī
PVOIL HSVEA	T	IERPESVEUS SAIMIRI (STRAIN !!)	т-	364.388	51.15	330.346			l	 	Ī
PVGS9 MEVII	ī	ICTAL UNLD HE REESVINUS 1	ī	367.389	ī						
PVGS SPV4	GENE S PROTEDY	SPIROPLASMA VIRUS 4	43-44				П	H	H		
PVOGO HBVIII	HYPOTHETICAL GENE 60 PROTTIN	IL TALLWID IN PPECCIFUS	36-51	53.75							

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PVCLE HOVEA	CLYCOPROTED B PRECURSOR	EQUINE KEXPESVIRUS TYPE I (STRAIN ABI)		1						Γ
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	AL LANCES FOR THE CHIEFOR	S VIRUS (STRAIN 632)		197-621	140-758				1	
		PARECENTAGE ABOVACOTE ACHEITS VIRUS (STRAIN SA.2)	266-285	24 119-109	750-764				-	
PYCE BETYS		CONTROL OF TANAMAN CURITY CHIEF (\$79 ATM TUMBNE VIS)	266-285	107-631 75	26.76					
PYCLE B.TVT		IN COLUMN LOCAL COMPANY AND EASTERN	Т	Т	738.765		-			
PWCS MOVIN		CONTRACTOR CALUNIANS (STRAIN PAILTT)	T	T			-			
PWGLB PANT		PSEUDORABIES VIRUS (STRAIN INDIANA: FUNKTIAUSER CHICKER)	17-702	†			+			
PVOLE VZVD	CLYCOPROTEDY B PRECURSOR	VANCELLA-20STER VIRUS (STRAIN DUNIAS)								Ī
TO ST. VALUE	CL VOCESOTTE DE PRECIDE COM	EXPES SOCIET VIRUS (TYPE 1 / STRAIN 17)	1.22	447-403		-				
	Co. Under Artista P. Self C. III CO.	GENER SAMPLEX VIRUS (TYPE I / STRAIN KOS)	1.12	467-403						
THE HOUSE		WEBBER KINDS BY VIBING (TYPE 2)	135-264			_		;	_	•
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PVGLC HSV33	CLYCOPROTEIN C PRECURSOR	HEATER MARLEA VIACOLITATE & STRANG SEL	100	<u> </u>		-	: :		:	:
PVOLC HISVING	CLYCOPROTEIN CHI PRECURSOR	DOVING INDICES VINUS 1 FFE 1 13 MAIN CAM I. II		+	-	-			-	
PVOLC HSVSA	GLYCOMOTEIN C PRECURSOR	EQUING HEIPESVIRUS TYPE 4 (STRAIN 1942)		1		+		<del> </del>	ļ	Ī
PVCLC HSVED		EQUINE HEAPESVIALUS TYPE I (STRAÍN ABAP) AND ISTRAÍN KEN THEN		+	1	+	1		t	Ī
100	CECHETORY CLYCOMOTERN CP17-45 MECURSOR	MAREK'S DESEASE HERPESVIRUS (STRAIN HC·I)	100-421						1	Ī
	THE PARTY OF TAXABLE PARTY AND	MARRIE DICKAGE HERPESTALIS (STRAIN RB-19)	166-431							į
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MOL HSWIC	SECTION OF THE WASHINGTON	ALL PRING PARK ARE ARE BECKER IN A CONT.	169.621			  -	-			
PVCIC HISMON		MALES SUSCESSION STATES (STATES)	180.107	446.477		-		!		
PVCLC MVB		SEUDOIGHES VIRUS ISTRAIN INCOMA COMMISSION INCOME.			-				-	
DWG/C VZVD	CL VCOPLOTED GPV	VALICELLA-ZOSTEA VIRUS (STRAIN DURIAS)		+			+			
PVOLC VZVI	OL YCOPLOTED OPV	VANCELLA ZOSTER VIRUS (STRAIN SCOTT)		1		1	+		$\frac{1}{1}$	
PURE A PROPER	CH VCOPE OFFIN D PERCURSOR	HEIDES SOCILEX VIXUS (TYPE I / STRAIN IT, AND (TYPE I / STRAIN				-			$\dagger$	
20 E	CH WOMEN CHARLES BEACH RECORD	AEAPES SDOLEX VINUS (TYPE 1)					4		1	
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100 mm	CALVICOROTIFICATION	VARICELLA-2031ER VIRUS (STRAIN DURLAS)	469-493			•			1	
	THE SAME OF VANDANTED PRICE IN CO.	BOVING RESPIRATORY SYNCYTIAL VIRUS (STRAIN AS 1904)	125-221	265-287	482-504				1	
2	STATE OF LANGE OF THE PARTY IN COM-	MOVINE DESPIRATORY SYNCYTIAL VIRUS (STRAIN COPENHAGEN)	305-331	265-180	484-306					
	FUSION OF TOWNS INCOME.	BOWNE BECOME ATORY SYNCYTIAL VIRUS (STRAIM RB94)	105-221	265-280 4	464.506					
WC BSW	PUNCH OF TOWNS IN THE WASH	CANNAR PACTEADER VIRING (STRADE ONDERSTEPOORT)	336-361	396-414	\$43.589					
200	FUSION CLYCUPTO FILM MELLINSON	A MANAGEMENT A TORY STOLEY WAS A STRAIN IN		Γ	484-506				-	
TYCE HELVI	-	TOTAL STATE AND STATE OF THE CORP AND ASS.	305.331	Ť	484.506					
FVOL MASYA	_	HUNDAR RESPUENTION 1 STIME TIME VINUS (STIME)		Ť	484.506					
TYCE HIST	FUSION CE YEUMOTERY PRECUESOR	TANKS AND A PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY	304.233	Т	404.506	-				
PVOLD HESVE	FUSION GLYCOPHOTED! PRECURSOR	TOPON TENTON STORY STORY CONTRACTOR CONTRACTOR TO STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY OF THE STORY O	234.245	Т	451-477					
TO LOASE	FUSION CL. VCOPILOTIED PRECUASOR	PERMITTED AND COMPANY (P. 1. CA.)	227.248	Т	454-480	<u> </u>	-			
MOT NEAS	٦	ACCOUNT OF STREET AND VALUE OF ALL	334.346	Τ	161-433	-			-	
TYOU DOWN		ALCOHOL VINCE (STOCK)	8	Ť	446.463	-	-			
PVOLT MADE		MUNICO VICTOR (STRAIN SOC.)	376 300	T					-	
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TYCH MUSICAL		MORPS VILLE (STRAIN RW)		Т	446.463	-				
PYCL MODES		MANGES VINUS (STRAIN SBL.)	22.5	Т		1				
TWO DOVY		NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTURUA))	107-672		1	+				T
WOL LOV		NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	273-289			1	+		1	
DIACK & FOAT	PUSION OLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN HEAD))	273-269							
ALVON CHONG	Т	NEWCASTLE DISEASE VIRUS (STRAIN BI-HITCHMEN47)	273-269				$\frac{1}{1}$			
MON E PONS	FUSION CLYCOPHOTEON PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN LAS/46)	273-289						1	
	FINAL OF VECOROTERY PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN MIYADERANSI)	273-289			_				
CACH TON	FLISTON OF YCOPROTEDY PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN QUEENSLANDMA)	273-289						1	
TACK TON	FUSION CLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS)	273-289				1		$\dagger$	T
PAGE 1 NOVICE	1	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B /48)	273-289		1	1		†	$\dagger$	Ī
WOLUM	Т	NEWCASTLE DISEASE VIRUS (STRAIN ULSTERAS)	273-280	T	٦		+			
AQQ-II IIA	Τ	PHOCONE DISTEMPER VIRUS	269-313	103-126	167-383 531-558	25	-	1	1	]

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PVQ FIIHC	FUSION CLYCOPROTEIN PRECURSOR	HOMAN PARAINGLUENZA I VIRUS (STRAIN C19)		<b>;</b> -	T		Г	Т	1	Т	T
PYCL PUR	FUSION CLYCOPROTEIN PRECURSOR	HUMAN PARATMELUENZA 2 VIRUS (PIV.2)	150.02							f	
PVGU MIHO	FUSION GLYCOPROTEIN PRECURSOR		450-471								
PYCLE PLINT	FUSION GLYCOPROTEIN PRECURSOR	HUMAN PARAINFLUENZA ? VIRUS (STRAIN TOSIUIA)							•		
Wall Mile	IFUSION GLYCOPROTEIN PRECURSOR	BOYINE PARAINFLUENZA 3 VIRUS	2	٦						-	
30	FUSION CLYCOPROTEIN PRECURSOR	HIDAAN PARAINT (UEŅZA ) VIRUS (STRAIN MII 47185)	Т	╗	453-474				1	1	
NO.	PUSION CLYCOPROTEIN PRECURSOR	ADMINISTRATION (STRAIN KABETE O)	220-24	783.708	447.47				+	+	T
VG V SDDS	FUSION OF VOOPROTEIN PRECINGOR	SENDAL VIRUS (STRAIN 2 / HOST MUTANTS)	Τ	Τ		ŀ			1	$\dagger$	1
WGJ ENDY	PUSION OLYCOPACTED PRECURSOR	SENDAI VIRUS (STRAIN FUSITINITY	117-03					-	!	<u>:</u> :	:
WOLL SENDY	FISSION CL. VCOPACTEIN PRECURSOR	SEMBAI WIRUS (STRAIN HARRIS)	3							t	Ī
Wat tom	FUSION GLYCOPIOTEIN PRECURSOR	SEMBAL VIRUS (STRAIN HV.)	460-431					l	l	+	
Wal serbs	PUSION CLYCOPROTEIN PRECURSOR	SENDAL VIRUS (STRAIN 2)	460-481								
PVQLF SV41	FUSION GLYCOPROTEIN PRECURSOR	SEGAN VIRUS 41	453.476			•				<del> </del>	Γ
PVQL SVS	FUSION GLYCOPROTEIN PRECURSOR	SOUTAN VIRUS S (STRAIN W))	401-425	646.467							
INCLE TRIV	FUSION GLYCOPROTEIN PRECURSOR	TÜRKEY KHIMOTRACHEITIS VIRUS	٥	452-474		-					
700 B	SPIKE GLYCOPROTEIN PRECURSOR	INTECTIOUS NEMATOPOIETIC NECROSIS VIRUS (STAAIN ROUND BUT	17.99			-					
PVGLO PABVE	-	RABIES VIRUS (STRAIN ERA)	1			1					Ī
MOLO BABYE	7	RABIES VIRUS (STRAIN HEP-FLURY)	T	434.474				1			
Wad by	SPIRE CLYCOPROTEIN PRECURSOR	RABIES VILLE (STRAIN PV)	434.474			•		1	1		1
WOLD BANK	SPIKE GLYCOPIOTED PRECURSOR	KABLES VIRUS (STIAIN SAD BI9)						1		+	
ACC PAC	STIKE GLYCUPROTEIN PAECURSON	KABLES VIKUS (STRAIN STREET)	2/ TX					1	1	1	
WG.6	MANOR SURFACE CLYCOPROTEIN G	TURKEY INGRACHEITIS VIRUS	100-210					+		+	
MONO WISK		VICAL REMOUSHAGIC SEPTICEMIA VIRUS (STRAIN 07.71)	7	T						+	
ANGE HOW	CALYCOPHOTEIN N PRELUXOR	HUMAN CYTOMEGALOVINOS (STRAIN ADISS)	107-117	787.44	374.398			$\dagger$	$\frac{1}{1}$	$\dagger$	
	7	PLEADURE OF TOMBE OF UNITY (STRONG TOWNS)	Т	T	, ac-1, c	+			1	1	T
אינה דו דולאונ	AN ACCORDING IN PRECIOUS	NEBER COMPLEX VISITS (TVPR ( / STRANDER))	Т		101.877	1				$\dagger$	Ī
T ELAN	Ca voneoffe all besone	HERBES SOLD EX VIEW CIVE & STRAIN CS	Τ			ŀ		t		$\dagger$	T
WOLLDWIN	CLYCOMOTEM HPRECIASOR	EQUAL HERPESVIKUS TYPE 4 (STRAIN 1942)	Τ	814-839				1		$\dagger$	T
PVOLM HEVED	GLYCOPROTEIN W PRECURSOR	EQUINE HERPESVIRUS TYPE I (STRAIN ABAP) and (ISOLATE HYSISA)	Γ	107-112		-		┢		H	T
PVOLH MSVSA		HEADES VIRUS SABAIRI (STRAIN 11)		638-670							
PYGLM MONY		MURINE CYTÓMEGALOVIRUS (STILAIN SMITH)	670-690								
PVGLI HOAVA	М	HEDGAN CYTOMEGALOVIRUS (STRAIN AD 169)	138-180								
PVOLT MSVII	GLYCOPROTEDVI	HERDES SOULEX VIRUS (TYPE I / STRAIN I?)	45								
YOU BYES	CLYCOPROTEIN I PRECURSOR	EQUIDE HELVESYINUS TYPE I	£					<del> </del>		1	
PVGU VZVO	GLYCOPROTED ¹	VAUCELLA-COSTER VIRUS (STRAIN DUMAS)	278-297		1			1	+	$\dagger$	
7 100	т	BINAVAVIRIE LA CENCES CICM ATE I 741	Ť		116, 481	1134 1544	0171 2011		+	$\dagger$	T
PVOLE MERCH	M POLYPROTEDY PRECISEOR	BUNYAVIKUS SNOWSHOE HARE	T	T	18.2	138:136		$\dagger$	$\mid$	$\dagger$	T
PVGLM MANY		BUNYAWERA VIRUS	_	ş						+	Ī
PVOLM BUGBV	-	DUCAE VINUS							-		
PYCEN KANTE		HANTAAN VIRUS (STRAIN B-1)	П	Г	600-915	969-1019					
PYCLM HANTH		HANTAAN VIDUS (STRAIN HOJO)	П	П	1000-1020					_	
MOUNT HAME	-	HANTAAN VIXUS (STIVAIN LEE)		П	1001-1021				-	_	
WOLK HAND	_	HANTAAN VIRUS (STRAIN 16-118)	2		=						
VOLK DISV	M FOLYPROTEEN PRECURSOR	DAPATIENS NECROTIC SPOT VIRUS (INSV)	7	18. 78.	746-367	331-331	3			1	
NOV.	IN POLYPROTEIN PRECURSOR	PROSPECT HELL VINUS	Т					1	1	1	
ALL PLANT	M POLYPROTEIN PRECURSOR	PUNTA TORO PRI EBUVIAUS BIRMATA MARIR ATRANIAN TANDAN	745-765	907.1016	1775-1302			†		+	T
	-	PUBLISH VISITS (STRAIN COTE ALLO)	T	T		1000		+		+	
	-		Т	T	27.71	111.2001		1		+	
WG V IV	-	(STRAIN 214.548 M12)	Τ	344.346	Т	1154-1174			+	+	T
PYCEM SECUR	_		Ę	Г	\$10.00	1013		T		t	Ī
PYCEN SECUR				П	Г	1000-1020		<del> </del>			
PYCLM SEOUS		AIN SR.11) (SAPPORD RAT VIRUS)	П	П	П	999-1019		H	H	Н	
PYCEM USE	M POLYPROTEIN PRECURSOR	UNKUNTEMI VIAUS	\$81-383	129-659	200-928	925-952	684-996			H	Π
ļ											

POSSAN	417.11.814	All Virgary (No Bacterioghoges)			_	77497	AREAS	AREAG	AMEA 7 AB	AREAS	AREAS
FILE NAME	PROTELI	YIRUS		Г	1009-1124		Т				
PVGLP BEV	PEPLONGA GLYCOPROTEIN PRECURSOR	BEANE VIRUS	Т	Τ	+						
PVCL X HSVEB	GLYCOPROTED4 X PRECURSOR	EQUING HELPESVICUS TYPE I (STRAIM ABAP)		Ī		ŀ		-	-		
PUCE Y HEWEK	CLYCOPHOTEDY GX PRECURSOR	EQUINE HELVES VIAUS TYPE I (STRAIN KENTUCKY A)		T	l	Ī	İ			-	
PVC X HSVEL	GLYCOPROTED ^N OX	EQUINE HELDES VIRUS TYPE I (STRAIN KENTUCKY D)		Ì		T			ŀ	<u>-</u>	.
TANK A PONE	SECRETED GLYCOPROTEIN GX	PSEUDORABIES VIRUS (STRAIN RICE)	2	1						T	
KINDY A FOAM	GLYCOPROTEIN POLYPROTEIN PRECURSOR	JUNIN ALENAVIRUS ;		***	177 777			$\mid$		-	
ONE VIASO	ALVEGRACIEM FOLIPROTEIN PRECUASOR	LASSA VIRUS (STRAIN GA191)	T	Т	-	T			-		
1000 01 400	CH VCOPROTEIN POLLYPROTEIN PRECURSOR	LASSA VIRUS (STRAIN JOSIAH)	T			Ī				T	
AVTV V VVV	THE VERNESTEIN FOL YPROTEIN PRECURSOR	LYNDHOCYTIC CHORIOMENINGITIS VIRUS (STRAIN ARAISTRONG)	T		1	ŀ			t	t	
	ON VOICES OF STANDARD VARIOUS PALECUASOR	LYGHOCYTIC CHORIOMENINGITIS VIRUS (STRAIN WE)		201.62		1	1	+	+	T	I
	OF VOCABE OF THE VEROTE IN PRECINCOL	MOPELA VIRUS	12.15	43,7467	1	-		+	+	t	T
	CLICORDIEM TOLIVED BEILDING	PROMINE AREMAVIRUS		441-466				1		1	
MOLY PARY	GLYCUMOI EIN POLITIKUI EIN PRECONSON	4 - 7 - 4 - 7 - 4 - 4 - 4 - 4 - 4 - 4 -	113.38							1	1
PVCLY TACV	GLYCOPROTEDA POLYPROTEDA PRECURSOR	I ACADES VINOS	1		-	•				7	
PVCLY TACVS	GLYCOPROTEIN POLYPROTEIN PRECURSOR	TACALINE VIRUS (STRAIM V.)		Ī	<del> </del>	1	Ī				
PVCLY YACVI	CLYCOPROTEIN POLYPROTEIN PRECURSOR	TACABLE VIRUS (STRAIN V?)				-				T	
TATAL A TACAT	CLYCOPROTEIN FOLYPROTEIN PRECURSOR	TACALIDE VIRUS (STRAIN TRVL 11596)	T		***	3447 5111	1146.1164	t		T	
200	CENTRACE BOX VOROTEIN B	COWPEA MOSAUC VIRUS	٦	٦	7					T	
2	Charles of the Original of	COWPEA MOSAIC VIRUS		741-764		-				$\dagger$	
2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	CENCIEM FOLTERNIEM M	ESCHERL BARR VIRING COTRAIN BOS BY CHIDACAN HERPESVIRUS 4)	637-481		_	7					
WG72 EBV	PROBABLE NEWBOARDE ANTIGEN UP 250	THE PERSON OF THE ACT AND MACHINE STATE OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF T	854-878								
PVGP) EBV	ENVELOPE OL YCOPROTEIN GP)40	EVELOCIONES AND CONTRACTOR OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY O	47.88								
PVCM EBV	PROBABLE MEMBRANE ANTIGEN OPIS	EPSTEIN-DARK VIRUS (STRAIN BY)-1) (NUMBAN TIEN ESTINGS 7)	Ī		1						
ACES COAS	STRUCTURAL CLYCOPROTEIN PRECURSOR	EBOLA VIRUS	T	Т		-			l	T	
TANKY CONG	STRIKETIERAL CHYCOPROTEDN PRECURSOR	MARBURG VIRUS (STRAIN MUSOKE)	200-300	170-100		I					
	CONTINUE AT OR VANCE OFFICE PRESCRIPTION	MARBURG VIXUS (STRAIN POPP)		607-627		-			+	1	
200	STRUCTURE OF LOWER STRUCTURE AND	VACCINIA VIRING (STRAIN COPENHAGEN)	26-91	103-121					1	1	
PVH01 VACCC	PROTEIN: 1 TRUSING PROSTACIOSE	UACCOUR VIEW AND WAY	76-92	105-121							
PVHDI VACCV	PROTECN-TYROSINE PROSPINATASE	A ACCOUNT A DATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY O	Γ	105-121		-					
PVHOL VARV	PROTED4 TYROSDAB PHOSPHATASE	VACULA VIRUS	60.00								
PWIET VACCV	LATE PROTEIN H?	VACCINIA VIDUS (STRAIM WR.)				Ī					
PWINT VARV	LATE PROTEDIN	VARIOLA VIRUS	1	I						T	
WIE FOR	PROBABLE WELLCASE	FOXTAIL MOSAUC VIRUS	202			1			l		
SAME I	December of the Att	PAPAYA MOSALC POTEXVIRUS	23-166			-			1		
	Section 11	VACCINIA VIRUS (STRAIN COPENHAGEN)	120-135						1	T	T
	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	VALIGIA VIRUS	120-135						1	1	
	rro i cara is	VAPPRITA VIBITS (STRATH COPENHAGEN)	194-220								
PVID VACCE	PROTEIN	VACCINA VIDIO (CTE ANA VIDI)	194-220								
PVIO VACCV	PROTEIN IS	CARLA A CRESC	194-220								
PVIO) VARV	PROTEIN (3)	VACULA VINO:	104.178	133-155						ľ	
PVIDS VACCV	PROTEIN 16	TACCING THOS (SINGLE WA)	106.138	135.155							
PVIOS VALV	PROTEDNIA	YALULA VINUS	7	144 749							
PVIOT VACCE	PROTEIN 17	VACCINIA VIRUS (STRAIN CUPEMIANCEN)		57, 77,						İ	
PVIOT VACCV	PROTEIN !?	VACCINIA VIRUS (STRAIN WR.)								T	
PVIOT VARV	PROTEIN 17	VAROLA VIRUS	Т	- Br - 10 5					t		
PYIOR VACOC	PUTATIVE BYA HELICASE IS	VACCINIA VIRUS (STILAIN COPENHAGEN)	T						t	Ì	
PVIDE VACCV	PUTATIVE BYA HELICASE D	VACCORIA VIDUS (STRAZIN WR.)	212-041							T	Ī
VALVA VARV	MATATIVE RNA HELICASE 10	VALUELA VIRUS	198-2112						1	Ī	I
AVE. INC.	т	HUDALN CYTCHAEGALOVINUS (STRAIN AD169)	77-100	33-350						1	
	Т	HUMAN CYTOMEGALOVIRUS (STRAIN TOWNE)	77.100	113-150						1	I
WE BE	STATE TO THE PARTY OF THE PROPERTY OF	HI BLAN CYTOMEGAL OVIRUS (STRAIN AD 169)	14-32	907-681							
YES TO A	4) to metal legant moters	IN BANK CYTOMEGAL OVINIES (STRAIN TOWNE)	14-32	388-405							
PVE2 HOVY	49 KD DOGDIATE EAULT PROTEIN A	LATERIAL PROPERTY OVER 18 CATE ANY SAILTH	211.17								
PVIEZ MONYS	DOCEDIATE-EARLY PROTEIN 2	MUNICIPALITY PROPERTY OF THE STREET TOWNER	14.13						-		
WIES HOW	30 KD MARDIATE-EARLY PROTEIN 2	MUMAN CTIONEGALUVIAGO (SIAMIN IUWINE)	***						l		
PVED HSVSA	DOJEDIATE-EARLY PROTEIN IE-O	HEADESVILUS SADADU (STRAIN II)	21.00	900						Ī	Ī
PVEN NPVAC	DOCEDIATE EAST, PEG PROTEIN IE.N	AUTOCILAMIA CALIFORNICA MUCLEAR POLYHEURUSIS VIRUS	911	21.	::						
PVIND EBV	-	EPSTEDLBARK VIXUS (STRAIN 899-E)	() - 100	761-67	*******				t		Ţ
AVACH GOVY		HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	PH-110	7.0						T	Ī
PADO HISVII	-	HEAPES SO/PLEX VIRUS (TYPE I / STRAIN 17)	031.0	2	T	.,,,					
WOOD HISVED		EQUING HEAPESYTHUS TYPE I (STRAIN ABAP)	24-49	20.00	2 2 2	2.7	77:100	2007	+		T
PVDO HSVSA	Т	HERPES YRUS SAMIN (STRAIN 11)	101-94		1						
	1										

POGENE	Prichale	All Virunes (No Bacteriophages)				П			Г	
THE KAME	PROTEIN	YARUS	OREAL	П	IJ	AREAS	1478	AREA AREA?	A. AREAL	AREA?
7VD VZVD	PROBABLE INTEGRAL MEMBRANE PROTEIN	VAUCELLA-ZOSTER VIRUS (STRAIN DUMAS)	273	ž	230-233	+		+		
TANK ANCE	PROJECT II	VACCINIA VIKUS (SIRAIN COTENHAGEN)	200			+	1	1		
PVJOI VACEV	PROTEIN	VACCINIA VIRUS (STRAIN WR)	89-110			7	1		-	
VAXV	PROTEIN JI	VALIDICA VIRUS	19-110			1		$\frac{1}{1}$	-	j
WKS VACC	MOTEIN K4	VACCIMIA VIRUS (STRAIN COPENHAGEN)	61.13	201-234	319-317	†				
TAKE WALK	TACIETY AS	VACCINIA VIDE (STRAIN COSEMACEM	104.11	Т	1	T	1	1	1	
A CONTRACTOR	PROTECTION OF	VACCEDIA VIBILE (STRAIN CIPENHAGEN)			$\dagger$	T		-		
Т	PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFICATION OF THE PACIFI	VACTORIS VIEWS (STAIN WE)	130		† 	T	Ī	-	1	:
_	PROTEIN 13	VARYA WRITE		i	-	1.	•	:	:	-
PV M VACATE	Phorent 1	VACCIDIA VIBIR (CTBAIN COPPNIACEN)	149.144	104,301	202.115	-			-	
	MOTENIA	VACCINIA VINUS (STRAIN WR.)	10.10	10,73	202-315	+				
1	MOTENT	VANOLA VIRUS	147.163	185-207	291-314	ŀ				
PVLBS VACCV	PROFESSILS	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPENIIAGEN)	16.39			ŀ				
PVLOS VARV	PROTEINLS	VARIOLA VIRUS	16.70		-			:	_	
PYLI CUPVK	PROBABLE LI PROTEIN	COTTONTAL RABBIT (SHOPE) PAPILLOMAVIRUS (STRAIN KANSAS)	299-317			-				
PVLI JOVIS	PROBABLE LI PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 18	20-55			:				
PVLI HOV41	PROBABLE LI PROTEIN	HEMIAN PAPELLOMAVIRUS TYPE 41	36-63			-,				
PVLI REOVO	MAJOR CORE PROTEIN LAMBDA 1	(REDVIRUS (TYPE 1/STRAIN DEALING)	327-346	351.366	152-774	-				
PVL2 KPV08	PROBABLE L2 PROTEIN	HUNGAN PAPELLOMAVIRUS TYPE 8	254-270							
PVL2 HDVII	PROBABLE L2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 11	32-58							
PVL2 HPVIS	PROBABLE L2 PROTEIN	HUMAN PAPILLOMAVIRUS TYPE 13	13.59							
PVL3 HDV16	PROBABLE L2 PROTEIN	HIBAAN PAPILLOMAVIRUS TYPE 16	34-40							
PVL2 HDVIB	Probable L1 Protein	HIDAAN PAPILL CHANINUS TYPE 18	33.59							
PVL2 HPV1A	Probable L2 Proted	HEBICAN PAPEL COLAVIRUS TYPE 1A	213.228							
PVL2 HPV2A	Probable L1 Protein	HUDGAN PAPILLONIAVIRUS TYPE 1A	88.114			1				
	PROBABLE L2 PROTEIN	HUMAN PAPELIOMAVIRUS TYPE 31	14-40	443.462		^				
I	PROBABLE LI PROTEIN	MUMAN PAPEL CALAVINUS TYPE 33	3.5	8	1					
7 1 10 VI	PROBABLE LA PROTEIN	HUMAN FATILLIAMA VIRUS 1 V.E. 33	8		+	1				
PVI JOVE	PROBABLE 13 PROTEIN	HAMAN PAPAL CALAVIRUS TYPE 42	31-30	0.6.971		T		+	 	
PVL3 IBV47	PROBABILE LY PROTEIN	HIDAAH PAPILLOMAVIRUS TYPE 47	250-265							I
PVLS NOVS7	PROBABLE L2 PROTEZN	HEDLAN PAPILLOMANIKUS TYPE ST	33-58		$\mid$	T				Ī
PVL2 HPVSE	PROBABLE L3 PROTEDU	HIDAAN PAPILLOMA VIRUS TYPE SE	13.59	98-114		-				
PVL HVG	PROBABLE L3 PROTED	HUMANY PAPILLOMAVIRUS TYPE 6B	13-59							
MLS PAWE	PROBABLE L3 PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS	30-56			Ī				
202	PROBABLE LI PROTEIN	RHESUS PAPILLOMA VIRUS TYPE I	45-71							
	MOSALL LY MOTEIN	HORAN PAPELLINA VINUS 177E SE	2.5		1	1			1	
TAN SEGVI	NUMBER OF THE PROTECT AND A 1	RECYCLOS (1975 27 STRAIN DEVICES)	3(4.7)	1017.1161	+	1		1	1	
WI LOW	ADVOR CORE PROTEIN LANGEDA 3	REOVINUS (TYPE 1/ STRAIN LANG)	214.537		$\dagger$					
PALM DIVI	LM MOTEIN	TOULA INDESCENT VIRUS (TIV) (INSECT INDESCENT VIRUS TYPE 1)	) 144-170	196-320	606-711	198.54				
PASSI VACCC	PROTEIN MI	VACCINIA VIRUS (STRAIN COPENHAGEN)	134-159	133.195	281-302					
PVIADI VACEV	PROTEDUMI	VACCINIA VIRUS (STRAIN WR)	83-108	П	130-251					
PYNO! VARV	PROTEIN MI	VALOLA VIRUS	81-10¢				Г			
MI ROW	ACHOR YOUCH STRUCTURAL PROTEIN MU-2	REOVEN'S (TYPE 1 / STRAIN DEALING)	141-166	П			П	454-477		
WAI KEOM.	MINOR VILLON STRUCTURAL PROTEIN MU.2	REOVINUS (TYPE I / STRAIN LANG)	3	27.245	20.304 20.304	9779	454.477			
ANG! STOKE	MACOR VINCON STRUCT PROTEIN MICHAROLIC	JEDVICIO (TVP. 1751ANIN DEALING)	164-192					1		
2000	MAJOR VINCEN STRUCT PROTEIN ACCOMUSE.	REDVINOS (1775-37 STRAIN DEADING)	24 97		1	†				
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TANGE SECOND	MANOR VICKOR STRUCTROTEIN PROFINGER	MEDINAME (TITE IT STRAIN LAND)	1	37,	1	1	1		1	
WAYT BESYA	MATRIX PROTEIN	BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN ASSOCIA	17.62	AK:176	+	†		+	-	
WANT COVO	MATRIX PROTEDY	CAMINE DISTEMBER VIRUS (STRAIN ONDERSTENORT)	2	283-309		T	1	+		
PVAAT HOSVA	MATRLY PROTEIN	HUMAN RESPONSTORY SYNCYTIAL VIRUS (STRAIN A2)	Γ	139.160		<u> </u>	T			
TWAT LTNY	MATRIX PROTEIN	LA PEDAD-MICHOACAN-MEXICO VIRUS	311-338							
PWAY MEASE	MATTUX PROTEIN	MEASLES VIRUS (STRAIN EDMONSTON)	283-309							

	ROTTUR ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER ALTUR MOTER	NAMES OR STRAIN INT. E. S. S. S. S. S. S. S. S. S. S. S. S. S.	201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-200 201-20	137-130 195-200 195-200 195-200 196-205 117-101 15-193	316-330 316-339 306-339 306-338 306-338 306-338 306-338 306-338 306-338 306-338 306-338 306-338					
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	OTEN OTEIN	ALIN AUSTRALIA-VICTORIAVIS)  ALIN BEAUDETTE CV4)  S (STRAIN CV9)  S (STRAIN CV9)  US (STRAIN C4-33)) (PIV-4)  US (STRAIN C4-33)) (PIV-4)  ET E O)  ET E O)  ET E O  CEPIALITIS VIRUS (STRAIN DIKEN)  CEPIALITIS VIRUS (STRAIN DIKEN)  S THE  MEDUS)  THAIN ASP  TRAIN ASP  TRAIN ASP  TRAIN CORDANIRUS (STRAIN ROCKIN DIKEN)  REAIN ASP  TRAIN ASP  TRAIN ASP  TRAIN ASP  TRAIN STRAIN RAM4)		95-208 95-208 195-209 116-338 116-338 137-161 174-193	365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-328 365-36 365-36 365-36 365-36 365-36 365-36 365-36 365-36 365-36 365-36					
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EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH EBECH	OTEIN OTEIN OTEIN OTEIN OTEIN OTEIN OTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN ACTEIN AC	CEPILALITIS VIRUS (STRAIN BIKEN)  (PALABDOVIRUS CABRA)  US  MEBUS)  12761  CC-1)  CC-1)  CC-1)  CC-1)  CC-1)  CC-1)  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-1  CC-		116-138 132-148 137-161 137-161	306-328 306-328 171-190 177-181					
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	OTEIN OTEIN OTEIN OTEIN OTEIN OTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN A			114-138 180-205 132-148 137-161 174-193	304-328 308-328 171-190 137-161	-1: -1 -1 -1				
	OTEIN OTEIN OTEIN OTEIN KOTEIN			172-148 177-161 174-193	301-338 301-338 [7]-190	:   -   -				
	OTEIN OTEIN OTEIN KOTEIN KOTEIN KOTEIN KOTEIN PRECINSOR KOTEIN PRECINSOR	(STEAD W)  TACKER STAND WINGS (SHADDOVIRUS CARPIA)  TACKER STAND WEBUS)  AVRUS (STEAD MEBUS)  AVRUS STAND ARE)  AVRUS HOV (STEAD ASE)		132-148 137-161 134-193	)(1)-1)-1)-1)-1)-1)-1)-1)-1)-1)-1)-1)-1)-1	-1 -1				
	OTEIN OTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN AOTEIN PAECINSOR AOTEIN PAECINSOR	US (STRAI		37.161 54.83 174.193	171.190	7.				
	OTEN AOTEN AOTEN AOTEN AOTEN AOTEN AOTEN AOTEN AOTEN AOTEN PECLASOR AOTEN PECLASOR	US (STRA) US (STRA)		17.161 54.85 176.193	171-190	.           -				
12/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/2/	ROTEIN ROTEIN ROTEIN ROTEIN PLECUSOR ROTEIN PRECUSOR			137.161 54-83 174-193	137:161					
1212121212121212121	ROTED ROTED ROTED ROTED ROTED PRECISOR ROTED PRECISOR			34-193	137:161	1				
	KÖTEN KOTEN KOTEN PECLASOR KOTEN PECLASOR KOTEN PECLASOR			174.193	137:161	-				
	KOTEIN KOTEIN PLECURSOR KOTEIN PLECURSOR KOTEIN PLECURSOR			174.193						
	KOTEIN KOTEIN PRECUASOR KOTEIN PRECUASOR KOTEIN PRECUASOR			174-193		į	+			
4-4-4-4-4-4	ROTEIN PRECURSOR ROTEIN PRECURSOR ROTEIN PRECURSOR			174-193						
4-4-4-4-4	ROTEIN PRECURSOR ROTEIN PRECURSOR		П	174-193						
+-+	AOTEIN PRECURSOR		134-193			,	4	_	+	
			I						_	
_				137.161	21-140					
П	LOTEIN	1	2			1				
	KOTEIN	7	74-101			1				
	KOTEN	ETTENMEN	101-2			1			1	
Г	ROTEIN	US (STILATIN KBES23)		100		1			1	
	PROBABLE MEMBERING PROTEIN	ESTEDI-LACE VIRUS (STRAIN BY)		27.50	167.30	1				
PYNE CALYC MOVEMENT PROTEIN	FROTEIN		T	147.164	183-201	T				
THE CAME INCOMENT MOTERS	THOU EAST		Γ	147.164	102-101					
	Pentred	(8)	116-134	147.164	107:(81					
т	PROTEIN	OURG)	П	127-164	183-201	1				
•	T PROTEIN	TRAIN W260)	<u> </u>	47.164	183-201			1	1	
Ī	T PROTEIN					1				۱
П	AÖVEMENT PROTEIN	FIGWORT MOSAIC VIRUS (STRAIN DIXS)		160-190		1				
7	MOVEMENT PROTEIN	ANCHA! DUCK ISOLATE SS	Т	306.304		T	-		-	١
PANCA HARD MADE SU	MAKUR BURYALE AN INEN CRECORDON	T	Γ	266.294						
_	MAKOR SURFACE ANTIGEN PRECURSOR	Г	Γ	231-259			H			
1	MAJOR SURFACE ANTIGEN PRECURSOR	INGHAI DUCK ISOLATE S)!)	154-331	269-295						
1	MAJOR SURPACE ANTIGEN PRECURSOR	ITIS VIRUS	П	271-295	180-195					
_	MAJOR SURFACE ANTIGEN PRECURSOR	B VIRUS	<u> </u>	201.00					1	
98	MAJOR SURFACE ANTIGEN		٦	200			-		1	
Ħ	MAJOR SURFACE ANTIGEN PRECURSOR		7	344-370						
•	MAJOA SUMPACE ANTIGEN PRECURSOR		T	244.270						
_	MAJOR SURFACE ANTIGEN PRECURSOR	STRAIN 991)	T	***			+	+		
	MACE ANTIGEN PRECURSOR	AI)		10-10		1	1			
PYNESA HPBYD MAJOR SUR	MAJOR SURFACE ANTIGEN	7		R						١
-	MAJOR SUIVACE ANTINEM PRECUASOR	THE PROPERTY OF A CASE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P	Τ	311.310			ŀ			

INCERNE	Prizenzie	All Vivan (Ne Becierdeshares)			L	Ī			-	ŀ	Γ
PILK NAME	PROTEIN	VIRUS	AREAI	AREA?	AREAJ	AREAD	AREAS	AREA 6	AREA? AR	AREA! AR	AREA?
PYMEN HEBYL	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIRUS (STRAIN LSH / CHIMPANZEE ISOLATE	134-191	652-562					П	П	
PWKK HEEVN		HEPATITIS B VIRUS (SUBTYPE ADR / STRAIN NC·1)	:: ::	8.2						_	
PWGA MBVO		HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN OKINAWARODW202)	174.191	233-259						-	
		HEPATTIS B VIRUS (SUBTYPE ADW / STRAIN PHILIPPINOTEDW294)	207-501	244-270		1		1		1	Ī
100 V	MANOR CHRISTING ANTIGEN	HEPATTIC B VIRIA (CIBITYPE AB)	1.3	200		1			1	+	
	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIRUS (\$UBTYPE ADW)	174-191	233-259		T	T			-	Ī
_	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIRUS (SUBTYPE AYW)	174.191	233-239		Ī	İ				Ī
PVACSA HOBVZ	MAJOR SURFACE ANTIGEN PRECURSOR	HEPATITIS B VIRUS (SUBTYPE ADYW)	134-191	557-((2		·					
PWASA WITVI	MAJOR SUBFACE ANTIGEN PRECURSOR	WOODCHUCK REPATITIS VIRUS I	207.134	166-243	378-393	•					
PACK MINSS	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS 59	213-236	274.20	393.394						
	MAJOR BUILTACE AVINGEN PRECURSOR	WOODCHUCK NEPATITIS VIRUS 7	212-239	274.295	183.398						
WW.Y	MAJOR SURFACE ANTIGEN PRECURSOR	WOODCHUCK HEPATITIS VIRUS I	212-239	24.70	383-398	·	_ <u>-</u>	:	:		
		WOODCHUCK HEPATITIS VIRUS & (INFECTIOUS CI.ONE)	212-239	274.298	343-394	1			- 1		
PVICA WHYWE		WOODCHUCK HEPATITIS VIRUS W64 (ISOLATE PWS2)	125-149	234.249							
		DIFLUENZA A VIRUS (STRAIN AVAINN ARBORANO)	37.46			-				1	
WITH THE	MATRUX (MC) PROTEIN	INDLUERZA A VIAUS (STRAIN ABANGROWITY)	25-46			•				1	
Т	MATHUM (MJ) PROTEIN	INCLUENCA A VIAUS (STRAIN APORT WALKEN 170)	2			1		1		1	
E MA	MAINUX (MO) PROTEIN	INCLUENCE A VIRUS (STRAIN APOWL PLACUE VIRUSAROSTOCK)				+		1		+	
MAIN THAT	MATRIX (RQ) PROTEIN	INCLUENCE A VIKUS (STRAIN APOWL PLACUE VIKUSWE YBRUDGE)	23-48				1	1		1	1
Т	MAINTA (MJ) PROJESIA	INTURACE A VIRUS (STRAIN ALEXINGRADITOS)					1		1	1	Ī
Τ,	MATERIA GAN PROTECTO	INCLUSION A VIRGINIA TO A MALALLI ABRAGE VARIATION					Ī	1	+	$\dagger$	1
Т	MATERIX OF PROTEIN	MET LENGT A VINIT COM AND REPORT BECOMES				1	1	1	+	$\dagger$	
	MATERIX OUR PROTEIN	DELIENCA A WEIG CETAIN ACTION POLICY	1			-		1	+	$\dagger$	Ī
WATE ALEDO	MATRIX OWN PROTEDI	DOLLIDOZA A VIRUS (STRAIN AUDORNIO)/2)	1			1	T	T	+	+	T
PWATE TAWAL	HATTELY (NO.) PROTEIN	DIFLUENCA A VIRUS (STRAIN AMILSON-SMITH))	77			-	Ť				T
	MT + PROTEIN	MYXOALA VIRUS (STRAIN LAUSANNE)	226-341				T	T	$\mid$	-	T
\$	NONSTRUCTURAL PROTEIN NSM	BOVINE ROTAVIRUS (CROUP C / STRAIN SHINTOKU)	334-351			·					
PAGE PASE	10 7 KD PROTEIN	POTATO VIRUS & (STRAIN PERUVIAN)	21.36							-	
PVNO ENCESSE	NB CLYCOPROTEIN	INTLUENZA B VIRUS (STRAIN BUDELLING/IAT)	13.39			-					
PVNB DENK	NB GLYCOPROTEIN	DIFLUENZA B VIRUS (STRAIN BHONG KONGAZI)	13.30			-					
PWG DGLE	NB CLYCOPROTEIN	INCLUDICA B VIRUS (STRAIN MALE/40)	2								
PVKS INSUA	NB CLYCUTION SIN	INCLUENCA B VINUS (STRAIN BALCINI MANALY)			1		1			+	T
PWG BALO	NB GLYCOPROTEIN	INCLUENCA B VIRUS (STRAIN BAGACHICATES)			+	Ť	T		+	+	T
PVNB DOOR	NB GLYCOPROTEIN	DIFLUENZA B VIRUS (STRAIN BYOREGON/S/80)	5.5			T		T	-	$\mid$	T
PWICE ABVO	HONCAPSID PROTEDY NS.1			169-190						$\mid$	
PANCS AEDEV	MONCAPSID PROTEIN NS. I	VIRUS (STRAIN GKV 001 002) (AEDES DENS								Н	
MAN CA STANK	MONCAPATI MATERIANE.	MANCAGE DAR VOYDER HI	100.00		+	1	1	1		$\dagger$	
PVICE) ALSTV	NONSTRUCTURAL PROTEDY NS!	4/STRAIN VACCINES	236-272		1	T	1	T		+	T
PYRSI (MALA	NONSTRUCTURAL PROTEIN NSI	Т	3:5	114.137	167-192	Ī	T	T	-	l	T
П	NOWSTRUCTURAL PROTESNINS	DELLENZA A VRUS (STRAIN AVANA ARBORANO)	31.30	114-137	167-192						
PMG IACAO	MONSTRUCTURAL PROTEIN NSI	INFLUENCY A VIBLIS (STRAIN ACANGLANCHICALIA)	10.10								
PARE IACK	MONCHELL LUNCK TRUITER ASI	DET (ENTR A VISITE (STRAIN ACCRECATION)	2 5		107-192	1	1	1	1		
PWSI MOK	MONSTRUCTURAL PROTEIN NS!	DIFLUENZA A VIXUS (STRAIN ACHICKEN/JAPANZA)	2 7	1		1	1	1	+	+	T
PVNSI JADA2	MONSTRUCTURAL PROTERN WSI	INFLUENZA A VIDUS (STRAIN ADUCKVALBERTANO76)	31.50	167.192		T	1	T	$\frac{1}{1}$	$\dagger$	T
PVNS1_LADE1	NONSTRUCTURAL PROTEIN NSI	INFLUENCA A VIRUS (STRAIN A/DUCIVENCILAND/1/36)	28.47	- FE		T	<del> </del> -	Ī		+	T
PYNS! LADUS	NOWSTRUCTURAL PROTEIN WSI	INTLUENZA A VIRUS (STILAIN A/DUCKAIKRAINE/IAS)	26-47	164-189		Ī	ľ	T		$\vdash$	Ī
PVNSI IAFOM	NONSTRUCTURAL PROTEIN NSI			114-137	167.192					-	
PVASI IAFOV	NONSTRUCTURAL PROTEIN NSI	INFLUENZA A VIRUS (STRAIN AFORT WARRENIISO), ANDISTRAIN AJ		14.139	167-192					H	
PWS IAM	MONSTRUCTURAL PROTEIN NS			167-192						H	
PWS MEN	NONSTRUCTURAL PROTEIN NSI	DOLUENZA A VIRUS (STRAIN AA ENINGRADASA))	2 5	7	7 (0) (V)	†	1	1		+	
PVNSI LAMA6	NONSTRUCTURAL PROTEIN NS!	INFLUENZA A VIRUS (STRAIN AMALLARDALBERTAND/16)		167.197	741-701	Ť	†	†	1	$\frac{1}{1}$	7
			l		1	1	1	1	1	1	7

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PCCENE	PINCHIZIP	VIBITA	AREAL	AREAJ	AREAL	AREA	AREA S	AREAS	AREA? A	AREA!	AREAS
PVNS: IAMAN	HONSTRUCTURAL PROTEIN NS!	INFLUENZA A VIRUS (STRATH AMALLANDAREW YORKATSOTS)	31.50	167-192		-					
PANSI IAMAO	_	DELLIENZA A VIRUS (STRAÍN AMALLARDNEW YORKM874/18)	8:1	167-192						1	
PVNS1 JALMYN	_	DOLUENZA A VIRUS (STRAIN AMYNAWIANEDA-THAU76)	28-47	EA.189							1
PWGI MB	MONSTRUCTURAL PROTEIN MS!	DIFEUENZA A VIRUS (STRAIN APINTALIJALBERTA/11979)	167-192								
PVISI JATI	MONSTRUCTURAL PROTEDY NSI	INTLUENZA A VIRUS (STRAIN APINTAILALBERTA/121/79)	3:50	167.192						1	
PANSI LAND	HONSTRUCTURAL PROTEIN NSI	BRELIENZA A VIRUS (STRAIN APINTALI/ALBERTA/268/78)	8	24.79					+	†	T
PVNS1_LAPID	MONSTRUCTURAL PROTEIN NS!	DIFLUENCA A VIRUS (STRAIN APPRITATIVALIBERTATION)	2 5	741-701	101	I				1	T
WAS LANGE	NOWSTRUCTURAL PROTEIN NSI	INTUING A VIKUS (STRAIN AFTER 10 ALCHEM)				-				Ì	T
PYNG! LATKE	MONSTRUCTURAL PROTEIN INSI	INPLUENZA A VIRUS (STRAIN ATURKEY/BETHLENEM GULLTIVIANZ-BY	2 5			-				T	T
MISI WIKE	MONSTRUCTURAL PROTEIN INST	INPLUENCE A VIKUS (STRAIM A) UNACTALANAMAS)	2 5			-				T	Ī
WIGH WIKE	MONSTRUCTURAL PROTEDY MS I	DIFLUENCA A VIRUS (STRAIN ATURICE TARECORVI)	2 :	441 177		1				$\dagger$	Ī
PWGI LATES	NONSTRUCTURAL PROTEIN INST	INTELLEGIZA A VIAUS (STRAIM ATELMISCULIN AFRICAGE)	5	143.103		Ī				T	T
PWS! WIRT	NONSTRUCTURAL PROTEIN INSI	INPLIENZA A VILUS (STRAIM AT ELIMI URCHEMIATOR)	2		201.071	1				İ	Ī
PARSI MUDO	MONSTRUCTURAL PROTEIN NSI	(DOLUBEZA A VIRUS (STRAIM AUCUNA)9772)	2			Ŧ				T	
PWSI MUSS	NONSTRUCTURAL PROTEIN NS:	DEPLOYER A VICUS (STRAIM AUGSMONT)	2	201	***					$\dagger$	T
	NOWSTRUCTURAL PROTEIN NS!	DOLUMEACA A VIRUS (STILAIM ANSWING-NUMALINSO)	200	76		-				1	Ī
	NONSTRUCTURAL PROTEIN NS	INPLUENCA C VIXUS (STRAIN CANN AGRICULTOS)								T	T
PWS! MCC	MORGITEUCTURAL PROTEIN MSI	INTELLEGICAL CARGO (STRAIN CONTINUADA)		101		1				T	Ī
MAKES BLAIG	POPETRUCTURAL PROTEIN NS	SELVE CONTROL VIOLE (SESTIMATE OF FIGURE OF FIGURE OF FIGURE)		201.21		Į.					
PWES BIVIN	NONSTRUCTURAL PROTEIN MS.	BLUE LOWGED VINDS (SENDING LINES AND	191.19							T	Ī
ALCOHOLD STATE	MONESTRUCTURAL PROTEIN POS	INTERCONCUE VINIS (SEROTVPE 10)	191-50							T	T
-1-	WANTED THE AT BEATERN WAS	EPIZOCOTIC HEMOREHARDIC DISSACE VIRUS (SEROTYPE 2 / STRAIN AL									
-1	Concession of the Artist Cons	THE SENTA A VIBIG (STRAIN APPENDING BLCOADA)	1.20			-			ļ		Ī
	MONEY FILE HIGH PACTED INST	INTLUENZA A VIRUS (STRAIN ATTERNISOUTH AFRICAN)	8 3			-					
	MANAGEMENT AND A PROTECT 2	PRETINCHALA VIXILS OF MOCE.	53-66								
Ŀ	MANAGEMENT IN ALL PROPERTY I. I.	PORCHAIN TRANSLASSIBILE GASTROENTERLITIS CORONAVIRUS (STRAI	177.201			_					
	MOMENTAL PROTEIN 1.1	PORCINE TRANSLAISEBLE GASTROENTENTIS CORONA VIRUS (STRAI	121-122								
	NONSTRUCTURAL PROTEIN 3-1	PORCEME RESPERATORY CORONAVIRUS (STRAIN RM4)	17.201								
	NONSTRUCTURAL PROTEIN NSS	RICE STRIPE VIXUS				1					
_	MONSTRUCTURAL PROTEIN 4	HUMAN CORONAVIRUS (STRAIN 229E)	94-100			•					
PYNS4 CYNCS	HONSTRUCTURAL PROTEDY 4	(MURIDE CORONAVIRUS MAY (STRADYS)	17.38			•					
1 1	HONSTRUCTURAL PROTEIN 4	PORCENS TRANSPOSSIBLE GASTROENTES CORONAVIRUS (STRAI								1	
	MONSTRUCTURAL PROTEIN 4	PORCEME TRANSMISSIBLE GASTROEMTERITIS CORDRAVIRUS (STRAI				1			+	1	
	NONSTRUCTURAL PROTEIN 4	PORCING RESPIRATOR Y CORONAVIRUS (STRAIN RAW)	3							1	T
>	NONSTRUCTURAL PROTEIN NSA	MAKES STRUTE VIKUS	2 3	44	697 691					$\dagger$	T
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	MONETHIEFT BAL PROTEIN 7	FELDIE DIFECTIOUS PERITOMITIS VIRUS (STRAIN 79-1146)	3								
	NONSTRUCTURAL PROTEIN C	HIDAAN PARATNTLUENZA I VIRUS (SITIAIN C) S)	76-97								
ŧ	NONSTRUCTURAL PROTEIN C	HUBALM PARADOLUENZA I VIRUS (STRAIM C19)	76-97								
PYNSC MIND	NONSTRUCTURAL PROTEDNIC	HUMAN PARANGLUENZA I YINUS (STRAIN CI-5/1)	76-92	179-197							
PVNSC MIKE	NONSTRUCTURAL PROTEIN C	HUMAN PARAMOLLENZA I VIRUS (STRAIN CI-1413)	2							1	
PWST CYBO	33 KD NONSTRUCTURAL PROTEDY	DOVING CARCHAVILLES (STRAIN QUEBEC)	601-00							1	T
PAST DOC	NONSTRUCTURAL PROTEDIS MS1-NS2	INTEREST C VINES (STRAIN CAREAT LANES/118/79)								†	T
PVNSI DACH	NOVE THE COURT PROTEINS NOT AND	INTERIOR OF VIEW CONTROLLERS	33.348							$\dagger$	
TO THE PERSON NAMED IN COLUMN 1	NOW THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER	DOT LENZA C VIRIS (STRADA C/VAMAGATA/1091)	22.348			Ī	Ī			T	
1	MOMETER CHIRAL PROTEDINGS	MONTA TORIO PREBIOVIDUS	9	T		Ī	T			T	Ī
WACT BOW	NONSTRUCTURAL PROTEIN NS-S	SANDFLY PEVER SICILIAN VIRUS	7.4							t	
PVNST ULK	NONSTRUCTURAL PROTEIN MS-S	ULIKUMENA VIRUS	3.73	20.00		Γ			T	<u> </u>	Γ
PYNUK HIVKA	$\Box$	PSEUDORABIES VIRUS (STRAIN KAPLAN)	136-777	1543-1583							
PVNUC DHVIII	MUCLEOPROTEIN	DHORL VIRUS (STRAIN INDIAN/1713/81)	123-139	197-324							
PVNUC EBOV	П	EBOLA VIRUS	159-136								
PVNUC LAANA	П	INFLUENZA A VIRUS (STRAIN AVANAS ACUTAPRIMORIE-89576)	173-197	266-287							
PVNUC LADOR	╗	INTLUENZA A VIRUS (STRAIN AZBOINÁMO)	17.19							†	T
PVNUC MBIA	MUCLEOFKOTEIN	INPLUENCE A VISUS (3) EASIF ABEAGIL/11/19)	113-131						1	1	]

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PILE HAMIL	PROTER		7	ABLA ABLA	4	1	T V V V V V V V V V V V V V V V V V V V		4
PWACE MAKED	_	KKAILLEIVI	201.00						
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PWRUC LACKO	MUCLEOPROTEIN	T	101					1	
PWILL IACK	MUCLEOPROTEIN	1100							
PYRUC INDAU	MUCLEOPROTEIN	Olembi A		-				T	
PYNUC INDBE	MICLEOPROTEIN		131.101	-	1			ľ	
WALK MAKE	MUCLEOPROTEIN	INTELLEGIZA A VIRUS (STRAIN AMBIERREMOLECTORIO)	173.197						
WHILE LANGE	Main sopeone	Ī	193-197		_				
WHIT LINE	MICHEOPOLEN	5	13)-109						
PANE LANGE	MARY FORESTEIN	INSTITUTOR A VIRUS (STRAIN ADUCKA(EMPHIS92074)	13:197						
PVAIL LAINA	NICE POROTEIN		193:197						
PVAUC LADRZ	MACI EDPROTEIN	(91/16	193-197						
PYNEL LADER	INVOLEOPROTEIN	INFLUENZA A VIRUS (STRAIN ADUCKAIKRAINE/2/60)	133.197						
PWRUC MENS	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN A/ENGLAND/19/55)	193-107						
PYNUC INFORM	NUCLEOPROTEIN	INFLUENZA A YIRUS (STRAIM AFORT MONIMOUTH/1/47)	177-197					1	l
PVNUC LABOW	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AFORT WARREWIYS)	177-197					Ī	
PVAUC MIPD	INICLEOPROTEIN	INTLUENZA A VIRUS (STRAIN AFOWL PLAGUE VIRUS DOGSON/DUTG 17)-197	177-197			$\downarrow$		1	
PWRUC WITH	MICLEOMOTEIN	INFLIEDZA A VIRUS (STRAIN AFOWL PLAGUE VIRUSAROSTOCKOTA)	117-197	1		1			
PWRC MORE	MUCLEOPROTEIN	INPLUENZA A VIZUS (STRAIN ACALET TEAL/AUSTINALIA/A/A)	131 141					Ī	
PWRUC IAGUI	NUCLEOPROTEIN	INSTITUTE A VINCE STRAIN AND LIMAN TANK TO SEE	17.101			1			
PARCE MODE	MALEOTRO I EIN	INSTITUTE A VIDIS (STEAM ARTHEL ARREST AND 12478)	17:197						
TARRE MOUSE	-	INSTITUTION A VIRING (STRAIN AKHILLAKAR YLANDVIBISMS)	137-197			L			
A LANGE LA PARTY	Main Possonen	INFLUENCE A VIRUS (STRAIN AGULLASTRAKIIAN227/n4)	132.197						
PANCE MOLES	_	INSTITUTION A VIRUS (STRAIN ACULLAASSACHUSETTS26/40)	193-197						
PYNUC JAGUN	۲	DOT URKEA A VINUS (STRAIN AGULLAMMESOTAMASAN)	173-197						
PWINE TABLE		DOLLENZA A VIRUS (STRAIM AMICKOXMO)	132-197						
PYNUC LAHIT		DOT DENZA A VIRUS (STRAIN A/EQUING/JILL IN/1/19)	13.197	-				1	
PWRC MEO	MUCI BOPROTEIN	DOLUEYZA A VIRUS (SIRAIM AREQUINEAUMONIUM IN IN	17.107			1			
TANKE MEN	NOTES AND LEAST	DATE DESTA A VIRIA ESTRADA AMONO KONGUMB	17:197					Ī	
	Manage Charles	DETAILING A VIBLIS (STRAD) AMONG KONGAN)	173-197	-		L			
PVAIR LABOR	NECT FOROTED	INTLUENZA A VIDUS (STRAIN ARQUINE/PRAGUE/1/54)	172-197						
PYNUC IAHTE	+	DOLLEDIZA A VIZUS (STRAIN ARQUINE/TENNESSEE/596)	173-197						
PANC LAKE	•	INSTITUTION A VIRUS (STRAIN AREVISAM)	173-187						
PVNUC IXLEN	_	DIFLIENZA A VIRUS (STRAIN ALENINGRAD/S4/1)	173-197						
PVNUC IMMAA	-	DIFLUENCA A VIRUS (STRAIN AMALLARDASTRAKHAN24481)	13:197						١
PARK WAY		DOLLERCA A VIEUS (STRADA AMALLALDAREW YORLANDOWN)	17.19	+	$\frac{1}{1}$	1		Ī	۱
MACC ING	MUCLEUMOTEDA	INTELLEGIZA A VIRGIR (STRAIN ANTROKA)	13.10			1			
PAGE 1408	MICHEOPROTEIN	INFLUENZA A VIRUS (STRAIN ACHIGOAR))	173.197						
PVRUC LAPAR	Т	INFLUENCA A VRUS (STRAIN AFARROTALSTER/1)	133-197			L			
PYNUC LANCE	F	DOLLIEDZA A VIRUS (STRAIN APLIERTO IUCORIJA)	193-197						
PYANC LARUD	MUCLEOPROTEIN	INFLUENCA A VIRUS (STRAIN ARUDDY TURNSTONENEW JERSEYATI	133.197						-
PVNUC LASEO	MUCLEOPROTEIN	DOLLIENZA A VILUS (STRAIN ASEALAAASSACHUSETTSVIAO)	173.197					1	
WALL LASHE	NUCLEOPROTEIN	INFLUENZA A VINUS (STRAIN ASHEAKWATEWAUSTRALIA772)	10.10						
MAC ASP	NUCLEOPROTEIN	INPLUENCA A VIAUS (STRAIM ASIMUACOMOTIOS)	10.00						
PWRUC MTE	MUCLEOROTEIN	INCLUENCE A VIRUS (SERVIN ALEXANDE ELANDEMO)	11.101		$\downarrow$	$\downarrow$			
3	Ť	INSTITUTA A VIBUS (STRAIN A/TURKEY/ONT ARIO/7) 2566)	19):101						
2000	Ť	INGLIENZA A VIRUS (STRAIN ATTRINSOUTH AFRICAN)	173.197						
WATE LATE	NUCLEOPROTEIN	INFLUENZA A VIAUS (STRAIN ATTERMITURKMENIATION)	173.197						
PANIC MIX	-	DOLUENZA A VIBUS (STRAIN ACTEXASIO?)	173-197			L			
PVNUC INDO	-	INGLUENZA A VIRUS (STRAIN AUDORNIJOITI)	173-197						
PYNUC LAUSS	•	DØLUDIÇA A VIRUS (STRAIN AUSSRIVOTI)	133-197						
PVAUC LAVIA	NUCLEOPROTEIN	INFLUENZA A VIRUS (STRAIN AVICTORIA/SAR)	173.197	_					

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	_		133.187							+
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PVALC LAWIL	-		19:(1)	T						J
WALL LAST	-	INTELLERZA A VIXUS (STRAIN ASAMINOSSI)	133-193					1	1	+
WALLE LAZAI	_	THE INCENTOR	13.197							+
			173-197					1	+	┥
	INVOLEOPROTEIN C		193.161						1	+
			133-197		į		1	•		
PVHUC LAZALI	MUCLEOPROTEIN	-	173.197		<del>-</del>	 	-	+		i
PVMUC [AZH)	NUCLEOPROTEIN	:	133.197			-		+	+	$\dagger$
PYNUC LAZII	MUCI ECPROTEIN	=	173-107				i	<u> </u>	:-	:
PVHUC [A213	NACC EOPROTEIN		133.197			-		1	1	Ŧ
PARIC LASIS	INICI EOPROTEIN	(6)	173-197			1			1	$\dagger$
PVNIC INTH		8	193-107			•	1	1	:	:
PVRUC IAZIA			173-197			-			1	$\dagger$
PWRIC LAZAA		LANDS/12/85)	171.197					$\frac{1}{1}$		+
PVNUC LAZINE			131.10)			7		1		+
PWINC IAZOH		1151)	133-167			1		1		$\dagger$
PVICE LAZWI			133-193		1	·				t
PYRUC IAZY7	-	ADAPTED))	234-258							t
PVNUC INDAC	= 1		234-258		1	-			-	$\dagger$
PVIEUC DEBAD	-1		234-258					+		$\dagger$
PYNC MEE	_	ORE/12/19)	_					+	+	$\dagger$
PARCE POST			٦	=				1	+	$\mid$
PARIC MARVA			٦	┪		1			1	$\dagger$
WALL INDIV		VACCINGA VIRUS (STRAIN COPENHAGEN)	П	7	36.38	-				t
WORL WACE		VANICA VIRUS	٦	297.707						$\mid$
WOO! VAK	Moreovoi	CVRUS	┪							t
NOK INDIA	DO TO THOUSE	US		01010						$\mid$
AON ION	IN TO THOUSE	RUSSIAN	7	AND AND	_					
	STATE BOTTON	POTATO VIBUS S (STRAIN PERUVIAN)	1			0101			<u> </u>	<del> </del>
	LAST PROPERTY.	POTATO VIRUS X	T	007	Ť	24.0	1010,1030		-	r
	THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE PARTY IN THE P	POTATO VIRUS X (STILADN CP)	T	27.07	Ť	919191			-	
	TAKEN PROTECT	POTATO VIDUS X (STIVALIN XX)	T		T					
	List of the Contract	OS STILAWBEARY MILD YELLOW EDGE ASSOCIATED VIRUS	T						-	H
	SOCIAL SECTION OF STREET	WHOTE CLOVER MOSAIC VIRUS (STRAIN M)	T	917						l
OW CON TOWN	S 1147 KD PROTEDY	WHETE CLOVER MOSAIC VIRUS (STRAIN 0)	***	Ŧ	\$41.575	579-595	1031-1072		-	
AND THE PARTY	PROBABLE MENGRANE ANTIGEN 3	HERPESYRUS SADGRI (STRAIN !!)	Т	Т	Т					
PVP16 NPVAC	PIOPROTEDA	AUTOCRAPHA CALIFORNICA MUCLEAR PULTYELIKUSIS VIKUS	Ţ							
ONE! SIEVE	Pio PROTEGA	OROTA PEUDOTSUCATA MULTICAS SUBTACTIVICACISTS TECS		Ī						
PVPIS INVE	Pie PROTEDA	SPODOTERA EXCUA MULEAR FOL INEDAOSIS VINOS (STEWNS)		11:13	105.139	195-214	200-211	304-538		
PAPE LESSOV	PROTEDI SIO	INCENTAL STREAMS DAVING		165-291						1
VIN MAY	NOWSTRUCTURAL PROTEDY PHS10	WOUND TOWAR VINCE (WITH A PRINCE)	Ĺ	827.278	1124-1145					1
PVPIA IBV	PROBABILE MOMENTANCE ANTICEN PI 40		Π	344.364						1
PAPER DAY	PROB CAPSID ASSEMBLY AND DNA MATUR P	EFSTED CHANGE VICES (STRAIN BYS-1)	17.10	122-149	912-002					1
AVAIL BEAVA	PLOS CAPSID ASSEMBLY AND DNA MATUR P		216.265							
PVP IS ISVA	T	ENERGIES VIRUS SARMUD (3 I MALIN 11)	153							
DVEY BIND	CAPSED ASSEMBLY AND DRIA MATUR PROTEIN	VAUCELLA-COSTER VAUS (SIRAM DOWNS)	5							
TVP1 SSVI	STRUCTURAL PROTEIN VPI PRECURSOR	SULPULBUS VICUSTINE PARTICLE 33 **	3743							1
WILL ALCO	CORL PROTED/ P21	AATICAME MOTOR ON THE	5900							1
PVP31 CM	COME PROTEIN P21	CUCUMBERA RECANOS VANOS	(P)							†
PVF31 CRV	CORE PROTEIN PI	TOWATO BIRGHY STIME VIRUS (STRAIN CHERRY)	(9-0)							1
PVP31 TREVE	7	HEIMAN CYTOMEDAL DVIRUS (STIVAIN AD169)	141-165	187-202	261-212				+	†
WITH HOWA	A CONTRACT CAPSED PROTEIN V7.23	HEAPES SINGLEX VIAUS (TYPE I / STRAIN 17)	197.230					1		$\dagger$
PVP2 HSVII	CAND MUIEM VID	HERPES STACH DX VIRUS (TYPE 6/STRAIN UGANDA-1102)	206-232							١
MAY LAVEL	THE CAPSID PROTEIN V73	HEAVES SUMMEA TIMES (1115 V. 2120)								

100	41212314	All Vivaes (No Becteriophages)	П	П	П	$\Box$	П	$\mathbf{r}$	П	$\mathbf{T}$	
FILE HAME	PROTEIN	VIRUS	1	र रज्ञ	4 74.5	200	S T T T T T T T T T T T T T T T T T T T	T T	7		
CAZA (TAAA	PROBABLE CAPSID PROTEIN VP23	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS)	27.12			1	$\dagger$	T			
PVP26 NEVAC	P26 PROTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYTEDROSIS VIRUS	T	Т		1		T		T	T
PVP1 AUSV4	OUTER CAPSID PROTEIN VP2	AFRICAM HORSE STERNESS VIRUS (SEROTYPE 4/ STRAIN VALCINE)		100 434	787.73	19.66	T			ŀ	
PVP2 BTV10	OUTER CAPSID PROTEIN VP2.	BLUE UNICE VIAUS (SCAC) TTE 107 (SOC.A) E USA)	117	Т	Т						•
MAZ BIVII	OUTER CAPSID PROTEIN VP2	STUDIOS VINOS (SENOTITE DE LECONO ES TENTO A TELIFAN	Г	Т	Т	657-676					
WY BIVES	OUTER CAPAD PROTEIN VP2	SECOND CONTRACTOR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE	Т	Γ						=	
MAT BIMIN	OUTER CAME PROJECT VIZ	BUTETONICHE VIRIS (SEROTYPE I / ISOLATE AUSTRALIA)		189-159	П						
VIATE PARTY	WHEN A PROPERTY OF	BETRETONGLE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	14.31	111-140 42	420-438 6	654-681					
1000	COURSE CARRIED BACKERS VP3	EMZDOTIC NEMORAHACIC DISEASE VIRUS (SENOTYPE 1)	153-168	139-152	П	•					
	SALE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE SALES OF THE	NOVOVE ROTAVALUS (STRADA RF)	301-317	334-360 5	333-543 6	673-64	164-709				
1000	AND ASSESSED OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF TH	BOVING BOTAVILUS (STRAIN UK)	116-100	Г	H						
TO TO THE	TAX-BINDING TRUITED VYZ	MINIAM ROTAVILUS (SEROTYPE I / STRAIN WA)	309-325	343-363	\$32-553 6		114.700				
BUILDING SALE	ANT DESCRIPTION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT	PORCHER BOTAVIEUS (GROUP C./ STRAIN COWDEN)	21-75	916-606	406-425	114-53					
201	TOTAL BENEVICE TO THE TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TOTAL COLUMN TO COLUMN TOTAL	74-57	219-240	102.318	396-566	333-544	674-700	765-790			
	CALLAN ARICH WARRANTS VOID	MARKED VIRUS (STRAIN MUSOKE)	\$6.75			-					
	ALIPOR INCOME INTO THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF THE PART OF	AFRICAN SWING PEVER VIRUS (STRAIN BATIV)	174-197								
The state	TANK VARIA A LIK CYTACH LIX PROTTE IN VP15	EBOLA VILUS	233-254			-					
TOWNS TANKS	NAMES A CHARACTER STATE OF THE STATE OF VP.35	MARBURG VIRUS (STRAIN MUSOKE)		10-104							
SALVE STATE	POLYMERACE COMPUTER PROTEIN VPIS	MAKEUNO VILUS (STRAIN POPP)	45-75	76-104							
PVP15 VACES	INDIANABODAMIANT IDVITABLE PROTEIN P35	VACCINIA VILUS (STRAIN COPENHAGEN)	278-304		1						
PVP35 VACEV	BAGNODOMOVANT IDAVELOPE PROTEIN P35	VACCOUR VIRUS (STRAIN WR)	27-70					T			T
VALV	BAATHODOLOUNT DIVITIONE PROTEIN P15	VARIOLA VIRUS	278-305								
PVP18 HSWAD	_	MALEKS DISEASE REPRESVINUS (STRAIN CA)	255-270		1						
PVP38 HSWAN	-	MANEKS DEEASE HERPESVIRUS (STRAIN MOLLIPSCR2)	25.270	1	1	-					
PVP N NOVAC	+	AUTOCRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	296.311	1		1					
PVP IS NOTOP	•	ORGYIA PSEUDOTSUGAYA MIR. TICAPSID POLYHEDROSIS VIRUS	107:03	214-240		416.943		T			
PVPJ AIGSV4	VPJ CORE PROTEIN	AFIICAN HORSE SICKNESS VIRUS (SEROTYPE ASTRAIN VALCINE)		T	Т	2					
PVP3 BTV18	VATI CORE PROTECI	ELLETOWGUE VIRUS (SEXOT VPE 19715/A 19715/A)	131-144	100	1						
PVP3 BTV19	VP) CORE PROTEDI	BELUE ICHAGE VERUS (SERO) THE 17 TOWN ATE CONT	13.14	11:13	Ī	+					
MY BIVIA	VP) COME PROTEIN	TEMPORTUR MENOREMACIAC DISEASE VIRUS (SEROTYPE 1)	121.142	671-605							
W73 D40V	WY COLL PROJECT	EMPONING MEMORINADIC DISEASE VIRUS (SEROTYPE 2/STRAIN AUS	131-142	635-695			Г			•	
AND CAN	VED COME PROTECTION IN ALL BEATTERS	BET DWARF VIEUS GDW)	101-48	Г	367.393	640-717	342.760	374.374	840-975		
	CALLE PARE BOTTEN VET	PORCINE ROTAVILUS (CROUP C/STRAIN COWDEN)	401.439	П							
	notes coast professives	SDELAN II ROTAVIRUS (STRAIN SAII)	401-425	\$ \$50-927	313-536	746-822					
ANG ENV	CASE PROTEIN PO	EPSTEID-BARK VIRUS (STRAIN B99-4)	470.45								
PVP-0 HEVII	CANSID PROFEDI NO	HEADES SINGLEX VIRUS (TYPE I / STRAID) 17)	20-15								
PVP40 HSVED	CAND MOTERING	EQUINE METHES VINUS TYPE I (STRAIN ABAP)	3	11.6	Š						
PVP40 HSVSA	CAME MOTERN PA	MEDIESVEUS LABOR (STILAN II)									Ī
PVP-0 LTVI		TOPECTIONS LAKENCOLACIONS VINUS (31100M 1110MM Vers)	21.5								
PAPE KABAH	-	MARGUNG VEICES (STRAIN MUSICIES)			Ī						
MAN DAN	-	PONDUM VINCE DE PART PART AND VINE VINE VINE VINE VINE VINE VINE VINE	33.30	34.37	Ī				L		
1 0 K	STRUCTURAL GETCUTION PO	VANCELLA POSTER VIRIS (STRAIN DUMAS)	2								
OVZV OVZ	CANAD PROTEIN VYZA	AUTOCIALING CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	279-248	262.278							
THUS TOWN	CUTTER CAPETO PROTEIN VIA	SDELAN II ROTAVBUS (STRAIN SAII)	483-508								
Nece Lors	OUTER CARED PROTEIN VIN	SBEAN II KOTAVRUS (STRADI SAII)	10541	483-506							
WEST NOVAC	Т	AUTOGRAPHIA CALIFONNICA NUCLEAR POLYNEDROSIS VIRUS	14.1								
SOME SPANE	Т	ORGYNA PSEUDOTSUGATA MULTICAPSID POLYKEDROSIS VIRUS	136-157		1						
PYPAA VARV	1	VALIDLA VIRUS	27.78								
PVP4B VACCC	Н	VACCOMA VIAUS (STILAIN COPENHAGEN)									
TYPE VACCV	MAJOR CORE PROTED PAR PRECURSOR	VACCIFICA VINUS (STROOM WAS)	201:10								
TVPCB VARV	7	INTERTONGUE VINUS (SEROTYPE 10/15OLATE USA)	174-193	333-249	27.2						
TAN TAN	VACORE PROTEIN	BLUETONOUE VIRUS (SEROTYPE 11 / 15OLATE USA)	174-193	T	335-551						
	VPA CORE PROTEIN	INLURIONGUE VINUS (SEROTYPE 13 / ISOLATE USA)	174-193	133.249	535-551						
	VIA LOWE : mo : mi										

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,	PROTEIR	VIRUS	T	Т	1	Т	Г	Г			
Ţ	VAN CORE PROTEDY	BLUETOHGUE VIRUS (SEROTYPE 2/ ISOLATE USA)		Т	-	1	l				
Ī	CLITTER CAPSED PROTEIN VP4	NEBRASKA CALF DIARAHEA VIRUS (STRAIN MCDV-LIMCOLM)	J		357.75	t					
T	MANAGEMENT BAL PROTEDY PASA	RICE DWALF VIRUS	7	Ŧ		1	Ī			Ŀ	
Ţ	CATTER CAPSED PROTEIN VP4	BOVING ROTAVIRUS (SEROTYPE &/ STRAIN BAIL)	*		+						_
T.	CLITER CAPSED PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN CASA)			+	1			-  -		L
L	OUTEA CAPAID PROTEIN VP+	BOVING ROTAVIRUS (STRAIN UK)	936.364	5.5		T					
L	OUTER CAPSID (ROTEIN VIV	EQUINE ROTAVIRUS (STRAIN H-2)	M. 101	Т	487.507	T					
Γ	CUTTER CAPIED PROJECT VP4	MUMILAN ROTAVIRUS (SEROTYPE I / STRAIN 1076)		Т	193.693	ŀ					
T	CKITTE CAPEID PROTEIN VP4	HALMAN KOTAVIRUS (SEAOTYPE 27 STRAIN RV-5)	/07-191	Ţ	+	T					
77.44	WHEN CAPED PROTEDI VP4	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN 691)	2		100	T					
	ATHER PAREN PROTEIN WA	HUMAN MOTAVIRUS (SEROTYPE 1/STRAIN DS!)	102-191	Т	À A	1					
	ATHER CARES BEOTEIN VPA	HADLAN ROTAVIAUS (STRADN KS)	<b>3</b>	Т	Т	107.00					
	COLEA DE LE MANIEN VOA	HERIAN BOTAVIAUS (STRAD) KU)	76-91	٦	٦	Ř					l
A ROLL	COLER CATALOGUE TO THE	HEIMAN BOTAVIRUS (STRAIN L26)	181-207	П	483.507	1					
WA KUINE	COLEA CATAN MANTEN VIA	HAMAN BOTAVIRUS (SEROTYPE 1 / STRAIN M37)	141-207	П	482.507	-					
AN EGINE	COURT ALLERS AND LESS VILL	HIBADA BOTAVIRUS (SEROTYPE 37 STRAIN MCN13)	111.20	٦	483.508	-					
PVM ROTHER	COLEA CASA MANAGA WA	MEDIAN ROTAVIAUS (SEROTYPE 37 STRAIN P)	181-207	П	482.507	:					
2016	COLEA CASA MARININA	HIMAN ROTAVILIS (SEACTYPE 4/ STRAIN ST THOMAS 3)	181-207	234-249	482.20	1					
VA KOTHIT	COURT CASAL PROJECT VIA	HEBLAN ROTAVIAUS (SENOTYPE 4/ STRAIN VATO)	161-207	483-307	1	1					$\downarrow$
VP4 ROTHY	COTES CANDINGS AND	181-307	403.507		•					1	
WIN MOTHW	COLEA CASIO PROTEIN VAL	PORCEASE ROTAVINUS (SEACTIVE 5.1 STRAIN OSU)	115-250	\$. \$							$\downarrow$
CION N	COLEA CASO PROTECT OF	MORCEAR ROTAVIRUS (GROUP C / STRAIN COWDEN)	487-512			-					1
AN IOUR	CONTRACTOR SECTION VOL	POLCINE ROTAVIRUS (STRAIN COTTFALED)	234-349	£.50	†	T					1
MA KOING	MIER CASH PROTEIN VA	PORCINE MOTAVIRUS (STRAIN YM)	115-150	45.50		-					1
VA KOIPY	WHEN CARES PROTEIN UP.	INESUS ROTAMRUS	417-506			-					1
AND MOINT	CATTER CAPITO PROTEIN VP4	SDEAN II ROTAVIRUS (STRAIN SATI-PEM)	487-308			T					
2000	A THE CAPEIN PROTEIN WA	SDAGAN II ROTAVIRUS (STRADI SA II-SEAI)	117			1					ļ
VP4 SRAW	N PROTEIN	SOUTHERN BEAN MOSAIC VIRUS		***	200.000	19,73				L	L
VIVA WIV	NOWSTRUCTURAL PROTEIN PASA	WOUND TUNOR VIRUS	110	174.761	Т						L
VPS BTV10	OUTER CAPSID PROTEIN VPS	BLUETOWOUE VINOS (SENOTYPE 197130LATE USA)	¥(11)	126.345	494.517	-					
WPS BIVIE	OUTER CAPID PROTEDI VPS	BLUE LONGON VINCE (SCAC) ITE 11 (SCENE) CONTROL OF THE LIST	295.317	484.517							
ves brvis	DUTER CAPSID PROTEIN VPS	BITHERMAN WARRACE (VICE INTO A TENDERALIA)	17.103	711.28							
VPS BTVIA	OUTER CAPSID PROTEIN VPS	SALESTANDO DE VIDITA (CERCITADE I / 1901 ATP SOUTH AFRICA)	205-317								
VPS BPVIS	CUTER CAPSID PROTEIN VPS	SALIESTINGUE VIRUS (SEROTYPE 2/150CATE USA)	395-317								4
WHI BITTLE	OUTER CAPAD PROTEIN VP	ALC'S DWARF VILLS	265-284	613-639	\$16-069						1
AN NOA	OUTER COAT PROTECTION	IN LESTONGUE VIRUS (SENOTYPE 10/150LATE USA)	9-27	111-249	161-176						1
Wei Brylo	V TO LEAVE	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	321-137	438-462						1	1
VINI INVAL	STATE SOUTHERN	BLUETONCUE VIRUS (SEROTYPE 10/ ISOLATE USA)	2.13	22.22							
NAME OF THE PERSON	MACHINETER WITHOUT AND MED PROTEIN	MALZE ROUGH DWARF VIRUS	130-146							$\downarrow$	$\downarrow$
2000	MAKEN BAY CLYCOPROTEIN PREC	ORGYTA PSELDOTSUGATA MULTICAPSID POLYNEDROSIS YIRUS	66-13	232.32	286-313					$\downarrow$	1
VICT NOVAL	MANOR ENV CL. YCOPROTEIN PREC	AUTOGRÁPHA CALIFORNICA NUCLEAR POLYHEDRÓSIS VIRUS	101	38.33						$\downarrow$	
WIND NOVOM	MAJOR ENVELOPE OLYCOPROTEIN	GALLERIA MELLONELLA MUCLEAR POLYMEDROSIS MRUS	135-172								L
PVP6 BTVII	VM PROTEIN	BLANCONCUE VINUS (SEROTYPE II / ISOLATE USA)			11.60						L
PVP6 BTV13	VN PROTEIN	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)		336 346	1100						L
TYPE BEVIT	VP6 PROTEEN	BELIEFONGUE VIRUS (SEROITYPE 17/150LATE USA)	153	333.340	261.276					L	
PVP BTVIS	VP6 PROTEIN	ILLIETUNGUE VIRUS (MENOTITE I / ISOLATE SOOTH MINICAL)	100,000								
WPG BTVIA	VP4 PROTEDV	ELUCIONACION VINCO (SECO) TER ATTENDATE CONT	174.107								L
PVP6 WTV	STRUCTURAL PROTEIN PS	WOUND TURKEN VIEWS	374.397							Ц	
DATA MANA	STRUCTURAL PROTEIN PO	ALTIGORAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	254-275								4
PVP74 NeVAC	LECKS AND TEAM AND ANTICEM 25	HEDDELSVIRUS SAIMINU (STRAIN 11)	137-147								$\downarrow$
ALL CANA	79 KD PAOTEDA	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDRÖSIS VIRUS	274.301	605.470 605.470	678-704					$\downarrow$	$\downarrow$
STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STA	VP7 CORE PROTEIN	BLUETONGUE VIXUS (SEROTYPE 1) / ISOLATE USA)	187.333						$\downarrow$		-
PVP7 EMBVI	VP7 CORE PROTEDY	EPIZOOTIC KEMORANAGIC DISEASE VIRUS (SEROTYPE I)	703-177	17101					ļ	1	ļ
VOT TAVE	NONSTRUCTURAL PROTEIN PNS?	NICE DWALF VIRUS	100		#						ļ
	100000000000000000000000000000000000000						_	_	_		_

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PCCENE	Prictize	(All Virgos (No Bacterioghages)	-						1		
THE HAME	PROTEIN	YARUS	AREA! AREA!	A1 AREAL	AREAN	AREAS	ARFA 6	AREA?	AREA! A	ARCA?	
PVPED NOVAC	CAPSED PROTEDY P86	AUTOGRAPHA CALIFORNICA PUCLEAR POLYHEDRÓSIS VIRUS						Г	Г		
200	CAPSID PROTEDY P07	OROYTA PSEUDOTSUGATA MULTICAPSID POLYTIEDROSIS VIRUS	1871-593								
PVM BTV10	MONSTRUCTURAL PROTEIN PS	BLUETONGUE VIRUS (SEROTYPE 107 ISOLATE USA)	104-120		-				_		
IVA BIVII	MONSTRUCTURAL PROTEIN PO	BELIETOMGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	04-120		-				7		
PWR BTVE	NONSTRUCTURAL PROTEIN PO	BLUETOWGUE VIRUS (SEROTYPE 1) / ISOLATE USA)	21.20								
	MONSTRUCTURAL PROTEIN PS	BLUETONGUE VIRUS (SEROTYPE 17/150LATE USA)	81-18								
MA BIVIA	NONSTRUCTURAL PROTEIN PS	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE AUSTRALIA)	8 3		-						
	NONSTRUCTURAL PROTEDY PE	BLUETOWGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	10t 130						-		
PVPE BTV2A	MONSTRUCTURAL PROTEIN PO	BLUETONGUE VAUS (SEACTYPE 2 / ISOLATE USA)	813								
AOI MA	OUTER CAPAD PROTEIN PR (	RICE DWALF VILUS		٦							
AND MAN	OUTER CAPSID PROTEIN PA	INCE GALL DWAIF VIRUS	177-202 216-242	142 198-425							
WAY VACOC	STRUCTURAL PROTEIN VP9 PRECURSOR	VACCIDITA VIRLIS (STRAIN COPENHAGEN)	235-242						-		
PVPB VACCV	STRUCTURAL PROTEIN VPS PRECURSOR	VACCINIA VIRIIS (STRAIN WR)	225-242		-						
PVM VARV	STRUCTURAL PROTEIN VPS PRECURSOR	VALUOLA VIRUS	225-242				l	l			
PVP WTV	OUTER CAPSID PROTEIN PA	WOUND TUNOR VIRUS	111-129 214-241	141 251-271	179.405						
PVP9 LDV	NONSTRUCTURAL PROTEIN PNS9	INCE DWALF VIRUS	21:12		-					Ī	
PVP RCDV	HONSTRUCTURAL PROTEIN SP	NICE GALL DWARF VIRUS	151-175		-		T	T	t	Ī	
PVPACE NOVAC	29 KD POLYNEDRAL ENVELOPE PROTEIN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	145-166 225-245	3					İ	Ī	
PVPHE NOVOP		CALCYLA PSEUDOTSUCATA MULTICAPSID POLYHEDROSIS VIRUS	123-144				T		T		
PVPRT ADEL2	ENDOPROTEASE	HUMAN ADENOVIRUS TYPE 12	191-191		-						
PVPRT LOCTIVE		MOUSE MANOMARY TUMOR VIRUS (STRAIN BR6)	(3-5)	_			T	l			
PVPRT LONV	PROTEASE	SINDAN MASON-PFIZER VIRUS	80-88					T	$\mid$	Ī	
PVPRT SACKVH		SQUIRAEL MONKEY RETROVIRUS	134.71		-		İ		+		
PVPRT SAVI	PROTEASE	SDAIAM RETROVIAUS SAV.1	8.8		-			Ì	$\dagger$	T	
PVPU HVIBI	VPU PROTEDY	HUMAN INDICATE HEALTH VIRUS TYPE I (BILLO ISOLATE HEALT)	157		1			Ì	†	T	
PVPU HVIBS	VPU PROTEIN	HIDAAN BOALDAGOEFICIENCY VIRUS TYPE I (BITS ISON ATE)			1		T	Ì	$\dagger$	I	
MEINE DAVE	VPU PROTEIN		17.		-		<u> </u>   			Ī	
PVPU HVIBA	VPU PROTEIN	HUMAN DOMINODEFICIENCY VIRUS TYPE I (BRI) ISOLATE)	1:1	-							
PVPU HVIEL	VPU PROTEIN	1	1.26		ŀ	İ	<del> </del>	<u> </u>	!		
PVPU MV1H2	VPU PROTEIN	HUMAN INDAMODEFICIENCY VIRUS TYPE I (HXB) ISOLATE)	153	  -			<del> </del>	<del> </del>	<del> </del>	Ī	
PVPU HVIDE	VPU PROTEDI	HUMAN BANDWODERCIENCY VIRUS TYPE I (FICSF ISOLATE)	1.20		<b>~</b>						
PVPU HVINA	VPU PROTEIN	HUMLAN DOACHODEFICIENCY VIRUS TYPE I (AIAL ISOLATE)	13:33		-		-				
PATC NAMED	VPU PROTEIN	HUMAN DANGMODEFICIENCY VIRUS TYPE I (AIN ISOLATE)	3.30								
	VTU PROTEIN	HUMAN BOADNOCEFICIENCY VIRUS TYPE I (NDK ISOLATE)	3.20								
AIN PA	VPU PROTEDY	HUMAN BOARNODEFICIENCY VIRUS TYPE I (PV22 ISOLATE)	3.27								
TVPU HVISI	VPU PROTEIN	HUMOAN BOOKINGDEFICIENCY VIRUS TYPE I (SF162 ISOLATE)	3.28								
TAND HAVE	VPU PROTEIN	HUMAN BOAUNCIDES ICIENCY VIRUS TYPE I (SC ISOLATE)	2.5								
	VACUTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF	RUMAN DEPUTATION TO VIEW (22/CDC-2)4 (SOLATE) 1:23	7.21								
THAT ASSA	WELLEY DO NOT THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF	MINISTER FOLLMANANT AMERICAN LIGHTS VIRUS (TAAGUSEK IE SKEEF KE	5-5				1	1	1		
A SAME	VOX PROTEIN	MODAN BARBACKETIENCY WALL THE COLOR AND CANAL	25.4				1		1		
NAT ROBBI	Vex People	INTERNATIONAL PROPERTY VINES THE ACTOR AND	HIBAAN BAAANDOFFICENCY VIRING TYPE 2 (100 ATE 1000 T)	7(-0)	 	1		1	1	$\dagger$	T
PVPX HV201	VPX PROTEIN	MILKAN BARCHODES HEISTYN VIRUS TYPE 3 (150" ATE CHANA. 1)	101				1	1	+	Ī	
PVPX HVDG	VPX PROTEIN	HUMAN BOATHODEFICIENCY VIRUS TYPE 2 (ISOLATE NIH.Z)	100	+	-				+		
PVPX HV2BO	WAX PROTEIN	HUMAN BOADWOOFFICIENCY VIRUS TYPE 2 (ISOLATE ROD)	10.31				$\dagger$		$\mid$	Ī	
PVPX HV258	VPX PROTEIN	HUMAN BARCHODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLISY)	10.12	-			T		$\mid$	I	
PVPX HV2ST	VPX PROTEIN	HUBLAN BOMINODEFICIENCY VIRUS TYPE 2 (ISOLATE ST)	10-33				t	l	l	T	
wx CPV	VPX PROTEIN	LACTATE DENYDROGENASE-ELEVATING VIRUS	145-165						$\mid$	Ī	
PVPX SIVAL	VPX PROTED	SDALAN BANDNODEFICIENCY VIRUS (ISOLATE AGM / CLONE GRU-I) (S	76-79						-	Ī	
PVPX SIVA	VPX PROTEIN	SINGAN BIOADMODEFICIENCY VIRUS (ADMI 42-83 ISOLATE) (SIV-MAC)	10.33								
PVFX SIVACE	VPX PROTEDY	SDIDAN DIGITARODEFICIENCY VIRUS (K6W ISOLATE) (SIV-MAC)	10-33						-		
PVFX STAND	VYX PROTEIN	SDGAN DOGRODEFICIENCY VIRUS (K78 ISOLATE) (SIV-MAC)									
TANK YANG	VIA TROILEM	SDADAN DIGATINGOEFICIENCY VIRUS (F236/SMI4 ISOLATE) (SOOTY M	10-32								
TANK TANK	AT MALE A PROTEIN	BABLEY STRIPE ALCO ALC VITER OF SELECT ISOLATE) (SOOTY MA	2								
100	MONCHE STATE OF THE PROPERTY INC.	SOUNTE BOY AND IS COAN BE	T	g,			1		1	1	
	MASINGLICAN TROITER PLATA	DOVING RUINVING (STRAIM RL)	140-157 461-487	-			1	1	1	7	

W.C. Die	Pinchille	All Wrees (No Bectwieghs m)	ABTAIL	AREA 2 ARI	AREA J AR	AREAM ARI	AREAS AREAS	4 ABEA 2	4	1
TAY THE	PROTECT		Γ	T	Т	Г				_
	SOURCE OF THE AT PROTECT MCVP2		Ī	1	:	<u>:</u> :		•		
PWSS ROLLS	MONSTER PARTY AT DECITED INC.	(N.RIMO.) MI	~	:	:	-	-	_	: -	
VSS ROTE	MONSTRUCTURAL PROTEIN NO.		399-414			-	+			
VSes ROTS!	MONSTRUCTURAL PROTEIN PROTE	1 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	202-235						Ī	
VSB6 ROTBR	VPN PROTEIN	TRAIN GINTOKIN	54.45							
vsot nores	VP PROTEIN		201-125						! :- -	!
VSOL BOTTEU	VP6 PROTED(	BOVING ROLL WILL STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND STATE AND	202-225							
VSGS ROTE	VP6 PROTEIN	EQUINE ROLAVILLOS (STRAIN TRING)	207-225							
Vest BOTTUL	VP6 PROTEIN			-		-	L	_		
TANK POPUL	Vis lentros	AUCHEA ROLAVIAL		+	+	-	-		-	L
- T	A. MARCHA	ROTAVILUS (GROUP B / STIVATM IDIR)	2	+		+			-	L
	THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P	HEBLAN ROTA VIRUS (SEROTYPE 1 / STRAIN 1076)	30-23			+	+		-	ļ
EQUAL EQUAL	VP PROTEIN	LABAM BATAVIRIA (CROSTO C./ STRAIN BRISTOL.)	64-85		1		1		$\frac{1}{1}$	$\downarrow$
VSG ROTHE	VP PROTEIN		202-225			,	-			1
VSOL ROTHS	VP6 PROTEIN		202-225	-	ŀ	-				4
WCG IOTHW	VP4 PROTED ⁴	MUMAN ROTAVIRUS (SEAG) TPE 1/31 MAIN WA)	Ť	114.140		-		L		
VENT BOTTLE	VPA PROTEIN	PORCOGE ROTA VIRUS (GROUP C/STRAIN COWDEN)	Ī,				-	-	L	L
7	Use be of Fig.	PORCHE BOTA VIRUS (STRAIN COTTFRIED)	202-223	+			1		-	L
	AL COMPANIES OF 1	BOVING BOTAVIRUS (STRAIN KM-4)	21-122	1	$\frac{1}{1}$	:				ļ
WSOT ROTEU	G. TOUTION OF	AND THE BOTTA VIRILE (CROUP C / STRAD) COWDEN)	117-136	_		-	1			1
PVS04 ROTPC	CL VCOPROTEIN VP7 PLECURSOR	TOWNS IN BOTTANNIN CALL	274-295						+	4
VSOE ROTS!	MONSTRUCTURAL PROTEIN MCVP4	SECURITY IS NOT A CASE OF THE A PART AND A LAND	131-155	-						-
WOO LOTTE	CL VCOPROTEIN VP7	BOYING ROLATING (SCROTTE OF STREET)	11.11	-	ŀ	-				
ANTON BOTT	ICE VOOPLOTEIN VP?	BOVINE ROTAVILUS (STRAIN A44)			+	-				
Vers Britis	I/A VC/OPEDITED VP?	BOVING ROTAVIRUS (SEROTYPE 107 STRAIN 8421)			t					L
	As Acceptoring VP1	BOVINE ROTAVIRUS (STRAIN KKJ)		-			-			L
TO AND	COLON MONEY CAN	BOVINE ROTAVIRUS (SEROTVPE I / STRAIN TAM)	31-135	1	+		1			ļ
PVSOP ROTE	GLYCOPROJECT VY	CHICKEN BOTAVIBLIS A (SEROTYPE 7/ STRAIN CH2)	134-158			-	+	+		ļ
COLOR GO	CLYCUPICIEM VIV	GOLDAN BOTTAVALIS (STRAIN (.) 36)	131-155			1			-	+
VSOS LOTEL	CLYCOPROTEIN V/	PACA VIET A APPENDING THE AIM IDIO.	205-232				-			1
VSOF ROTGI	CLYCOPROTED V77 PRECUESOR	IN DANN BATTAVILLE (SPROTYPE 4/ STRAIN RV-4)	131-155	197-212		1	1		+	1
PVSOB INDITING		AMENIA DE BATA VIDERA (SEROSTYPE 2 / STRAIN HUS)	197.212			-			1	1
PVIOR ROTHLA		CARTAN MATANETH CONTRACT / STRAIN DS:)	197-212	-					$\frac{1}{1}$	1
CON TOTAL	_	THE AND AND AND THE POST OF STRAIN HAIZS				7				1
PVES ESTIM	_	TANALA BOT AVIRT (STEATH 126)	881-161	197.212			1			1
sos nome.	CLYCOPROTEIN V77	CARLAL BAFA CABIR (CERATIVE 1 / STRAIN M37)	1 581-161	197.313						4
tos Mother		THE A MENTAL WATER AND STRAIN BY STRAIN BY STRAIN BY	881-161	107-212					1	1
VSOF ROTHO	OLYCOPROTEIN VP?	AND	131-155	-				1		4
PASON ROTHO		HUMAN HULL A KAN LIMITE AND THE STRAIN BRA	131.133	-						4
to tone	г	HUMAN HUI AVIAUS (SENOTITE 37 STANIS MAY)			-	-				
PAYEN BOTHS	Т	HUMAN KOTAVIRUS (SEKOTTE 17 STEAL 24)		+		l			L	L
SOF ROTHEN	Т	HUMAN ROTAVBUS (SEROTYPE 47 STRAIN VA A)	T	107.919	İ				_	L
	Т	HUMAN ROTAVIRUS (SEROTYPE I / STRAIN WA)	I	717.141	1	t				l
	Т	PORCINE ROTAVIRUS (SEROTYPE \$ / STRAIN OSU)	1	117:711	1	$\dagger$		  -	<u> </u>	ļ
	Т	PORCEME ROTAVELUS (SEROTYPE 5/STRAIN TFR-41)	131-155	1		1	+			$\downarrow$
2	CHICAGO TENTO	PORCINE ROTAVIAUS (SEROTYPE 4 / STRAIN BEN-144)	197-212	+		1	+	1	+	ļ
24102 605/	7	PORCING BOTAVILLIS (SEROTYPE 4 / STRAIN BAU-1)	197-213					1		+
VSO9 ROTTE	7	INEGR BOTAVILIS	131-155						1	4
VSD9 ROTRIA	7	CONTANT OF BATAVARIES (STRADS SATI)	131-155						$\frac{1}{4}$	4
PVSDB_ROTS!		PAYANDER COM BE LETEATH AND WITATH T DIARRES ROTAVIRU	1136-153	-	-	_			-	4
SII ROTCA		AUTA TRUE (AND TO STANK TO STANK AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AND THE AUTO AUTO AND THE AUTO AND THE AUTO AUTO AND THE AUTO AUTO AND THE AUTO AUTO AND THE AUTO AUTO AUTO AUTO AUTO AUTO AUTO	1				-			4
PVSH IGESVA		HUMAN MENDATURE STATE TIME VINOS (STRAIN AS)	2,5		T		-	L		
WSH MEDGE	SMALL HYDROPHOBIC PROTEIN	MUNUS VIRUS (STRAIN SOLT), AND MUNIS VIRUS (STRAIN	×							
VIII MADE:	SMALL HYDROPHOBUC PROTEIN	MUMP'S VILLOS (STEAMED PROTECTION)			l				L	L
WELLERA	SALALL HYDROPHOBIC PROTEIN	MANOS VIXUS (STRAIN EDINGBURGH 4)	,		T					L
VEH LEBER	Г	MUMO'S VICUS (STRAIN MATSUTAWA)			t		-			L
VSJ JAUGO	Г	MUNDS VIRUS (STRAIN BELLAS))			1		-			
PVSH MUNOE	Г	MONGES VINUS (STRAIN ENGERS)	2.5		T	t				
PVSH MUMO!	Г	MUMOTS VIRUS (STRAIN SEATL-LINN)	¥.1		T					Ц
WSH MUMOR	SMALL HYDROPHORIC PROTEDI	MUNUS VIKUS (STRAIN RICHAM)			T	t	-			Ц
PVSM MUMOL	Г	MUNCS VIRUS (STRAIN BIOSTOL 1)					$\mid$			L

	Janes of the						Ì			
1000		An Versen (No Becteriophales)		7	_	Т	Т	٦	7	
WENT LABOR	SMALL HYDROPHYRIC PROTEIN	LATERAGE SETTE A SALE WAS	Ī	70-70-0	ONE OF ORDER	- XMI	O TOWARD	Z Z Z	AREA &	ORIGINA.
PVSH MODER	SMALL HYDROPHOBIC PROTEIN	MIDAPS VIRLIS (STRAIN TAKALIASIR)	0.0	<u> </u>	1	1		1	$\dagger$	
PVSH MUMOU	SHALL HYDROPHORISC PROTEIN	ADAPS VRUS (STRAIN (RABE VACCINE AMS)	1			-			$\dagger$	
PVSII REOV.	SIGNA I PROTEIN PRECURSOR	REOVINGS OF VPE 1 STRAIN LANGS	21.01		1		İ		+	Ī
PVELD REOVE	SIGNA 3 PROTEIN	REDWILLIS (TYPE) / STRAIN DEALING)	152-170		-			1	-	T
PVSD REOVI	SIGMA 3 PROTEIN	AEOVRUS (TYPE 2 / STRAIN DS/JONES)	152.170		-  -			-	$\dagger$	T
PVSIJ REOVL	SIGMA 3 PROTEIN	REOWING (TYPE 1/ STRAIN LANG)	133.130							I
PYSUS REOVE	SIGMA I-S PROTLIN	LEOVILUS (TYPE I / STRAIN LANG)	79-101		-					T
PWST3 HEVBU	STRUCTURAL PROTEIN 2 PRECURSOR	HEPATTIS E VIRUS (STRAIN BURMA)	192.311		-					T
PWIT HEVE	STALICTURAL PROTEIN 2 PRECURSOR	HEPATITIS E VIAUS (STRAIN MEXICO)	292-311							Ī
PVST3 HEWAY	STRUCTURAL PROTEIN 2 PRECURSOR	MEPATITIS E VIRUS (STRAIN MYANMAR)	116-244						-	Γ
PVST3 HEVPA	STRUCTURAL PROTEIN 2 PRECURSOR	NEPATITIS E VIRUS (STRAIN PAKISTAN)	116-292						$\mid$	
PVST2 HEVDH	STRUCTURAL PROTEIN 3	HEPATITIS E VIKUS (ISOLATE KLIESUS)	80-130		-	-		-	-	Ī
PVT2 MYXVI.	TUMOR MECROSIS FACTOR SOL RECEPTOR PREC	MYXOMA VIRUS (STRAIN LAUSANNE)	261-283						$\dagger$	T
PVT2 SPVICA	TUMOR NECKOSIS FACTOR SOL RECEPTOR PREC	SHOPE FIRECOLA VIRUS (STRAIN KASZA)	170-289						$\dagger$	T
PVTIA CAIVII	PROTEIN TOA	CAPAINOXYIAUS (STRAIN INS-1)	116-138	-	-			$\mid$	$\dagger$	T
PVT4 SFVKA	TA PROTEIN	SHOPE FIBROALA VIRIS (STRAIN KASZA)	135-148				<u>†</u>	1	$\dagger$	Ī
PVTER EBV	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-DARK VIRUS (STRAIN 199-6)	ī	146-197	وا	!	1	<u>.</u> [	+	!
PYTER HOMYA	PROBABLE DNA PACKAGING PROTEIN	HUBAAN CYTOMEGALOVIRUS (STRAIN AD169)	T	Т		1			$\dagger$	T
PYTER HSVII	•	HERPES SINOL PE VIRES (TYPE 1 / STRAIN 13)	T	491.400	1				1	Ī
PYTER HSVAU	PROBABLE DRIA PACKAGDIG PROTEIN	HERPES SDOCLEX VIRUS (TYPE 6 / STRAIN (IGANDA. 1102)	Т					+	1	
PYTER HISYED	PROBABLE DRIA PACKAGDIO PROTEIN	EQUING HERDESVIRUS TYPE I (STRAIN ARAP)	Ne. bi	1	  -				1	Ī
PYTER ILSVII	PRODABLE DNA PACKAGING PROTEIN	ICTALUNIO HEUPESVIRUS I	T		!			•	-	:
PUTER HEVEA		HEAPESVIRUS SAIMIN (STRAIN !!)	Т		ŀ		+	1	$\dagger$	
PUTER VZVD		VARICELLA-ZOSTER VIRUS (STRAIN DIBLAS)	172.180						+	T
PX IDEOS		CAROLDIO SOUTUREL HEPATITIS VIRLIS	1		1			1	+	
PX WHV!	PROTEINX	POODCHUCK REPATITIS VIALUS I	15 23						$\dagger$	T
PX WHOSE		WOODCHUCK HEPATITIS VIRUS 50	55.77					1	$\dagger$	T
PX WHV1	PLOTEIN X	WOODCHUCK HEPATTHIS VIRUS ?	58-83						+	T
PX WHV8	PROTEIN X	WOODCHUCK HEPATITIS VIRUS &	5.5	$\mid$					$\dagger$	Ī
PX WHVE		WOODCHUCK HEPATITIS VIRUS & (INFECTIOUS CLONE)	20.00				+		+	T
PX WHVW6		WOODCHUCK HEPATITIS VIRUS WER (ISOLATE PWS23)	200	-				+	$\dagger$	T
PYION ADED!	KOTEIN	HUMANA ADENOVIRUS TYPE 7	35.73		-				+	T
PYICE SSVI		SULFOLOBUS VIXUS-LIKE PARTICLE SSVI	24-30	-				ł	$\dagger$	T
PY10K MSVS	HYPOTHETICAL 16 9 KD PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFINCAN ISOLATE)	ž.	-	-			-	$\dagger$	T
PY118 55VI		LAFOLOBUS VIRUS-LIKE PARTICLE SSVI	42-59		-				$\mid$	Τ
PYIIK PASV		PANICUM STREAK VIRUS	29-52						-	
THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S	KWA-J KITOTHETICAL II 6 KD PROTEIN	REST NECKOTIC YELLOW VEIN MOSAIC VIRUS (ISOLATE GI)	15-42						-	Γ
T		CTHOLOGOL MOSAUC VIXUS (STRAIN SPICANORE)	Q.							
Т		PARRENA ADEMO MANDA I TETE 2	9	1					H	
Τ	INPOTAGRICAL IN THE PROTECT	CASSAVA EATENI VIDUS (SIRAIN WEST RENTAN 1941)	74.55	1						
Т		COMATO VELLOW FAR CITIES VINITE REPRACTOR AND ACCOUNTS	24-55	1						
PYIJK TYLCV		TOWATO YELLOW LEAF CURL YIRUS	1		1				+	
PY145 ADEOT	HYPOTHETICAL 14 SKD EARLY PROTEIN	TUNAN ADENOVIRUS TYPE ?	104.113				1	1	+	Ī
		CHECOLIS STREATE MOSANC VIRUS	99.3	+	+		1		1	T
		SULFOLORUS VIRUS LIKE PARTICLE SSVI	_	141.162			1		1	T
П	HYPOTHETICAL 26 6 KD EALLY PROTEIN	HUMAN ADENOVIAUS TYPE 1	T		-		1		+	T
╗		BEET NECROTIC YELLOW VERN MOSAIC VIRUS (ISOLATE F1)	163-188					$\frac{1}{1}$	1	T
PY39K NOVAC	OTEN	UTOCRAPHA CALIFORNICA MUCLEAR POLYNEDROSIS VIRUS	90-106	-			$\frac{1}{2}$		1	T
200	MYOTHER CAL PROTEIN 2	SOVEZAN CALOAOTIC MOTTLE VIRUS	95-90						$\mid$	T
מאלאלי לכניו		SOLVOLOBUS VIAUS-LIKE PARTICLE SSVI	122-143				-		-	Ι
PYTK4 VACCV		VACCINIA VIRIIS (STRAIN WA)	*							
PYTK SEEASH		MEASUES VIRUS (STRAIN HALLE)		1					$\frac{1}{1}$	
		SOYBEAN CALCACTIC MOTTLE VIRUS	96178				1	1	<u> </u> 	1
PYISK SSVI	HYPOTHETICAL 15 7 KD PROTEIN	SULFOLOBUS VIAUS-LIKE PARTICLE SSVI	Τ	146.131	413 434			+	1	
			7	7	7		1	1	$\frac{1}{1}$	7

PY SOCKY					TVARY S VARY	7	7 7 4 4 7		74.7	ARFA 9
YYY ADEOT	PIOTEN	COVERAN CHARACTER MOTTER VIRIUS	I	_	1	Т		Г	Т	
LIV ANCO	MATCHINAL PROJECT	LUMAN ADEMOVIBLIS TYPE ?	25.73	-						
	HYPOTHETICAL 62 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	П	63.77						
YALI EBY	HYPOTHETICAL BALF! PROTEDY	EPSTEIN-BALR VIRUS (STRAIN 899-4)	205-220							
PYROI KORMA	HAPOTHETICAL BALGUORFI PROTEIN	FOWLPOX VIRUS (ISOLATE HP-438[MUMICH])	354.374			1			1	1
PYBOT FOWPA	HYPOTHETICAL BANGO COST PROTEIN	FOWLPOX YIRUS (ISOLATE HP-438[MUNICH])	104-121	1	1				Ť	·
PYBOS FOUTM	_	FOWLPOX VIXUS (ISQLATE IP-434)AUANCHI)		+		+			+	
PYBIG FOWPM	_	FOWLTON VICOS (SOUNDE RY - SUPPLIED BATCHIS)	Ī.	24-168		 			Ī	
PYBIL FOWEN	7	CONTACT TO CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CON	T				-			
Water State	7	CHEAN COURT VINCENTER OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE COURT OF THE CO	\$1.78						Ī	
PYELS FOAM	UNITED STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STATES THE STAT	HERBEROTERING CANADA SCHOOL CONTRACTOR	206-230	+	-	-				
SALES INC.	7	HERPESYTRUS SATARITY (SUBGROUP C / STRAIN 418)	69-90							
200	7	PPATPINALBARE VIRIES (STEATN BOLD)	200,222	-	_				_	
	Т	ILARBERY PREMATE WERPSYILLS (STRAIN BC.)	175-130	t						
ACA HAVE	A LIVERTHAND STATE OF THE PROTEIN	MAREK'S DISEASE HERPESVIRUS (STRAIN MDS)	175-190							
1000	_	NIDAAN CYTOMEGALOVIRUS (STRAIN AD169)	161-131	H						
2007	_	VACCINIA VIRUS (STRAIN WR.)	16-102							
WAY CAN	HYP PROTECULO NATION FOCAPSID ORP	ACCREPE CONCINA VIBUS NEIV	141-154			, ,				
PYOR CVAI	Т	MUNIBER CORONA VIRUS MATV	141-156							
PYIOR CVICE	HYP PROTEIN IN MUCLEOCAPSID ON	MURDIE CORONAVIRUS SORV	3.33	-						T
PYKEL EBV	HYPOTHETICAL BICARS PROTEIN	EPSTEIN-BARR VIXUS (STRAIN B95-1)	67-90	+						
PYLIZ ADEA!	HYPOTHETICAL 4 0 KD PROTEIN	HUMAN ADENOVIALIS TYPE 41	٦	٦	٦					
PYNOL EBV	ELOU'S PROTEIN	(EPSTEIN-BARA VIAUS (STRAIN B95-0)	2€ IB	121-155	215-241 330-350	8			1	
PYLES BAY	Т	SUMULIUM DEDESCENT VIRUS (INSECT INDESCENT VIRUS TYPE 22)	_	1						
PYOK! ADEG!	1	AVIAN ADENOVIRUS GALI (STRAIN PRELPS) (FOWL ADENOVIRUS I)	7	1					1	
PYORI COTACY		COMPACTION YELLOW MOTTLE VIRUS		+	+	+	+			
PYORE TIVE	Ī	THEOLOGICUS TENAX VINUS I (STRAIN ICAL)			+	-			T	T
PYORU COYNY	_	CAMPELIAN TELLOW MOTILE VALUE	141	$\dagger$		<u> </u>	1		T	Ī
PYON LAV	HTPOTHETICAL 25 6 KD PROTEIN	I FLYSTAD VIDIS	194-213			-				
	INVESTMENTAL IN THE PROPERTY	(a.y vans x	71:52	-		-				
2000	INVESTIGATION IN THE PROTEIN	NARCESSUS MODAIC VIRUS	9:7		-					
PYON PVX	Т	POTATO VILLE X	11-34							
PYOU PVXO	т	POTATO VIRUS X (STRADS CP)	11:M							
PYON WOWN	1	WHETE CLOVER MOSALC VIRUS (STRAIN M)	2	1					1	
PYON WOW		WHITE CLOYER MOSALC VILLIS (STEALN O)	40.00	$\dagger$	1	+	1		T	
	1	Frimes Angeltis Vincis	•				-			
AND PACA	WANTER TO A THE PROTEIN	NARCESUS MOSAIC VIRUS	10-26	T		L				
Proper Privil	HYPOTHETICAL 16 6 KD PROTEIN	THEBLACOPIOTEUS TENAX VIRUS I (STRAIN KRAI)	13-33		-					
PYCHL TTVI	HYPOTHETICAL 16 5 KD PROTEIN	THERMOPHOTEUS TENAX VIRUS I (STRAIN KRAI)								
PYCOUN TIVE	HYPOTHETICAL 38 6 KD PROTEDY	TREBLICHTOTEUS TEMAX YIRUS I (STRAIM KRAI)		313-256						
PYCOLD TIVE	HYPOTHETHEAL SO IND PROTEDY	THEISMOPROTEUS TENAX VIRUS I (STTAIN KIA!)	2						1	
VILLA ALTEV	HYPOTHETICAL PA PROTEIN	INCE TURGED BACELLE OUR VIRUS		921-0		+	-		1	
WITH KAYA		MCE TURGEO BACILLE ORM VIXOS (ISOLATE PRILITATIVES)	67-7	% 8	1	+			1	Ī
PYTHE NEVAC	7	AUTOGRAFIA CALIFORNICA MOLLEAN POL TREDAUSIS VINUS	_	$\dagger$	-		+		T	
DAG TALL	HTTOTHER HAND IS NO PROTEIN	CANTA PETINOTSUGATA ANT TICAPSIN POLYMEDIROSIS VIRUS (OP	27.54	215.230		+			T	
	HYPOTHETICAL PTS PROTEIN	TOBACCO NECROSIS VIRUS (STILAIN D) (ThV)	15:51		-					
DIVEN BOTTO	Т	LYMANTALA DISPAR MULTICAPSED NUCLEAR POLYMEDROSIS VIRUS	16-33							
DAVEL LEVE	T	HEAPES SDAPLEX VIRUS (TYPE 6 / STRAIN GS)	43-56							
PYRUT HEVED	Т	HERPES SDIFLEX VIRUS (TYPE 67 STEATH OS)	55-74			H				
PYRES HISVED	Г	HERPES SDAPLEX VIXUS (TYPE 6 / STRAIN GS)	35.8	1					1	
PYRPI IRV6	REPETITIVE PROTEDI ORFI	CHILLO DUDESCENT VIRUS (CIV) (INSECT INDESCENT VIRUS TYPE 6)	į	+	+	-			1	
PARK DV6	REPETITIVE PROTEDY ONE 4	CHELD INDESCENT VIAUS (CLV) (INSECT INDESCENT VIAUS 1 TPE 9)		100	300.076	+	1		1	
PYNES TAVE	NEPETITIVE PROTEIN ONES	CHILD INDESCENT YINDS (CIT) (INDESCENT VINUS LITE 9)	121-2	7	1				1	]

27.0	9:0			ľ					-	-	
FILE MAME	PROTEIN		AREAL	AREAL	AREAJ	AREA	AREAS	AREA 6 AP	AREA? AR	AREA . A.	AREA 9
PYKRI EBV	HYPOTHETICAL BRASTI PROTEIN	N-BARR VIRUS (STRAIN 095-8)	П	I	П		П		Г	Т	
PYRU EBV	HYPOTHETICAL BRUE? PROTEIN	EPSTEIN-BARR VIRUS (STRAIN 693-4)	281.191	-						_	
PYSRI EBV	HYPOTHETICAL BSIL! PROTEIN	EPSTEIN-BARA VIAUS (STRAIN 895-8)	611-26								
PYTRI EDV	HYPOTHETICAL BIRF! PROTEIN		183-401							-	
PYURS NEVOP	HYPOTHETICAL 24 6 KD PROTEIN	POLYHEDROSIS VIRUS (OP	133-152								
PYAR VACC			1	20	1					1	
TANK VACCE	HATOMETICAL FARD PROTEIN	VACCINIA VIXUS (STILAIN COPENHACEN)	3 5		1			$\dagger$	+		T
PYVAT VACO			77.00	$\dagger$	Ť			$\frac{1}{ }$		1	T
PYVBE VACEV	-		173	T					+	t	T
PYYBG VACCC	AVPOTHETICAL 11 1 KD PROTEDI		17.54		Ī	-					Ī
PYYCA VACC	HYPOTHETICAL BOKD PROTEDY		53	T	T				+	t	
PYYDZ VACCY		VACCINIA VIRUS (STILAIN WILL AND VACCINIA VIRUS (STILAIN COPE	2	2		-		-	-	$\mid$	
PYYDA VACCC		•				•				-	
PYVDA VACCV				32-38	44	1				-	
PYVFA VACCC	HYPOTHETICAL 7 I KD PROTEIN		48-67								
PYYFF VACOC	KYPOTHETICAL I I KD PROTEIN		13-42							-	
PYYGA VACCC		VACCINIA VIRUS (STRAIN COPENHAGEN)	105-127			7			_	-	
PYYKE VACCC		VACCINIA VIRUS (STILAIN COPENHAGEN)	54-70						_	-	
WELL ENV	HYPOTHETICAL BZLP1 PROTEIN	EPSTEIN-BALK VIRUS (STRAIN B95-4)	35-156			•			-	-	
PY MK CSMV	HYPOTHETICAL 14 S KD PROTEDY	CHEORUS STRUATE MOSAUC VIRUS	24-80	1					L	$\vdash$	
PYISK SSVI	HYPOTHETICAL 15 6 KD PROTEIN	ATICLE SSVI	100-125	141-162							
PYYOU ADEST	HYPOTHETICAL to 6 KD BARLY PROTEIN		50-73							$\mid$	Γ
PY2SK BNYVF	ANA.3 HYPOTHETICAL 24 7 KD PROTEIN		111-691							_	
PYZK NEVAC	HYPOTHETICAL 39 9 KD PROTEIN	A POLYHEDROŠIŠ VIRUS	901-06			,					
772 SOCIA?	HYPOTHETHCAL PROTEIN 2		65-30								
PYTH SEVI	HYPOTHETICAL 31 7 KD PROTEIN		123-143			•					
PYGKO SSVI	HYPOTHETICAL 6 6 KD PROTEIN	TICLE SSVI	7							1	
PYTE VACEV	HATOTHETICAL 7 & ILD PROTEIN	VACCINIA VINUS (STRAIN WR.)	97-17	1	1	•			1	+	T
2 10	INVESTMENT INVESTMENT	N. P.	50.73	$\dagger$	1	1		1	+	+	Ī
Pyrite REDI	INVESTIGATION IN THE PROPERTY	EVI	T	2000	177.00	2157 517	744 744	1		†	Ī
VICOS IN	HYPOTHERICAL PROPERTY		Ť	Т	Т	2/4/2	¥/-B/	+	$\dagger$	+	Ī
PWer Abbits	HYPOTHERICAL 6 7 KG EABLY PROTEIN			+	Ī				+	+	T
PYWC2 SEV	HYPOTHETICAL 9 3 KD PROTEIN	MICHISSVI	Τ	63.71	T	I			+	$\dagger$	T
PYALI EBV	HYPOTHETICAL BALF! PROTEIN		2						+		
PYBOI FOWING	HYPOTHETICAL BANGE-ORF! PROTEIN		34.34					-	-	t	
PYBO! FOWPA	HYPOTHETICAL BAMPS-ONLY PROTEIN		104-121						_	H	
TARON FORES	WATCHELL BANGE CREVETOLES	FOWLAND WALLS (INCLAID IN AUGUSTICAL)	į	1	1					+	Ī
TOOM STAN	_		3171	171	†			+	+	+	T
WELL SPORT	-		Т		T	T		+	+	+	
PYBL3 FOAMV			52.78								
TOTAL MAYSC	HYPOTHETICAL 28 7 KD PROTEIN IN DAGA TREGIO		204-230								
PYDED HSVSC	N DIGHT TREC	£	2								
PYECA EBV	MITOTRETICAL ECANA PROTEIN	ENTERNAME VIRUS (STRAIN BOSE)	700-222	1						Н	
STATE OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PERSON OF THE PER			81.6		1				1	-	
AND THE				1	1	T		1	+	1	
PYING VACEV			103	T	Ť				1	$\dagger$	Ī
PYIOT CYAKS	HYPOTHETICAL PROTEIN IN MACLEDICAPSID ORF		251.10		T	Ī			1	$\dagger$	
THOS CAR!	HYPOTHETICAL PROTEIN IN MUCLEOCAPSID ONS		35	$\dagger$	T	Ī	T	1	+	$\dagger$	
PYTOR CVAS	HYPOTHETICAL PROTEIN IN MUCLEOCAPSID ON		2					+	+	1	
PYKR2 EBV	HYPOTHETICAL BEAT? PROTEIN	D95.8)	67.60							f	I
PYLI3 ADEA!	HYPOTHETICAL 8 6 KD PROTEIN		П		П					-	
PYARU EBV	BAGUS PROTEIN	EVSTEIN-BARR VIRUS (STRAIN 805.8)		138-155	118:311	061.066			Н	H	П
PTMSF INTE	HINING IN ALL INVIEW	SUMULTUM INDESCENT VINUS (INSECT INIDESCENT VINUS TYPE 22)   23-46	7	1	1	]	1			1	7

2000		All Virgas (No Bacteriophages)		П	П	П	П		П	
THE WALTE		YIRUS	ARGAL	ABEA1 AF	ABEAL AREA	I	AREA JAHEAL	PREAT	o avad	ABIA!
PYOR! ADED!		AVIAN ABENOVIRUS GALI (STRAIN MIELFS) (FOWL ADENOVIRUS I)	200	1		$\frac{1}{4}$		+		
PYOR! COYLAV		COMMELINA YELLOW MOTTLE VIRUS	2			+		 		Ī
PYOR! TIVI		THERMOPROTEUS TENAX VIRUS I (STRAIN KIRAI)	240	+	+	+			1	T
PYORE COTAN	HYPOTHETICAL 15 KD PROTEIN	COMMELINA YELLOW MOTTLE VIRUS			+	$\dagger$		+		T
PYOLI EAV	INTROTHETICAL 25 6 KD PROTEIN	EQUINE ARTERITIS VIRUS	761	+	1	$\dagger$				
PYORE LELY	HYPOTHETICAL 28 4 KD PROTEDM	LELYSTAD VIRUS	11.03			$\dagger$	1		-	
PYORU LVX	HYPOTHETICAL (18 KD PROTEIN	LILY VIACOS A				ł				
PYORU JOAN	HYPOTHETICAL MKB PROTEDI	NARCISSUS MOSARC VIRUS	2 2			+		-		
MOD WX	HYPOTHETICAL 12 KD PROTEDY	OTATO VIKUS A				<del> </del>		-		
PYORU PYXCD	-	POTATO VIDUS X (STRAIN CP)	¥			+		1		
PYON WOLVE		WHITE CLOVER MOSAIC VIRUS (STRAIN M)			+	+		 		
PYOR WOW	-	WHITE CLOVER MOSAIC VIRUS (STRAIN 0)	2			+	+	1	1	
PYORS ADECU	-	AVIAN ADENOVIRUS GALI (STRATH PIELPS) (FOWL ADENOVIRUS !)	3		$\frac{1}{1}$	-	1			
PYCES EAV	INTOTALTICAL 28 7 KD PROTEDY	EQUINE ARTERITIS VIRUS	136-158			1			1	
AND VALUE	SAVOTACTICAL 18 KD PROTEIN	NAICHSUS MOSAIC VIRUS	10-36			1		1	1	
MULTI INVA	MYSOTHETICAL 14 & KD PROTEIN	THERMOPROTEUS TENAX VIRUS I (STRAIN KIA)	13-33			-		-		1
	WYPOTHE TIEAL 14 S KD PROTEDA	THERMOPROTEUS TENAX VIRUS I (STRAIN KRA!)	16-34			-				
1000	INTERPORTED TO BE AND PROTEIN	MEXIMOPROTEUS TENAX VIRUS I (STRAIN KRAI)	201-21	333-236		1				1
1000	WASHINGTON TO BE DECITED.	THEREGORD TENAX VIRUS I (STRAIN KRAI)	\$11.19							
	LIVERTIE TICAL PAR PROTEIN	ALCE TUNGED BACKLIFORM VIRUS	52.5	104-126						
2744	LIVERTHER PLANTED	RICE TUNCKO BACHLIFORM VIRUS (ISOLATE MIILIPPINES)	57.5	104-126	_					
1000	LIVERTHERS AT A REPRESENTATION PAY THE CHOIN	ALITOGRAPHA CALIFORMCA NUCLEAR POLYHEDRÓSIS VIRUS	P(E-112			-				
		ORGYIA PSEUDOTSUČATA MILLTICAPSID POLYITEDROSIS VIRUS (OP	23·108							
	MANAGEMENT AND RESIDENCE IN PASSIBLE OF THE GLOSS	CARGY IA PSEUDOTSUCATA MAR, TICAPSID POL YHEDROSIS VIRUS (OP	27.54	015-230	_					
		TOBACCO NECEDSUS VIRUS (STRAIN D) (TNV)	Ē			-				
TANK THAN	HATOING IN A TABLE TO BE SEED OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE O	VALANTAIA DISPAR MER TICAPSED MUCLEAR POLYITEDROSIS VIRUS	<u>•</u>			ŀ				
	HINDING INC. 1 TANKER BE	MERPER CLARK BY VINUS CTYPE 6 / STRAIN GS)	***			-				
SAC TAL	WAYNING THE PROPERTY OF	HERPES STAPLEX VIRUS (TYPE 6 / STRAIN GS)	55.74			H				
	CANADA MAINTENANCE OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONT	HERPES SINGER BY VINUS (TYPE 67 STRAIN GS)	32-56			$\mid$				
PYLL) HSYRO	HATOIRE IN ALTHOUGH IN	CHIED PROFESSION VIRUS (CIV) (INSECT INDESCENT VIRUS TYPE 4)	Ş			-				
-	REPERTURE FROM CONT.	CHILD REDSECTED VIEW (CIVI INSECT REDESCENT VIRUS TYPE 6)	\$ 3			-				
	KEYETITIVE PROTEIN ONLY	CARL & INDESCRIPT VIRUS (CIVI (IN)SECT (NDESCRIPT VIRUS 17PE 4)	1213	179-204	240-285					
5	ACTURE PROJECT BANK	FPSTEINLINGER VIRUS (STRADY BPS-0)	194-223			$\vdash$	-			
	MITOTORIUM INCAL BEAN I PROTECTI	EPSTEIN-BARE VIRUS (STRAIN 1991-4)	125.122							
	WASHINGTON BEEN PROPER	EPSTEIN-LEARN VIRUS (STRAIN 1995-1)	11:26		L	$\vdash$				
DH I	Investigation and Profession	EPSTEIN-BARR VIRUS (STRAIN 1995-8)	313-401							
AND LAND	HYPOTHETICAL 24 8 KD PROTEIN	OROTTA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OP	133-132			1		+		
WAY VAN	7	VACCINIA VIRUS (STILAIN COPENHAGEN)	13-99	140-156						
PYVAJ VACCE	т	VACCINIA VIRUS (STRAÎN COPEMHAGEN)		35.2		1		$\frac{1}{1}$		
PYVAL VACCV	т	VACCIDITA VIRUS (STRAIN WR), AND VACCIDITA VIRUS (STRAIN COPE				1				
PYVAT VACEV	+-	VACCIDILA VIRLUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE				1				
PTVIII VACCV	_	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE	27		+	1				
TAY O VACOL	+	VACCDRA VIRUS (STRAIN COPENHAGEN)	X.			+	1			
PYYCA VACCE	•	VACCINIA VIRUIS (STRAIN COPENHAGEN)	ŝ			1		$\frac{1}{1}$		
PYVED VACEV	_	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPE	ž	25.2		1				
PYYDA VACCC	-	VACCINIA VIRUS (STRAIN COPENHAGEN)	22.2	7	$\frac{1}{1}$	†	1	-	1	T
PYYDA VACCV	+-	VACCORA VIRUS (STRAZH WR)	=	23.38	2 2	1				
PYYA VACC	7	VACCINIA VIRUS (STRAIN COPENHAGEN)	2			+	-			
PYYET VACCE	۳	VACCINIA VIRUS (STRAIN COPEMHAGEN)	77			1	-	-		
PYYOR VACCE	₱	VACCDATA YORUS (STRAIN COPENHAGEN)	- 12 - 12 - 12 - 12 - 12 - 12 - 12 - 12			1				T
PWILE VACCE	+-	VACCDRA YDRUS (STRAIN COPENHAGEN)	2 3		1	1		$\frac{1}{1}$	1	
VALLE BAV	┯	EPSTEIN-BAUR VIRUS (STRAIN BOS-1)	25 156		_	1	-			7

## TABLE XIV

SEARCH RESULTS SUMMARY

FOR P23TLZIPC MOTIF

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OI G ENICYB	ENONIE POLYPROTEIN	STATE STATE VIBILE VIBILE AND BARC D DIADE TOCENIC)	18-131	1465-1503					1
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IVON DIO	GENORIE POLYPROILIN	PUOLI AND MICHIEL DISCASE CIPETO SEPARA AND A PRINCIPLICANI	1034-1074	1046-1133	1167-1199	1465.1501			
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		LIEPATITIS A VIRUS (STRAIN 41C)							
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TAN C. III. AVIA		SIMILAN INPATITIS A VIRUS (STRAIN ACKL. 27)	1911-1161	1317-133			1		ļ
Prot G 117 NVS	GENCALE POCYPROTEIN	AND AND DESIRED CORP. ( 14 KM V. 14)	194:122	2005.304	_				1
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BIABI DI DAG	GENOME POLYPROTEIN		1446.1475	1900 1842	1976-2012				
1	GENOME POLYPROTEIN	IIIIII MIIIMUVIKIIS Z (TIKV-4)	1440.1492	9	_				
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PPOLG JAEVI	CENORIE POLYPROTEIN	TOTAL STATE WITH COURT OF BAIL CANNIE	\$0.18	1333-1369	1516-154		2779-2110 1274-1311		
PPO C IAFVS	GENOME POLYPROTEIN	TATAMESE ENI PRINCEITS TINGS TOTALS TO THE							

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5	GENOME POLYPROTEIN	IRUS (STRAIN JADARS982)	61.95	1213-1269	•	1182-0112	1174-1111		
PPOI G JAEVN	GENOMIE POLYPROTEIN	(SIRAIN HAKAYALIA)	1161-1197					İ	
Proj G KUNIM	GENOME POLYPROTEIN	ALIMIN VIRUS (STRAIN NIRAGOIC)	10.19	105-196	1115-2111				
PPULC LANY	GENOAGE PULYPROTEIN		1157-1166	1519-1551	2230-2264	1166-1198	1005-3133		
PPOLG MCFA	GENOME POLYPROJEIN	LAVIVIRUS)	174.1706	1330-1356					
PPOLG MIDMV	GENONIE POLVPROTEIN		2.2						
PPOLG MVEV	GENOME POLYPROTEIN	SVIRUS	(6-10)	707:1345					
70.0	GENONE POL VPROTFIN	ORNITHOGALUM MOSAIC VIRUS	916-306						
PLOE DENVO	GENDATE POLYPRUICIN	(FEFFER AIOTILE VIRUS (CALIFORNIA ISOLATE) (FEATV)	18-13	11.980					
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Prote Police		POLICY HOS ITTE (15 IRAIN W.2)							
10.00		POLICYING TYPE I (STICKING PILE)							
Prod C Pour	GENOME FOLVERIN	TULKINIANS TITE JUNEAN PLECON AND PACCON LAND	100.000	111111111111111111111111111111111111111					
	GENUALE POLITICAL								
PPOLG PPVEA	GENOMIE POLYPROTEIN	THE UNITOR FOLLY WINDS (STEAM) (FTV)							
PPOLG PPVNA	GENOMIE POLYPROTEIN	FIGURE FOX POT VIROS (ISSUEATE MAT) (FFV)	\$147.00	1000					
POLG PIVIA	GENORIE POLYPROTEIN	FLUM FOX POLYVIRUS (STRAIN RANKOVIC) (FPV)	2030-2000	301.3112					ĺ
PPOLG PSBNV	GENCHIE POLYPROTEIN	PLA SEED HOUSE AKISARC VIRUS (STRAPH HPD)	90		1100				
Proice Valid	CENONIE POLYPROTEIN	POINTO VIETS Y (STRAIN HITMCARIAN) (FVV)	107	1004-1001					
PROLG PUT	GENOVIE POLYPROTEIN	FOLATO VIRUS Y (STRAIN M) (PVY)	102.1316						
PROI C PYFVI	GENOMIE FOLVFRUIEIN	!	210.262	10.113	1701.1031				
TCG C SALVE	CEMONE PON YPROTEIN		23.24						j
POLG STEVA	GENOME FOLVPROTI IN	ST LOUIS EMEPHALITIS VIRUS (STRAIN MS) 3)	61.05	1301-1331					
Proj. C SUMVS	GENOME POLVPROTEIN	SUGARCANE MUSAIC VIRUS (STRAIM SC)	307.136						
Proka Svovi	GENOWE POLYTRUIT IN	SWINE VEGGULAR PISCASE VIRUS (STRAIN IV) '16)	1385-1617						
היסוב ביסיוו	GENOVIE POLYPHOTEIN		20.0					İ	
PPOLG TBEVS	GENOVIE POLYPROPERS	TICK PORT TECT TICK CHIES (STRAIN SOUTH) (TRICK)	200	=	2164-2378	341.130			i
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	CENORE POLYTROILIN	1D.104)	137.1106	1336-1366	1664-1531	101.7140	1093-1133		!
	GENOVIE POLYPROTEIN	ZIVCHINI ALITON MOSAIC NIAUS (ZYMY)		1	:	:	:		
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MAN SEVA	NONSTRUCTURAL FOLYPROTEIN	AIN TRIMIDAD INDUKLYS		14)6.1466				Ī	Ì
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PPCH N PCVF4	MON-STRUCTURAL POLYPROTEIN	FELINE CALICIVIRUS (STRAIN JAPANESS. F4) (FCV)	300-333						
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IN THE	MANACATA TOTAL IN VINCELLIN	III PATILIST, VIRUS (STRAIN INTRAIA) (III.V)	(618-1652	İ					i
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PPOLN IEVPA	_	HEPATITISE VIRUS (STRAIN PAKISTAN) (HEV)	19.18				-		İ
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MALE STREATHER CHORNORANGE REDUCTARE LANGE (AVAILABLE ASSOCIATED MILES STRAIN BOANS) 10'20')  MALE STREATHER CHORNORANGE REDUCTARE LANGE (AVAILABLE STRAIN BOANS) 10'20')  MALE OF TREATES, SECOLATED THANSEQUENCY AND ASSOCIATED WILLS STRAIN WHO AND VACCHIA VINUS STRAIN COPERATOR WAS ASSOCIATED WAS GOVERNORANGED STRAIN COPERATOR WAS ASSOCIATED WAS GOVERNORANGED STRAIN WAS ASSOCIATED WAS GOVERNORANGED STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA VINUS STRAIN WAS AND VACCHIA WAS AND VACCHIA STRAIN WAS AND VACCHIA WAS AND VACCHIA STRAIN WAS AND VACCHIA STRAIN WAS AND VACCHIA WAS AND VACCHIA STRAIN WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA STRAIN WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA VALUS STRAIN WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND VACCHIA WAS AND V	Ī		VAKULA VIRUS	٦						
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	IS CORDINAVIRUS RAÎN DEAUDETTE! (IBV) HEMORBHAGIC FEVER VIRUS)	705-740 941-949 746-780 177-207 80-113 186-170	1137.2166 2137.2166 214.214 217.2166 127.216		1611.7661 2646.2730 2336.2391	3096-2728	<del>                                      </del>
	IS CORDHAVINUS AAIN DEAUDETTE; (IBV) HEMORRHAGIC FFVER VIRUS)	146.380 146.380 177-307 16-113 16-113 101-311	1137.3164 684.314 122-350 1094.1128		2556-2730	3696-2728	
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	IS CORGNAVIRUS RAIN DEAUDETTE! (IBV) HEMORRHAGIC FLVER VIRUS)	146-380 173-307 86-113 103-331	122-350 122-350 1094-1128	1687.1720	1116-11191	3046-2728	
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MAPO RCWIV	7	BLOVELS 1 VERAIN DUNINESS	111.113						
ALCON DECOM	-+	ROVINE ROTAVILLS (STRAIN RS)	23.60	200-231	347.276				ı
	MAN DIRECTED BUT PARENCE ACE SURING	ROVINE ROTAVIRUS (STRAIN IR.)	100-331	311.316					
	MANAGED BY ANA CHEST AND ANA CHEST	PORCINE ROTAVIRUS (STRAIN COTTFRICT)	100-211	147.236					
	MAN DIRECTED BAN POLYACE AND STATE	SIMIAM II ROTAVIRUS (STRAIM SAIL)	<b>9</b>	200.231	147.176				
200	PNA PCH VALERASE	TACARINE VIRUS	17.51	100.138	1078-2112				
100	Ť	TONIATO BUSITY STUNT VIRUS ISTRAIN CHERRY) (TRSV)	470-501						
	PROPARIS BUA DIRECTED BUA POLYMERA	TUBNIP CRIMILE VIRUS (TCV)	360-318						
TACAL	MITATIVE BNA DIRECTED RNA POLYNERA	TOBACCO MILD GREEN MOSAIC VIRUS (TMV STRAIN UZ)	41.47	130.159	209-244		450.483	135-1117	33.63
201		TOBACCO MOSAIC VIRUS (VULGARE) (TMV)	120-159	176-406	700-728	1533-1565			
2	TOTAL STATE THAT CHEET AND THAT POR VALERACE	PORACTO MOSAIC VIRUS (STRAIN KOREAN) (TAIV)	138-139	116-406	300-728	1333-1565			
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O STATE OF THE PERSON NAMED IN COLUMN 1	-	IOBACCO NE CROSES VIRUS (STRAIN A) (TWV)	331-363						
212	-	TOPACCO NECROSES VIRUS (STRAIN DICTINV)	9	114.270					
	BUY BOX ONED AT BUY CORDINE	CANNE DISTENDER VIRUS (STRAIN ONDERSTEPOORT) (CDV)	365.333						
200	SWA POLYNERACE ALPHA SIBINIL	NIEASI ES VIRUS (STRAIN EDMONSTON)	265 202						
PART LEASE	Ť	AFEASLES VIRUS (STRAIN IP.3.CA)	195-132						
APP MEASY	N.	ALES VIRUS (STRAIN YANAGATA-1)	\$16.213						
PHRPP MIDE	N.	ANIMAPS VIRUS (STRAIN SRL-1)	311.349						
PRRPP MILLAPE	RAN POLYNERASE ALPIN SUBLINIT	NIUMPS VIRUS (STRAIN ENDERS)	312-340						
RPP MUSEL	3	ATUMES VIRUS (STRAIN MIYAHARA VACCINE)	312.349						1
PRRIP NOVA	3	MEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIAJI) (NI)V)	230-355						
RAPP NOVE	ž	NEWCASTLE DISEASE VIRUS (STRAIN REAUDETTE CAS) (NUV)	220-255						
HEFF PIZH	ANA POLYMERASE ALPHA SUBURIT	HERITAN PARAING LUCKZA Z VIRUS (PIV. 2	10.13						
PREP PISHT	ANA POLYMERASE ALMIA SUBUNIT	INTERIOR PARAIMELUENZA 2 VINUS (STRAIM TOSHIDA) (TIV-2)		777					
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THE CANAL	ANA PUL TRIERASE ALTIN SUBURIT	RABIES VIRUS (STRAIN FRA). AND RABIES VIRUS (STRAIN PM)	116.244						
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27.47	1	RABIES VIRUS (STRAIN SAD BIR)	16.31						
AREA SENDS	ANA POLYMERASE ALPHA SUBINIT	SENDAL VIRUS (STRAIN Z / HOST MUTANTS)	230.00						
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PARFF SENDS	ANA POLYMERASE ALPHA SUBUNIT	SENDAI VIRUS (STRAIN HARRIS)	270.564						
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Ī	PROTEIN A4		207.241					
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	SA KD ABONTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN COPENIVACEN)	200					Ī
VACOV	SA KO ABORTIVE LATE PROTEIN	VACCINIA VIRUS (STRAIN WR)	100 431					
	SO KD ABORTIVE LATE PROTEIN	VARIOLA VIRUS						
	PROTEINA	VACCINIA VINITY (STRAIN COPTINIACIEN)	====	170.70)				
VAN VANV	TEOLEMAN AND	VARIOLA VIRUS	111.11	170.701				
1	PROTEIN A ST	VACCINIA VIAUS (STRAIN COPENIAGEN)	41.76					
1	PROTEINAL	VACCINIA VIRUS (STRAIN WR)	41.16					
PVAII VARV	PROJETA A 11	VARIOLA VIRUS	42.76					
1	FROIL IN A 12	VALCINIA VIRUS (STRAIN WR) AND VACTIMIA VIRUS (STRAIN - CITINITAC)	£.3		_	_		:
	THEORET ON A 12	VARIUR A VININ				1		
PVÁMO VÁCEC	PROJEIN A40	VACCINIA VIRUS (STRAIN COPENHAGEN)	5					
PVA41 VACCC	PROTEIN AU	VACCINIA VIRUS (STRAIN COPENHIAGEN)	2		+	-		
PVA01 VACCV	PROSESIN A41	VACCINIA VIRUS (STRAIN WR)	2				1	
PVA41 VARV	PROTEIN A4)	VARIOLA VIRUS	8.130					
PVAN VACTO	TEST IN A C.	VACUINTA VINITS (CIRAIN COPTINIACION)	3.5	,		-	į	-
WALL VALLY	PROHITS ASI	VALCINIA VIRINGSIRAM WILL	10.10			-		
PVAL BOT	ALIPOTEIN	BEET CUALY TOP VIRUS (BCTV)	19:118					
PVALLEGATV	ALI PROTEIN	REAN COLDEN MOSAIC VIRUS	=					
3	AL I PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST KENYAM B44	86-117					
7	NISTORIAL RIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA NISTORIA N	CASSAVA (ATENT VIRUS (STRAIN NICERIAN)	611.5					
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PVAL) TYLCM	AL! PROTEIN	TONIATO TELLOW LEAF LURE VIRUS (STRAIN MANNIANOE) (1111-1)		$\dagger$	T			-
PVAL) TYLCV	ALI PROTEIN	TONIATO YELLOW LEAF COAL VINOS (1 TECY	١		İ			
VAT CAMVC	APHID TRANSMISSION PROTEIN	CALL PLOWER PROJAC VIROS (STRANG CHITCALL)	5.00	107.130	T			L
VAT CAMO	APHID TRANSMISSION PROTEIN	CALLIFORER PROPRIE VINOS (STRAIN DRICKTAMY)	200				<u> </u>  -	L
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PVB04 VACCV	PROTEIN De	VACCINIA VIRUS (STRAIN WR)			Ť			+
PVB04 VARV		VARIOLA VIRUS		İ	Ì	1		1
PVBIG COWPX	INTERLEUKIN-I BINDING PROTEIN PRECURSOR	COMPOX VIRUS (CPV)		İ	Ì			1
PVB16 VACCV	INTERLEUKIN: I BINDING PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN WR)	70.0		1	1		+
PVB16 VACCC	SURFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN COPEMIAGEN)		1	1			$\frac{1}{1}$
PVB19 VACCD	SUMFACE ANTIGEN S PRECURSOR	VACCINIA VIRUS (STRAIN DAIREN I)	~		1			-
PVB19 VACCV	SURFACE AMTIGEM SPRECURSOR	VACCINIA VIRUS (STRAIN WR)	11.762		j		<u> </u> 	1
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VARIE ROMV	BRI PROTEIN	BEAN COLDEN MOSAIC VIRUS	166-198					4
PVC01 CCVKA	C. PROTEIN COUPLED RECEPTOR HOMOLOG C)	SHOPE FIDRONIA VIRUS (STRAIN KASZA) (SI V)	96.130					_
PVCM VACCC	PROTEIN C	VACCINIA VIRUS (STRAIN COPENHACI N)	109-139	107-210				
VICE VALLE	PROTEINCE	VACCINIA VIRUS (STRAIN WR)	611 601	103.215				
ı	77.212000	VARIOLA VIRUS	96.136					
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	100 Maria Cara Cara Cara Cara Cara Cara Cara	VACCINIA VIRUS (STRAIN WR)	19:01		Ī			
200	TO POSSESSED	VARIOLA WALLS	20.00					
	TOPOLITATION PROPERTY CO.	VIRUS (STRAIN RASZA) (STV)	19.03					
ALTO STATE	PEOPLE CO.		331-010					!  -
מולים מילים	PROFESS TO		533.410					
PYC 10 CF VIKA	HYPOTHETICAL PROTEIN CIO	SHOPE PIRADAIA VIRUS (STRAIN KASZA) (SFV)	111.5					
PVC 10 VACCC	PROTEIN CIO	VACCINIA VIRUS (STRAIN COPENHACE N	95:12					
PVC 10 VACCV	PROIFINGIO	ראלולוא אושנוע ועודא אוא ואין	21-12					
PVC 10 VARV	PROTEINCIO	VARIULA VIRUS	131-158					
PVC31 VACCC	PROTEIN C21/817	VACCINIA VIRIIS (SIRAIN COPENHAGIN)	1.1					
PVCAP FBV	MIAJOR CAPSID PROTEIN	FPSTEIN DARK VIRUS (STRAIN DO) D) (HUNIAN HERPESVIRUS 4)	148-163	П				j
PUCAP IKNIVA	MAJOR CAPSID PROTI IN	HERITAN CYTCHIC CALOVINIS (STRAIN ADICA)	=	191-101	710.746		<u> </u>	-
Ficke iistii	MAKON CATSID PROJES	III BPLS SIMPLEN VIRUS (TVPE 1/STBAD)	Ī	┪				
PICAP HISVAL	NAJOR CAPSID PROTEIN	HERPES SIMPLEY VINUS (TYPE 6/STRAIN UCANDA-1102)	_	ī	41.16			
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TOTAL PROPERTY.	_	VACCINIA VIRUS (SIRAIN COPINIACIEN)	8:5	701-901				L
LYID! VACE V	_	VALUE AND VIEW VIEW	9	211-491				
PVIEW VARV	_	VARIE A VIRIS	9	166-112				
PVINO FOUND	93 6 KD PROTEIN	FOWLPOX VIRUS (STRAIN FP.1)	113.353					
PVD05 VACCC	-	VACCINIA VIRUS (STRAIN COPEINIAGEN)	130.143					-
PVD05 VACCV	7	VACCINIA VIRUS (STRAIN WR)	330-348					4
PVD05 VAIV	_	VALIGICA VIRUS	330-348					4
PVDIG FOWP!	PROTEIN DIO	FOWL POX YIRUS (STRAIN FP.1)	116.13					+
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NENY VAFE	MANUAL CANCELLIST	VACCINIA VIRUS (STRAIN L.IVP)						L	L
PVENV VACCE	MANON ENVELORE PROTEIN	VACCINIA VIRUS (STRAIN VR.)	7.00						Ļ
A LUTA DATE	NITTO CONTRACTOR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER								-
THE ARTIST	VINARIA CINTERIOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR CONT		2	7.					

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30000	1517-15719	All Vieuzet ine becterioghaget)	П		П	П	П	П	
	PROTEIN	VIRUS	4	ARA	3	444	रमार रमार	Т	4
PYTO VACCO	PROTEINE	VACCINIA VIRUS (STRAIN COPENTIAGEN)		3				+	
	PROTECUE	VACCINIA VIRUS (STRAIN WR)	1	-	1			+	Ī
VAWOI 191V9	PROTEIN FPI	FOWLPOX VIRUS	2017.120		1	1		+	
PUFPA FOWPY	PROTEIN FPA	FOWLPOX VIRUS	707-107			1	1	+	1
PVIPT CAPVK	PROTEIN F?	CAPRIPOXVIRUS (STRAIN KS-I)						+	Ī
PVFUS VACCE	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN COPI:NIIAGI:NI						+	
PVFUS VACCV	14 KD FUSION PROTEIN	VACCINIA VIRUS (STRAIN WR)			1	1		$\dagger$	Ī
PLEUS VARV	14 KD FUSION PROTEIN	VARIOLA VIRUS				Ì		t	
PVC01 HSV11	HYPOTHETICAL GENE I PROTEIN	ICTALUND HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	-			1		+	I
PVC02 HSVEB		EQUINE INTRPESVIALIS TYPE I (STRAIN ABAP) (EMV-I)						+	
PVG02 VACCV	ISATIN-BETA-THIOSEMICARBAZONE DEPENDENT PROTE		_					+	
PVC03 VARV	ISATIN-BETA-THIOSEAIICARBAZONE DEPENDENT PROTE							$\dagger$	
PVCA1 HCVI		•	102-136					+	Ī
IN MEN	HYPOTHETICAL GENE & MEMBRANE PROTEIN	ICTALUND HENDESVIRUS I (CHANNEL CATRISH VIRUS) (CCV)	54-13					+	
מיניים מיניים		VACCINIA VIRUS (STRAIN COPENHAGEN)	9(1.66					-	
7000	PROTEIN CA	VARIOLA VIRUS	96.136						
2000	THOUSE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PART	VAPCINIA VIRUS (STRAIN COPENIAGEN)	113-145						
ארני איני	TRUICIN C	VARIO A VIRILA	\$ C					_	
200	TROISIN C	VACCIMA VIDIG 1819 AIM COPENIACIENI	103.338					L	
PVC00 VACCC	PROTEIN	VACCINIA VIACO (STANIA VIA)	104.101					-	
PVC09 VACCV	PROTEINF	TACLINIA VIAUS (SIRAIN WA)	101-118						
PVC09 VARV		VANOLA VIACA	19		Ì			H	
PVG11 JISVII		ICTALUATE TESTED I CHANGE CARTAN VINUE (C. )				T		+	Ī
PVC12 IISVII	HIYPOHIE HCAL GENE 13 ZINC-BINDING PROTEIN	ICTALUEID IERFESVIRUS I (CHAMMEL CATPISH VIRUS) (CCV)				Ì		$\dagger$	Ī
PVGI2 HSVSA	HYPOTIGETICAL GENE 12 PROTEIN	HERPESVIRUS SAIMIN (STRAIN 11)	Ī			1		+	
PVGI SPVIR	CAPSID PROTEIN	SPIROPLASMA VIRUS SPVI-RIAZ B	7	701.137	414-472			+	Ī
PVG22 IISVI	HYPOTIGETICAL GENE 22 PROTEIN	ICTALUMID HERPESVIRUS I (CHAMMEL CATFISH VIRUS) (CCV)		647-678				1	Ī
יולאון	IVENTAGE TICAL CENE 33 PROTEIN	ICTALUAID HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	801-62					_	
PVCOA HISVII	INPOSITE TICAL GENE 26 PROTEIN	ICTALUNIO HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	94.135					-	
PVC33 HEVEA	INVESTIGATION GENE 25 PROTEIN	HENTESVIRUS SAIMIN (STRAIN II)	16-30					_	
PVC38 HXVIII	HYPOTHETICAL GENE 18 PROTEIN	ICTALUAID HENDESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	481-531						
PVG2R AMEPV	IIYPOTIETICAL GIR PROTEIN	AMSACTA MOOREI ENTORIOPOXVIRUS (AMEPV)	180-317					1	
PVG2 SPV4	GENE 2 PROTEIN	SPIROPLASMA VIRUS 4 (SPV4)	100.344					-	
rvgjs lisvii	HYPOTHETICAL GENE 35 PROTEIN	ICTALUNID IILRPESVIRUS I (CIJANNEL CATFISII VIRUS) (CCV)	15-46	90-236				+	
PVG16 HSVSA	POSSIBLE TYROSINE-PROTEIN KINASE	HERPESVIRUS SAIMIRI (STRAIN II)	٦					+	
PVG39 11\$VII	HYPOTHETICAL GENE 19 PROTEIN	ICTALURID HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	٦	21.612				+	
PVG40 HSVSA	IIYPOTITETICAL GENE 40 PROTEIN	III.NESVIRUS SAIMIRI (STRAIN II)	_			1		+	
PVC41, IISVII	IIYPOTITETICAL GENE 41 PROTEIN	IC I AL LIRID FIGRET: SVIRUS I (CITANNEL CATFISH VIRUS) (CCV)	Ī	£ 50		1		+	
FVCA2 IESVII	HYPOTHETICAL GENE 42 PROTEIN	ICTALURIDATES VIRUS I (CITAMMEL CATIFISM VIRUS) (CC.V.)	7					+	
PVC43 HSVII	HYPOTHETICAL GENE 4) PROTEIN I'	ICTALUNID (ENFESVINUS I (CITANNEL CATRISH VINUS) (CCV)	1			1		+	1
PVG46 HSVII	PROBABLE MAKOR GLYCOPROTEIN	ICTALURID HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	55				+	+	
PVG48 IISVSA	٠	HELPESVIRUS SAIMIN (STRAIN II)	120-137				1	$\dagger$	Ī
PVGS0 115VSA		INEACESVINOS SAMMING (STIMAINTI)		,		1	1	$\dagger$	
PVGS1 HSVII	IIYPOTHETICAL GENE STRUKANG TROTLEM	TO ALL THE STREET STREET TO TANKE TO STREET STREET STREET						$\dagger$	
PVGS2 IISVII	HIYPUSHE HCAL GENE STRUCKIN	CTALLIAND LEAVES VINOS I CHARACEL CATTERN VINOS (CCV)				1		+	
PVG35 IISVII	SIMPOTHER FLAL GENE 33 PROTEIN	ICTALINED HERESVIRIS I CHANNEL CATEISM VIRISINCOV	Τ	631.447	1091-1126			ł	
TACHE III	SCHOOL SENE SENE SENE	CHANNEL CATFISH VIRUS	Ţ	105.00				+	ĺ
1000	CENE AS PROTEIN	HERPESVIAUS SAIMIRI (STRAIN II)	Τ	105.233			-	$\mid$	
TO SECOND	IIVED TOTAL CANA SAMEANIKANE PROTEIN	ICTALUMIS IBBRESVIRUS I (CHARMEL CATEISH VIRUS) (CCV)	811:53						
1221	SIYPOTILETICAL GENE 61 PROTEIN	ICTALUNID IERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	74-109					-	
NCA IISVI	INTOTIETICAL GENE M PROTEIN	ICTALUALD HEAPESYINUS I (CHANNEL CATFISH VIRUS) (CCV)	55.49	163.401.	430-452		-	H	
PVCAS IISVI	HIYPOTHETICAL GENE 45 PROTEIN	ICTALURID HERPESVIRUS I (CHANNEL CATPISH VIRUS) (CCV)	9(7-101	1146-1174	1390-1326			L	
DSH COA	HYPOTIETICAL GENE 47 PROTEIN	ICTALUND HERPESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)	1150-1185					H	
PVG SPVIA	GENE 6 PROTEIN	SPIROPLASMA VIRUS SPVI-RBA2 B	99-09						
PVG71 ISVSA	IIVEDTHETICAL GENE 21 PROTEIN	HEAPENTIS SAIMINI (STRAIN H)							
PVGT IISVII	IIYPUTILETICAL GENE 12 PROTEIN	ICTALURID HERPESVIRUS I (CHANDREL CATFISH VIRUS) (CCV)	45.478	128-151	4911-9511	1253-1265			
PVG75 HSVII	HYPOTHETICAL GENE 75 PROTEIN ,	ICTALUND KENFESVIRUS I (CHANNEL CATFISH VIRUS) (CCV)		111-422					

1000000			Γ	ABFAI	AREAS	ABEAG	AREA S	ARCAG	ARIAN
10.74	PROTEIN	VIEWS CONTRACTOR OF THE CANADA VIEWS (CCV)	177	Т	T	Г	Г		
P. G. IISVII	HYPOTHETICAL GENE 16 PROTEIN		2	•	-				
PUCH SPVIA	GENE J PROTEIN	IAUS (STAATH BEAUDETTE) (4131.)	1319.1347	-	2109-2146	1601-3633			
3	CI COSSOCIEM INC. PRECISE COR		5 13	137-113		1			
1	_		1250.1204			1			
5	E) CI VEOPEDIFIN PRECURSOR		931-01			İ			
\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	Т	DUVINE CORONAVIRUS (STRAIM LY-138)				1			
PVG CVBN	Т	DOVINE COROMAVIRUS (STRAIN MEBUS)	707.00		j	İ			
0000	F) CL VCOPROTEIN PRECURSOR	DOVINE CORONAVIRUS (STRAIN QUEBEC)	1234-1294		j	Ì			
	ES CLYCOPEDIEIN PRECURSOR	INVINE CORONAVIRUS (STRAIN VACCINE)	1239-138-						
	ET CLYCOPEDIES PRECUBSOR	HUNIAN CORONAVIRUS (STRAIN 229E)	1033-1088			1			
	ET CLYCOPROTEIN PRECURSOR	MURINE CORONAVIRUS MILY (STRAIN WILD TYPE 4) (AUIV-4)	267.1304			1	T		
1	E) CI VEOPEDIEIN PRECUASOR	MILITIME CORONAVIRUS BOIV (STRAIN ASP	251 5121			1			
TAN COL	F1 CL YCOPROTEIN PRECUBSOR	MURINE CORONAVIRUS MIN (STRAIN MINIV / VARIANT CL-2)	20.						
1000	ET GI YCOPROTEIN PRECUASOR		28			1			
PIG 2 CVPS	ET CL YCOPROTEIN PRECURSOR								
P.CL2 CVP6	EJ GL YCOPROTEIN PRECURSOR		ī	17, 11,	171.	T			İ
FVGL2 CVPR	E1 GLYCOPHOTEIN PRECURSOR					Ī			
PVQL2 CVTFU	EJ GLYCOPROTEIN PRECURSOR	FORCINE TRANSMISSIBLE GASTROENTERITIS CORONAVIRUS		100					
PVGL2 CVPRE	Т		Т	13.460	104.1130				
PIGEZ CVPRA	1	ACT BAIN MED	197.00	1	136.136				
PVGL) CVPR!	EJ GLYCOPROJEIN PRECURSOR		414.446	719.767	3	T			
PVCL3 FIPV	EJ GLYCOPROTEIN PRECURSOR	1				Ī			
PVCL3 IBVB	_	Ī		177		<u> </u>			
PVGLD INCMVA	_	HUNIAM CYTUNICALOVINOS (STRAIN ALVIEN)		303.344					
PVGLB HCMVY	ı.	HUDAKA CYTORIECALOVINOS (STRAIM TOWNE)	1						
!	GLYCOPROTEIN B	HERDES SIMPLEY VIRUS (1775 B) SIRAIN COANGA-1192	234.263						
	GLYCOPROTEIN I PRECURSOR	STRAIN MANY MICKING MANAGED THE VIRILE							
	CLYCOPROTEIN IL-1 PRECURSOR								
	GLYCOPROTEIN I PRECURSOR	Ath 6121/11/17	40.472			Ī			
:	CA YCOTROLLIN I FRI CURNUM		63.403			Ī			
rven n.1vs	TO ACCUMENT THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH	AIN THORNE VARDUILIVE	137.413						
	CA VOORED FRANCISCO		135-163	118.776					
	CLYCOPOLETY OFFICURSON	TERPES SINITEX VIRUS (TYPE 1/STRAIN 17)	4 7 8						
רעמוני ווצעוג	7		8			j			
PVCLC 115V1	Τ.		95.465		j	1			
PYCH C HSV21	•		10-444						
PVGLC HSVBC	GLYCOPROTEIN GILL PRECURSOR I	DOVINE HERTENINGS TYTE I (STRAIN COUTER)	200						
PVCA.C. VZVD	CH VCOFBOILIN CPV			11.54		T			
PVGIC VZVS	_		160-170						
LACED IISALA	Control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro		12	2.2		<u>.                                    </u>			
33731			41.70	190-10					
PVCI F HRVE4	T		95-125						
PVG E INVEN	Т		8	27.00					
PVGLE INSVEL	Т		81-1	2			İ		-
TVCHE PRVA	CH. VC OFROIL IN CHERT URSON		_			•			:
TVIZE SINSVA	DEVENDED AT CHEMIST IN PROPERTY.	THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O					1		
PVCLF BRIVE		Т	117.07			Ì	Ī		
PVCLF BASVR	FUSION GLYCOPROTEIN PRECURSOR								
יימני פאס	ℸ	AIN 185373	3						
PVCLF HESVA	FUSION CLYCOPROTEIN PRECINSOR	П	(14-51)						
PV(H.F 1085VI.	_	SIRAIN LUNG)	3			1			
PVGLF HASVA		IUS (STRAIN RSS-1)				1	T		
PVGLF MEASE	FUSION GLYCOPROTEIN PRECURSOR	INEASLES VIRUS (STRAIN EDMONSTON)	7			1			

ULEEANE				3	AREAL	ANTAL	AMEAS IA		
	PROTEIN	VIRUS	113-150						
PVGLF MEASI	FUSION OLYCOPACIE IN PRECURSOR	.A1A.I)	124.356	131-484					
PUCLE MEASY	FUSION GLYCOPROTEIN PRECURSOR			646-474				1	
PVCLF AIUNDI			100				1	1	
PVC3 F SIGNIFA	FUSION OF TOTAL BIR TRECORDS	LIUNIPS VIRUS (STRAIN AW)	2				1		
PACE PROPER	_	AIUNIPS VIRUS (STRAIN SOL)		Ì			†	T	
VCI F KNVI	_	NEWCASTLE DISEASE VIRUS (STRAIN ITALIENAS) (NDV)	13.14				T	T	
VGLF NOVE	FUSION GLYCOPROTEIN PRECURSOR	NEWCASTLE DISEASE VIRIS (STRAIN LASSA) (NUV)	198						
PVGLF MIODV	FUSION GLYCOPROTEIN PRECURSOR		28.48						
PVGLF MISIC	FUSION GLYCOPROTEIN PRECURSOR	(STATINGS)	187-187						
PVGLF PISB	FUSION CLYCOPROTEIN PRECURSOR								
PVC F MIN	FUSION CLYCOPROTEIN PRECURSOR	4 4785)	Т	447.480			$\mid$		
PVCL F RINDK	FUSION GLYCOPROTEIN PRECURSOR (	O) (mov)	30.363	27,780			Ī		
PVCL I INDI	FUSION GLYCOPROTEIN PRECURSOR								
PUCT E CENTA	FUSION GLYCOPROTEIN PRECURSOR	SEKDAI VIAUS (SIRAIN Z / HOST ANTAMIS)	107 97						
PVCI E SENDE	FUSION CL YCOPROTEIN PRECURSOR	SEMBAI VIRUS (STRAIN FUSHING)							
PVCA F SENDH	FUSION GLYCOPROTEIN PRECURSOR	SENDAI VIRUS (STRAIN SIARUS)	10.01						
PVCLE SEND	Т	SENDAL VIRUS (STRAIN HVJ)	100						
PVGLF SENDZ	т	SENDAI VIRUS (STRAIN Z)	7.57						
PVGLF SVS	7	SINITAN VIRUS S(STRAIN W1)(3×3)	453.481						
PVGLF 181V	1	TURKEY MIMOTRACHELLIS VINUS (TRI V)	137.164						
PVGLG HSVEB	۳	EQUINE HERFESVIRUS I YPE I (STRAIN ABOT) (ESTV-1)	\$34.553						
PVGLG SYNV	_	SONCHUS YELLOW MEI VIRUS (3THV)	187 017						
PVGLG VSVIG	7	_	417.402						
PVGLG V\$VIO	-	VESICIA AR STONIATIONS VIRUS (SERVICE NEW JEASE VISING COLORS)	10.41						
PVCLG VSVO	_	_	11797						
PVGLG VSVSJ	_	(NAN)	201.310						
PVCLH HCMVA	-	HIGHIAN CYTOMEDALOVINOS (STANIN ADIMA)	210.718						
PVGLII HCMVT	_	HIMAN CYTOMEGALOVIAUS (STRAIN 10 WE)	315.263	640-677					
PVCLII IISVAG		LIERTES SINITER VIXOS (* 772 6 / 318A) (* 5)	14-650						
PVCLIN HISVE		EQUINE HERFESVINGS 1 THE 4	807.843						
BYGLII HSVEB	CLYCOPROTEIN H PRECURSOR	EQUINE HERTESVIKUS 1 VTC 1	18:18						
FVGJ 1HTMVA	Т	HUNTAM CY I DAN GALLON IS LANGE AND BY	107.233	11.464	983.1030	1049-1084			
PVGIM BUNGE	_	HINNYAVIRUS GERAIISTON	9						
PVCH M HIDNE 7	,		2,0	144.101		•	:	:	
FVGB M INBANI		(GINVAVIRIES NADVARIE)	100	100	23.634				ŀ
rviji ni nunyw	NI POLYPROJETY PRICERSOR	INDINAARSWERA VIRTIS		17.17		114.416	1801.1001		
VACT IN LAW ON	-	STEEN ALVERTAGE AND THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER	70.0			 	İ		
PVC2 AS STANIS	_	THE PART OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE	111.222	(3) ES	1062-1170				
PVCLM HANTH	M POLYPROTEIN PRECURSOR	TANA TANA TANA TANA TANA TANA TANA TANA	22.1	13.64	100				
PVC2 AL HANTI			10.23	100	100	<u> </u>			! 
VIN II IIVI	N MAN VIEW IN THE CHANGE	INCENTIONS NECROTIC SPOT VIRUS (INSV)	200-307	1028-1062					
PVCLN INSV	N POLYTROICIN TRECORSOR	FROSFI CT IIII L. VINIS (MIV)	616-649	1048-1121					
PVGLNI MIV	A PAR THURSDAY OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT	PUNTA TORO PHILEBOVIRUS	101-016	1375-1309					
PVCLN FIFV	Т.	PUUMALA VIRUS (STRAIM HALL: NAS IN)	159-029	1093-113					
NO. IN	- T.	FUUNIALA VINUS ISTRAIN SOFKAMMIT	620-653	1003-1135					
TWEE TO COME	⇁	AIFT VALLEY FEVER VIAUS (RVFV)	420-450	130.00					
		AIFT VALLEY FEVER VIRUS (STRAIN ZII. 148 MIZ) (RVFV)	22.5	30.65	= x		-		
	٠.	SEOUL VIRUS (STRAIN 60.39)	3	<u>=</u>					
		SECUL VIRUS (STRAIN #22)	2 2 2 3 3 3	2 2 2 2 2					
	C N POI VERDITIN PRICINGS	CI CHI, VIRIS (SIRAIN SR. 11) (SAFEMINENT VIRUS)	100	-					
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101 BEV	PEPLONIER CLYCOPROTILIN PRICURSOR	ALANE VIRUS (BLV)							
PVCL Y ICNIN	GLYCOPROTEIN POLYPROTEIN PRECUR	ILININ ARENAVIRUS	17.16						
PVGLY LASSG	GLYCOPROTEIN POLYPROTEIN PRECUR	I. ASSA VIRUS (STRAIN GAMI)							
NA LANGE	Т	I ACCA VIRUS (CIRAIN KISIAII)							

THE WANTE									
1		VINUS	3. 2.			1			
VCI V PIARV	ICLYCOPROTEIN POLYPROTEIN PRECURSOR		13:50						
	CLYCOPROTEIN POLYPROTEIN PRECURSOR	TACARIBE VINUS		19-124					
2012	ISI YEARDTEIN POLYPROTEIN PRECURSOR		9.2	12:13					
TANK A PARTY	CH YCOPACIEIN MR. YPROTEIN PRECURSOR	1803	T	19.134					
VALUE VIEW	CA YENTEDIEIN PIN THOTEIN PRECURSOR		1337-1555						
VCMB CPAIV	GENOME POLYPROJEIN®		100-343	141.111					
	GENOME POLYPROTEIN M		П	479-515					
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VENT BOND	_	INFRPESVIRUS 41	111111111111111111111111111111111111111						
VCP SBV	PRODABLE ANIANAME ANTIGEN CP110	-	71.111						
VCP1 EBV	ENVELOPE GLYCOPROTEIN GP340		21.53						
Alles VACCC	т		\$4.89						
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AND UARV	Т	VARIOLA VIRUS	15.148						
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1 N IN 1		I ACCINIA VIRUS (STRAIN COM: MIAGI:N)	36.5						L
בי או האכנינ	TROILEN D	CACCINIA VIRUS (STRAIN WR)	24-65						
אישו איכני	PROTEIN 15	VARIULA VIRUS	<u> </u>						$\downarrow$
PUDS VARY	ŀ	VACCINIA VIAUS (STRAIN COPENTAGEN)	2						1
PLKON VACCC	- 1	CACCINIA VIRUS (STRAIN WR)	2						1
VXO VACCV	_	VACCINIA VIRUS (STRAIN COPENIAGEN)	24-100						L
PVK03 VACCC	╗	VACCINIA VIRUS (STRAIN WR)	 					1	ļ
VK05 VACCV	Ť	VACCINIA VIRUS (STRAIN COPENIAGEN)	39.76						$\downarrow$
VI.03 VACCC	-	VACCINIA VIRIIS (SIRAIN WR)	36.76					_	1
VI OI VACCV	-	VARINIA VIRUS	2						1
FUI DE VARV	_	VACCIMIA VIRUS ISTRAIN COPENHAGEN)	261-122						1
PVL01 VACCC		VACCINIA VIRUS (STRAIN WR)	301-325						1
PLLOJ VACCA	-	VARIOLA VIRUS	20:162						$\downarrow$
PVIO VAR	_	VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPEMIAGE	-:						ļ
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T		REOVINUS (TYPE I / STILATIN LANG)		T				T	İ
ī	PROTEIN AND I AND IC	REOVINUS (TYPE 3/ STRAIN DEALING)					$\mid$		Ī
T	PROTEIN NU. IAIU-IC	REOVIRUS (TYPE 3 / STRAIN DEARING)	1				$\dagger$	$\dagger$	Ī
Т	PROTEIN MU.IAIU.IC	REOVIRUS (1YPE 2/STRAIN DYJONES)				$\frac{1}{1}$	$\mid$	+	l
BEDVI	PROTEIN MU-IAIU-IC	REOVINUS (TYPE I / STRAIN LANG)	4			+	l	$\dagger$	
T	OTERN MUNS	REOVIRUS (TYPE) / STRAIN DEARING)					1	1	
Т		SINIAN VIRUS S (STRAIN W)) (SVS)	308-305			1		t	
Ī,		TURKEY INDMOTRACHEITIS VIRUS (TRTV)	9			1		1	
T		BOVINE CORONA VIRUS (STRAIN MEBUS)	£-103			1		1	
Ī.		HUBIAN CORONAVIRUS (STRAIN OC4))	64-103				1	†	
. İ.,		ARCHINE CORONAVIRUS MIIV (STRAIN AS9)	63-103				+	1	Ī
		AUDINE CORONA VIRUS MINV (STRAIN MIM)	101-49				+	T	Ī
ī		TURKEY ENTERUC CORONAVIRUS (TCV)	£4.103		1	1		1	Ī
		AVIAN INFECTIOUS BRONCHITIS VIRUS (STRAIN BEAUDETTE) (IDV)	 0					1	
T,		AVIAN INFECTIOUS BRONCIUTIS VIRUS (STRAIN BEAUDETTE MAS) (IBV)	11.101					1	
	Z.S.	EPSTEIN BANK VIRUS (STRAIN B93.8) (HUMAN HERPESVIRUS 4)	136-213						
_	Á	CARNATION ETCHED RING VIRUS (CERV)	91-136						
-		SOYDEAN CHLOROTIC MOTTLE VIRUS	19.98	171.101			1	†	
SANISA LIPEDE MIANOR SILLE ACE ANTIGEN PRECURSOR	RECURSOR	DUCK HEPATHIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE S'HUHINY)	201-238	10.00		1		1	Ī
_	RECURSOR	DUCK HEPATITIS O VINUS (STRAIN CHINA) (DHBV)	194.227	2			1	İ	
τ	RECUASOR,	DUCK HEPATITIS B VIRUS (DIBV)	137.190	3.76			1	1	
7.	NECURSOR V	DUCK REPATITIS IN VIRUS (WIRTE SHANGILA! DUCK ISOLATE: \$11) (1)11111/1	2	264-302			+	1	Ì
Ţ	RECURSOR.	GROUND SQUIRREL INFATITIS VIRUS (GSIV)	204.243	71.101			+	1	Ī
T	RECURSOR:	HERON HEPATITIS B VIRUS	150.105	276-269			+	1	Ī
Т		INEPASITIS & VIRUS	30.08				1	T	
Т	RECURSOR.	HEPATITIS & VIRUS (SUBTYPE ADW2)	246-272			+	+	1	Ī
1	RECURSON	HEPATITIS B VIAUS (SUBTYPE ADRA)	244.272			$\frac{1}{1}$	+	T	
_	RECURSOR,	HEPATHIS B VINUS (SUBTYPE ADIV STRAIN WI)	777			1	+		Ī
_	RECURSORI	HEPATHIS DIVINUS (STRAIN ALTHAI)	107-107					t	I
	,	HEPATHIS BYRUSISCENTIFE AD)	10.00				T	T	
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_	BECI BSOL	HEPATITIS B VIRUS (SUBTYPE ADW / STRAIN PHILIPPHOPF DIVINA)	244-332						
┰	RECIPION .	HEPATITIS & VIRUS (SUBTYPE ADR)	344.277						
7		HEPATITIS B VIRUS (SUBTYPE AR)	14-01						
7.	RECURSOR	ILEPATITIS B VIRUS (SUBTYPE ADW)	133-361						
7	RECURSOR	HEPATITIS B VIRUS (SUBTYPE AYW)	333-361			1			
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BANKE WHILE MANDE SURFACE ANTIGEN PO	RECURSOR	WOODCHUCK HEPATHIS VIRUS I	203-241	266-305			-		
STATES THE PRECURSOR	RECURSOR	WOODCHUCK HEPATITIS VIRUS 59	212-246	274.310					
-	RECURSOR	WOODCITLICK HEPATITIS VIRUS 7	213.344	374.310					
T	-	WOODCHUCK HEPATITIS VIRUS 8	311.300	334-310			1	1	
L	ANTIGEN PRECURSOR	WOODCILLCK IEPATITIS VIXUS II (INFECTIOUS CLONE)	313.34	274-305		1	1	1	
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PVNCI AIISV4	MOMSTRUCTURAL PROTEIN NSI		116-146						
V 1241	MONETURAL PROTEIN MSI		10-144						
TANK I TANK	LOWER BUILDING PROTEIN WSI	1	19:14						
ASI IAAMI	CONTRACTOR OF PROPERTY INC.	INFLUENZA A VIRUS (STRAIN ACTILLUTA)	100						
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WALL TABILL	MONSTRUCTURAL PROTEIN MSI	INTUCENCY A VINCE COMPANY AND A MONTH WITH WAY	114-144						
١.	MONCHE LETTINAL PROTEIN NSI	INTLUENZA A VINUS (STRAIN ATOM MOCANOCIO	116.144						
- 1	POWETRING I PROTEIN NSI	INTUENZA A VIRUS (STRAIN ACORT WARRING TO COLOR	107-144						
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ı	CONTRACTOR AT DECISION MC	INTEREST A VINUS (SIRAIN AN EMINGRAIN)	,,,,						
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1	NONSTRUCTURAL PROTEIN NSI	INFIDENZA A VIRLIS ISTRAIN ATERNSOUTH AFRICANI)	104-141						1
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PVNSI INDPA	MONSTRUCTURAL PROTEIN NS!	THE LEAD A VIEW (STRAIN CARN ARBORTING)	387:22						
PVNS1 DECAA	NONSTRUCTURAL PROTEIN NSI	CAT TELY A C VIETS (STEAM CYCALIFORNIA/16)	222-255						4
PVNSI INCCA	MONSTRUCTURAL PROTEIN MS1	THINKS N. B. COMBATORY SYNCYTIAL VIRUS (SUBGROUP B) STRAIN 18517)	2.4						1
PVNS2 ICESVI	NOMSTRUCTURAL PROTEIN?	LIBRAN BECHRATORY SYNCYTIAL VIRUS (STRAIN A2)	10.49						1
PVNS1 ICRSVA	NONSTRUCTURAL PROTEIN 2	DATE OF UT A PURUS (STRAIN BALEDA)	44.93					1	1
PVNS1 INBLE	MONSTRIKETURAL PROTEIN MS2	THE LIENZA B VIRUS (STRAIN BY AMAGATAIN)	11.85					1	1
VNS1 INBYA	MONSTRUCTURAL PROTEIN 1932	LOTHER FORDMAVIRUS NINV (STRAIN S)	17-45						4
VHS4 CVMS	MONSTRUCTURAL PROTEIN	POSCINE TRANSMISSIBLE GASTROENTENTIS CORONAVIRUS (STRAIN FS?)	4.34						1
PVNS4 CVPFS	MONSTRUCTURAL PROTEIN	PORCINE TRANSMISSIBLE GASTROENTERITIS COROMAVIRUS (STRAIN PUR	6(-)				-		1
VINSA CVPPU		PORCINE RESPIRATORY CORONAVIRUS	4.39				1		
PVNSA CVIRM	7	LILIBINE CORONAVIRUS MITV (STRAIN AS9)	45.80						1
PVNST CVANS	_	MAINING CORONAVIRUS BOIV (STRAIN ABI)	49-64						$\downarrow$
VNST CVMBI	_	INTI LIENZA C VIRUS ISTRAIN CICREAT LAKES/1147/4)	111-115						1
PVMST INCGL	П	INST. UENZA C VIRUS (STRAIN CXXHANNESBURG'IMS)	<u>=</u>						ļ
VNST DATH	NOWSTRUCTURAL PROTEINS NOT 1963	DIFLUENZA C VIRUS (STRAIN CAUSSISSIPVIO)	222.23					$\downarrow$	1
PVNST INCAL		DATE UENZA C VIRUS (STRAIN CYAMAGATA/1041)	22.23						1
PVNST INCTA	_	PARTHEMANDING VIRING (STRAIN KAPLAN) (PRV)	2		•	! :	!	1	1

PCCENE	PINCTLLIF		ARFAI	ARCA I	ARCAS	AREAS	AREA S AREA S		AREAT
CILE MANE	PROTEIN	THE THE TAX A VINITE ISTRAIN ACHICKEN FENNSYLVANIA (II)	Г	П	П				
PVINUE JACKP	MUCL EOPHOTEIN		354-388					1	
PVNUC INITO	MUCLEOPROTEIN		154-110					1	
PYNOC INPR	MUCLEOFROTEIN	/34)	154-310				1	+	
PWACE INDICE	MOLLE OF FOREIGN	DKE)	1			1	+	$\dagger$	Ī
NAME AND ASSESSED.			T	101 001		†		$\dagger$	Ī
PVOOI VACCC		S (STRAIN COPEMIAGEN	00.11	100			+	+	
PVOO! VARV			91.15	641.671					
PVOR! YOUV	-	NARCISSUS MOSAIC VIRUS (MAIV)	(2)			T	-	+	
PVOR! PVACE	_	POTATO VIRUS M (STRAIN AUSSIAN) (TVPI)	2					-	
PVORI SAIYEA		T	462-493						
PVPO) HSVSA		HELPESVIRUS SAIMING (STRAIN 11)	3						
PVP10 NPVAC	PIO PROTEIN	10	4.10						
PVP10 NPV0P	Piophotein		266.79						
PVP10 PUSDV	PROTEIN \$10	(V.1)	339-268	287.525					
PVP19 HSVEB	2	TABLE OF COLONIES (CTRAN AD169)	141-172						
PVP23 HChVA	PROBABLE CAPSID PROTEIN VF23	LEADER CIAMI EX VIRIS (TYPE 6/ STRAIN UGANDA-1102)	6.30	106-238				1	
PVP23 HSV6U	PROBABLE CAPSID PROTEIN VEZI		7						
PVP33 HSVEB	PROBABLE CAPSID PROTEIN VP23	VANCEL A POSTER VIRIA STRAIN DERIASIVAN	124-253						
DV2V (19V9	PROBABLE CAPSID PROTEIN VF23	RAIN VACCINE)	108.901						
PVP3 AHSV4	OUTER CAPSID PROTEIN VY		649-643					+	
FVP2 BTV10	OUTER CAPSID PROTEIN VY		531.516	649-683				1	
	GOIER CARINGE STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE O		191-424	564.593					
1 PVP2	COLER CASSILL FROITER UP	(ALIA)	634-688				1	1	
LANT BIVIA	COLER CAPSID SECTION VE		634.688				1	1	
101010	COLUMN CARGO DEOLIE VON	DV-I)	170.915					+	Ī
10104	ENA BIXDING PROTEIN VP.		114.367	25.53		1	+	†	
100	ENA PROJECT CP2		114.167	33.53		1		$\dagger$	
WILDE COV	EXA. BINDING PROTEIN VP2	I STRAIN WA)	Ē	13.367				$\dagger$	
PVP2 #01PC	RNA-BIXING PROTEIN VP2	NIN COWDEN)	16.30	710-017			1		
PVP3 ROTSI	ANA-BINDING PROTEIN VP2			200		T	+	$\dagger$	
PVP35 VACCC	INTRINCUONINANT ENVELOPE PROTEIN PIS	VACCINIA VIRUS (STRAIN COPEMIAGEN)						$\dagger$	
PVP15 VACCV	INDIUNGDOMINANT ENVELOPE PROTEIN P35	_						+	
PVP15 VARV	ININIUMODOMINIANT ENVELOPE PROTEIN P15	VARIOUA VIRIOS	10					$\mid$	Ī
PUPIS MPVOF	MINKOR CAPSED PROJETS	_		214.770			-	T	
rvP) EIIDVI	VT) COME PROTEIN	ETTERATION IN MICHELLA DISEASE VINUS	10.412	31.30					
PVP) EIDVA	VT) COMI, PROTEIN		197.330						
	MAKE COSE PROTEIN VP.	RAIN SAIL)	633-628						
1000	CAPACID PROTEIN PAO	FPSITIN-BARR VIRUS (STRAIN DOLD) (HUNDAN HERFESVIRUS 4)	479-457					1	
FVP46 HSVSA	CAPSED PROTEIN PAR	III RIY SVIRIIS SAIMIRI (STRAIM II	3					1	
PVP40 ILTVI	CAPSID PRUTEIN P40	IMITECTIONS LARYNCOTRACHEITIS VIRUS (STRAIN THORNE VILL) (ILTV)	-					$\dagger$	
QAZA 014A4	CAPSID PROTEIN P40	т			1		+	$\dagger$	
PYP47 MPVAC	VIRAL TRANSCRIPTION REGULATOR P47	OL THE DRUSS VIKUS (ALAINEV)	27.477					1	
PUPAN VACCC		VACCINIA VIROS (STRAIN CUPENIACEN)						t	
PVP4A VACCV	_	VACCING VIAUS (STRAIN WR)	9						
PUPAN VARV	_	VARRALA VINOS	61.172	44.44			-	t	
PVP4 ROTG	OUTER CAPSID PROTEIN VP4	ROLAVINOS (UROUF BY STRAIN)	378.308	24.48			+	Ì	
ALM PANE	NOWSTRUCTURAL PROTEIN PASA	TOTAL VIEW MAIN MAIN MAIN MAIN MAIN MAIN MAIN MAIN		200			-	l	
745 EV	OUTER CAPSID PROTEIN VP3	BILLE DONCHE VIELLE (CEROTYPE L/1904 ATE ALISTRALIA)	201.324						
PVPS BTV1A	OCIER CAPSID PROTEIN VP3	THE LUMBER OF THE STATE OF THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY						l	
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PVPS EIIDVI	OUTER CAPSID FROTEIN VES	SELECT COMPANY (WIN)	911-169						
ALA 644	OUTER COAT PROTEIN PO	This to the tite to the total tree to ison at E USA	159-107						
PVP61 BTV10	VP6 PROTEIN								

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PCCENE	PDCILLI		35.10	0.345					
TIL FARIE		SOLATE OSA)	T	222-257					1
01 A 10	ASSET BY THE AL 14 3 KD PRO		285.313						
PVP62 NUCOV	TRUBALLE MAN TO VERDIEN PRECURSOR	7	281-316						
PVPIN MPVO	NAME ENVELOPE OF YCOPROTEIN PRECURSOR	AUTOCIALPHA CALIFORNICA NUCLEMA TOC TRESSOCIA VIETE CIAINTY	148-213						
1000 PM	LIA TOR ENVELOPE GLYCOPROTEIN		183-103						
	NI I I I I I I I I I I I I I I I I I I		155-183						
	N 11074 112	DI UE IONGUE VIRUS (SERVO) STE SOUTH AFRICA)	189-117						
	VERPOTEU		131-159						
West BTV1A	VPAPROTEIN		80.309						
VIV.	STRUCTURAL PROTEIN PA	7	180-209						
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1000	MAKE TROTEIN		047-950						
74.7	MONATRIKETURAL PROTEIN PMS?	WOUND TUBIOR VIRUS (WIV)	11.112						
2000	CARCID PROTEIN PL	+-	104-139						
200	MONETHINGTON PROTEIN PR		96.139						
	LOUIS DE LE LE POLICIE PO	BLUE TONGUE VIRUS (SEROTYPE 11 / 150LA E USA	60:00						
	WONDER OF PROPERTY PER		56.13						
ı	WONSTRIKE CONTRACTOR OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR		96.130						
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rvra ROV	COLUM CAPSUD CROSSING STATES	()1	T						L
PUR WIV	CALLER CAPSID PROTEIN TO	_							L
PUPIE NEVAC	19 KD POL VIEGRAL ENVELUTE TAUTEIN	=	151.52						L
PVPHE NOVOF	13 KO POL MEDIAL ENVELORE PROTEIN		-	Ī					L
PVPR HVIAZ	VPR PROTEIN							:	: -
FVFR HVINE	No. I Carlo	ī	+						L
FVFR HVM'A		1							
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PVPR HV3NZ	VPR PROJEIN	:		:	!	-		<u>:</u>	l
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LAPR HASSII			2 :						
LALE HASS	VIN CRUITIES			T					L
	VPR PROTEIN	SINITAN INTRIMODEFICIENCY VIRUS (NOVI 43-8) ISOLATE) (SIV-ALAC)							
PUPE SHYLII	VPR PROTEIN			;		_			
PVPR SIVLIK	VPR PROTEIN		<u> </u>					:	
FYPH SIVALL	A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND A LICE AND		3						ļ
PURE SAVSA	VI PRINT IN	SINIAM INITIDICIDE FOLENCY VIRUS (PUMPCI) ISOLATE) (SOOTY MANGADI	37.49						ļ
FVFR SIVSP	VIR PROTEIN	LATE	2.33					1	ļ
VPU HVIBI	VPU PROTEIN	III IN IN INTERPODE FICIENCY VIRUS TYPE I (BILL ISOLATE) (HIV-1)	=						ļ
FVPU HVIBS	VPU PROTEIN	HINDIAN INDRINGUALICIENCY VIRIS TYPE I (BRAIN ISCH ATITICITY II	<u>-</u>			_			_
FVP() SIVION	VPU PROTEIN	THE BANK DESCRIPTION OF BUILDING INTO COMPLEXACE AND PRINCIPLE							1
PVPI IIVIIII	VIII TRILLIA	HILLIAM ILLIAMINGHINE ICHENCY VIRIS TYPE I (HXD2 ISOLATE) (HIV-1)	4.11						1
FVFU IIVIII	VM) PROTEIN	THE TANK IN THE PROPERTY OF VIRIS TYPE I (IRCSF ISOLATE) (1114-1)	1.34						1
TVPU IIVIR	VEUTROIEIN	(1-VIDENTER TOTAL NEW VIEW TYPE ( IVV ) NAMED TO A STATE OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY	=						1
PVPII IIVIFY	NI I I I I I I I I I I I I I I I I I I	THE PARTY AND AND TO SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE OF SELECT STATE SELECT STATE OF SELECT STATE SELECT STATE OF SELECT STATE SELECT STATE OF SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT STATE SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELE	10-134						1
TVPU 35RV	VPU FRUITIN	STIEFT FULNIONARI AND WASHING VIBUSILDY	25.55				1		4
VOT XAV	VPX PROTEIN	SALLINE MANIPONE BUILDY VIRING (150) ATE 129 (BIV)	15-31						4
VPV BIVZ	Г	BARRIE V CTRIPE NOTANC VIRILS (DSMV)	190-319	676-708					1
PVENA BSMV	ALPITA-A PROTEIN	DAME I SINCE FROM COMPANY OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF TH	Γ						
PVSOS ROTH	T	HOPIAN ROLL VINITE CONTRACT CONTRACT	11:119	358-392					1
VSOS ROTHE	HONSTRUCTURAL PROTEIN MSS	CACINE ROLL WINDS (CACINE)	115:347						1
ISTON SOSA	HONSTRUCTURAL PROTEIN NCVP2	SCHAMING TO LANGE (STRAIN BS)	\$8.02						1
VSOG ROTBA	Г	BOUNTE BOTAVIETS (CROUP C / STRATM SHIMTOKU)		113.340					4
PVSOS ROIDS	VIN PROTEIN	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s	(4:4)		_	_			_
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FORD SELECTION ACCESSING PROTEIN   FEFTER-BAJE VILLS STIALAN HERPESYNUS   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199   194-199	T	11 -		7					T	Ī
		ROIEIN LIA		٦	3.50				+	Ī
VENDAGE DUA PACKÁGING PROTEIN   TETALURID NEWEYORUS I (CHANNEL CATTISH VARUS) (CCV)   194-119     FROBAGE DUA PACKÁGING PROTEIN   TETALURID NEWEYORUS I (CHANNEL CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (CATTISH VARUS) (TETALURID NEWEYORUS I (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS) (TETALURID NEWEYORUS		ROBABLE DAY PACE ACTUO PROTEIN		26-208				1	T	
YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN   YEOTHETICAL IS TO PROTEIN		POBABLE DAY PACK ACING PROTEIN		756-788				1	+	
HYPOTHETICAL 10 4 KD EAALY PROTEIN   HOLAGA ADEROVATIOS 1976.]   HYPOTHETICAL 10 4 KD EAALY PROTEIN   HALE STREAK VIRUS (SOUTH AFRICAN ISOLATE) (MSY)   12-59     HYPOTHETICAL 11 5 KD PROTEIN   HALE STREAK VIRUS (SOUTH AFRICAN ISOLATE) (MSY)   12-59     HYPOTHETICAL 11 5 KD PROTEIN   HALE STREAK VIRUS (SOUTH AFRICAN ISOLATE) (MSY)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE ARRIVAL STREAK VIRUS (STAIN AUSTRALLA) (TYDY)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE ARRIVAL STREAK VIRUS (STAIN AUSTRALLA) (TYDY)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE ARRIVAL STREAK VIRUS (STAIN AUSTRALLA) (TYDY)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE ARRIVAL STREAK VIRUS (STAIN AUSTRALLA) (TADY)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE ARRIVAL STREAK VIRUS (STAIN AUSTRALLA) (ALSO AUSTRALLA)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE ARRIVAL STREAK VIRUS (STAIN AUSTRALLA) (ALSO AUSTRALLA)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE ALSO AUSTRALLA FOLYPEBAGSIS VIRUS (ACKNOW)   13-51     HYPOTHETICAL 11 5 KD PROTEIN   HALE AUSTRALLA FOLYPEBAGSIS VIRUS (ACKNOW)   13-51     HYPOTHETICAL 12 1 KD PROTEIN   HALE AUSTRALLA FOLYPEBAGSIS VIRUS (ACKNOW)   13-51     HYPOTHETICAL 12 1 KD PROTEIN   HALE AUSTRALLA FOLYPER OUT C (STRAN AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRAL HALE AUSTRA	Т	PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION O		6					+	
ITTPOTITETICAL 19 KD FROTEIN   WHATE STREAK VARUS (SOUTH-ARICAN ISOLATE) (MSY)   19-14     ITTPOTITETICAL 19 KD FROTEIN   WHAT ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK VARUS (STACK) (TO NOTH ISOUAND WINDS AND STREAK WARD (STACK) (TO NOTH ISOUAND WINDS AND STREAK WARD (STACK) (TO NOTH ISOUAND WINDS AND STREAK WARD (TO NOTH ISOUAND WINDS AND STREAK WARD (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND WINDS AND STREAK WARD (CONTANT) (TO NOTH ISOUAND W	Т	VENTUE TICAL TO A KID EAST Y PROTEIN		5					+	
INTROTHETICAL	Т	SPOTTET TO A TO PROTEIN		Z			1		+	
INTOTICE ICAL	Τ	VPOTITETICAL 10 KD PROTEDY						-	+	
	T	VACABLE TICAL 11 9 KD PROTEIN		3					$\dagger$	Ī
INTEGLIEE INCL.   IN DEPOCIEEN RISEGLEENT SILL   RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEENT RISEGLEEN	Ţ	SPOTIETICAL II 9 KD PROTEDVIOUS VI)		7				1	+	
	٦.		7						+	
INTOTICE TICAL   15 KG PROTEIN RN 19 ED PROTEIN STEEL AUTOGRAPH CALIFORNICA NUCLE AND STEELS SYNLS (ACADRY)   15-101.	Т	VENTILETICAL IS NO PROTEIN	TOBACCO YELLOW DWALF VIRUS (STRAIN AUSTRALIA) (TYDV)	200					+	1
HYPOTHERICAL IN G KD PROTEIN (GRE 6-164)   SULFOLGEUS VIRUS - LIKE PARTICLE SSVI   100-112.	_	VACTILE FICAL 13 R KD PROTEIN IN 19 LD PROTEIN S'REC	AUTOGRAPHA CALIFORNICA PUCLEAR POLYPEDROSIS VIRUS (ACNIPAY)	63-10I.					$\dagger$	
ITTPOTIETICAL 76 TK D PROTEIN (ONE 6-711)   SULFOLORUS VRUGALINE PARTICLE SSY1   17-101		VANCTURE INCAL AL DIED PROTEIN (ORF B-166)	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI	200					$\dagger$	
HYPOTIE FICAL 31.7 KD PROTEIN   MANZE STREAM VIRUS (NICELIAN SOLATE) (MSY)   17.113.     HYPOTIE FICAL 31.7 KD PROTEIN (OWT 1)   10.113.     HYPOTIE FICAL 31.7 KD PROTEIN (OWT CPT)   10.113.     HYPOTIE FICAL 31.7 KD PROTEIN (OWT CPT)   10.113.     HYPOTIE FICAL 31.7 KD PROTEIN (OWT CPT)   10.113.     HYPOTIE FICAL 31.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 31.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 41.7 KD PROTEIN (OWT)   10.113.     HYPOTIE FICAL 51.7						1	$\dagger$			
ITYPOTICE INCL. 19 TO PROTEIN (OUT 1)   SOVREAN CRUDDOTIC MOTTLE VILLS		VPOTIGIEAL 21.7 KD PROTEDY		13.63			†	1	$\frac{1}{1}$	
INTROTIEGICAL 313 TO PROTEIN (OBS.)   AUTOCOMANIA CALI CRICAL TO TREE MASS THE PROTEIN (OBS.)   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116   114-116	Т	IYPOTHETICAL PROTEIN 2 (ORU IS)							╀	
HYPOTHERICAL 513 KD PAOTEIN (OM C-772)	Т	IYPOTHETICAL 11.1 KD PROTEDI (ONJ.1)	OLYNGORUSIS VIKUS (ACMANY)		41.400				-	
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## TABLE XV RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG CARBOXY TRUNCATIONS

X-YTS-Z X-YTSV-Z X-YTSVI-Z X-YTSVIT-Z X-YTSVITI-Z X-YTSVITIE-Z X-YTSVITIEL-Z X-YTSVITIELS-Z X-YTSVITIELSN-Z X-YTSVITIELSNI-Z X-YTSVITIELSNIK-Z X-YTSVITIELSNIKE-Z X-YTSVITIELSNIKEN-Z X-YTSVITIELSNIKENK-2 X-YTSVITIELSNIKENKC-Z X-YTSVITIELSNIKENKCN-Z X-YTSVITIELSNIKENKCNG-Z 15 X-YTSVITIELSNIKENKCNGT-Z X-YTSVITIELSNIKENKCNGTD-Z X-YTSVITIELSNIKENKCNGTDA-Z X-YTSVITIELSNIKENKCNGTDAK-Z X-YTSVITIELSNIKENKCNGTDAKV-Z X-YTSVITIELSNIKENKCNGTDAKVK-Z X-YTSVITIELSNIKENKCNGTDAKVKL-Z X-YTSVITIELSNIKENKCNGTDAKVKLI-Z X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQEL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELD-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVT-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQL-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-2 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLM-2 X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z

The ne lett r amin acid code is used.

Additi nally,

"X" may r present an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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## TABLE XVI RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG AMINO TRUNCATIONS

```
X-QST-Z
                                                X-MQST-Z
                                               X-LMQST-Z
5
                                              X-LLMQST-Z
                                             X-OLLMOST-Z
                                            X-LOLLMOST-Z
                                           X-ELOLLMOST-Z
                                          X-TELQLLMQST-Z
                                         X-VTELOLLMOST-Z
                                        X-AVTELQLLMQST-Z
10
                                      X-NAVTELQLLMQST-Z
                                      X-KNAVTELQLLMQST-Z
                                    X-YKNAVTELQLLMQST-Z
                                    X-KYKNAVTELQLLMQST-Z
                                  X-DKYKNAVTELQLLMQST-Z
                                 X-LDKYKNAVTELQLLMQST-Z
                                X-ELDKYKNAVTELQLLMQST-Z
                               X-QELDKYKNAVTELQLLMQST-Z
15
                              X-KQELDKYKNAVTELQLLMQST-Z
                             X-IKQELDKYKNAVTELQLLMQST-Z
                            X-LIKQELDKYKNAVTELQLLMQST-Z
                            X-KLIKQELDKYKNAVTELQLLMQST-Z
                          X-VKLIKQELDKYKNAVTELQLLMQST-Z
                         X-KVKLIKQELDKYKNAVTELQLLMQST-Z
                        X-AKVKLIKQELDKYKNAVTELQLLMQST-Z
20
                       X-DAKVKLIKQELDKYKNAVTELQLLMQST-Z
                      X-TDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                      X-GTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                    X-NGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                    X-CNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                  X-KCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                  X-NKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
                X-KENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
25
              X-IKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
             X-NIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
            X-SNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
           X-LSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
          X-ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
         X-IELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
        X-TIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
       X-ITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
30
      X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
     X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-2
    X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z
    The one letter amino acid code is used.
```

35 Additionally,

"X" may r present an amino group, a hydrophobic group, including but not limited to carbob nzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl gr up; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier

group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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## TABLE XVII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG CARBOXY TRUNCATIONS

X-FYD-Z X-FYDP-Z X-FYDPL-Z 5 X-FYDPLV-Z X-FYDPLVF-Z X-FYDPLVFP-Z X-FYDPLVFPS-Z X-FYDPLVFPSD-Z X-FYDPLVFPSDE-Z X-FYDPLVFPSDEF-Z X-FYDPLVFPSDEFD-Z X-FYDPLVFPSDEFDA-Z X-FYDPLVFPSDEFDAS-Z X-FYDPLVFPSDEFDASI-Z X-FYDPLVFPSDEFDASIS-Z X-FYDPLVFPSDEFDASISQ-Z X-FYDPLVFPSDEFDASISQV-Z X-FYDPLVFPSDEFDASISQVN-Z X-FYDPLVFPSDEFDASISQVNE-Z X-FYDPLVFPSDEFDASISQVNEK-Z X-FYDPLVFPSDEFDASISQVNEKI-Z X-FYDPLVFPSDEFDASISQVNEKIN-Z X-FYDPLVFPSDEFDASISQVNEKINQ-Z X-FYDPLVFPSDEFDASISQVNEKINQS-Z X-FYDPLVFPSDEFDASISQVNEKINQSL-Z X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z 25 X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a 35 T-butyloxycarbonyl group; a macromolecular carrier

group including but not limit d to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrat s.

## TABLE XVIII RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG AMINO TRUNCATIONS

X-DELL-Z X-SDELL-Z X-KSDELL-Z 5 X-RKSDELL-Z X-IRKSDELL-Z X-FIRKSDELL-Z X-AFIRKSDELL-Z X-LAFIRKSDELL-Z X-SLAFIRKSDELL-Z X-QSLAFIRKSDELL-Z 10 X-NQSLAFIRKSDELL-Z X-INQSLAFIRKSDELL-Z X-KINQSLAFIRKSDELL-Z X-EKINQSLAFIRKSDELL-Z X-NEKINQSLAFIRKSDELL-Z X-VNEKINQSLAFIRKSDELL-Z X-QVNEKINQSLAFIRKSDELL-Z X-SQVNEKINQSLAFIRKSDELL-Z 15 X-ISQVNEKINQSLAFIRKSDELL-Z X-SISQVNEKINQSLAFIRKSDELL-Z X-ASISQVNEKINQSLAFIRKSDELL-Z X-DASISOVNEKINOSLAFIRKSDELL-2 X-FDASISQVNEKINQSLAFIRKSDELL-Z X-EFDASISQVNEKINQSLAFIRKSDELL-Z X-DEFDASISQVNEKINQSLAFIRKSDELL-Z 20 X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-LVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-PLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-DPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z X-YDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, p lyethylene glycol, or carbohydrates.

## TABLE XIX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG CARBOXY TRUNCATIONS

X-ITL-Z X-ITLN-Z X-ITLNN-Z X-ITLNNS-Z X-ITLNNSV-Z X-ITLNNSVA-Z X-ITLNNSVAL-Z X-ITLNNSVALD-Z X-ITLNNSVALDP-Z X-ITLNNSVALDPI-Z X-ITLNNSVALDPID-Z 10 X-ITLNNSVALDPIDI-Z X-ITLNNSVALDPIDIS-Z X-ITLNNSVALDPIDISI-Z X-ITLNNSVALDPIDISIE-Z X-ITLNNSVALDPIDISIEL-Z X-ITLNNSVALDPIDISIELN-2 X-ITLNNSVALDPIDISIELNK-Z X-ITLNNSVALDPIDISIELNKA-Z X-ITLNNSVALDPIDISIELNKAK-Z X-ITLNNSVALDPIDISIELNKAKS-Z X-ITLNNSVALDPIDISIELNKAKSD-Z X-ITLNNSVALDPIDISIELNKAKSDL-Z X-ITLNNSVALDPIDISIELNKAKSDLE-Z X-ITLNNSVALDPIDISIELNKAKSDLEE-Z X-ITLNNSVALDPIDISIELNKAKSDLEES-Z 20

X-ITLNNSVALDPIDISIELNKAKSDLEESK-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKE-Z X-ITLNNSVALDPIDISIELNKAKSDLEESKEW-Z

X-ITLNNSVALDPIDISIELNKAKSDLEESKEWI-Z

X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIR-Z

X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRR-Z

X-ITLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a

macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

# TABLE XX HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG AMINO TRUNCATIONS

```
X-RRS-Z
                                  X-IRRS-Z
                                  X-WIRRS-Z
5
                                 X-EWIRRS-Z
                                X-KEWIRRS-Z
                              X-SKEWIRRS-Z
                              X-ESKEWIRRS-Z
                            X-EESKEWIRRS-Z
                           X-LEESKEWIRRS-Z
                          X-DLEESKEWIRRS-Z
10
                         X-SDLEESKEWIRRS-Z
                        X-KSDLEESKEWIRRS-Z
                       X-AKSDLEESKEWIRRS-Z
                      X-KAKSDLEESKEWIRRS-Z
                     X-NKAKSDLEESKEWIRRS-Z
                    X-LNKAKSDLEESKEWIRRS-Z
                   X-ELNKAKSDLEESKEWIRRS-Z
                  X-IELNKAKSDLEESKEWIRRS-Z
15
                 X-SIELNKAKSDLEESKEWIRRS-Z
                X-ISIELNKAKSDLEESKEWIRRS-2
               X-DISIELNKAKSDLEESKEWIRRS-Z
              X-IDISIELNKAKSDLEESKEWIRRS-Z
             X-PIDISIELNKAKSDLEESKEWIRRS-Z
            X-DPIDISIELNKAKSDLEESKEWIRRS-Z
           X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
20
          X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
         X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
        X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
       X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
      X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
     X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
    X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
```

The one letter amino acid code is used.

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Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

# HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG CARBOXY TRUNCATIONS

X-ALG-Z X-ALGV-Z X-ALGVA-Z 5 X-ALGVAT-Z X-ALGVATS-2 X-ALGVATSA-Z X-ALGVATSAQ-Z X-ALGVATSAQI-Z X-ALGVATSAQIT-Z X-ALGVATSAQITA-Z X-ALGVATSAQITAA-Z 10 X-ALGVATSAQITAAV-Z X-ALGVATSAQITAAVA-Z X-ALGVATSAQITAAVAL-Z X-ALGVATSAQITAAVALV-Z X-ALGVATSAQITAAVALVE-Z X-ALGVATSAQITAAVALVEA-Z X-ALGVATSAQITAAVALVEAK-2 15 X-ALGVATSAQITAAVALVEAKQ-Z X-ALGVATSAQITAAVALVEAKQA-Z X-ALGVATSAQITAAVALVEAKQAR-Z X-ALGVATSAQITAAVALVEAKQARS-Z X-ALGVATSAQITAAVALVEAKQARSD-Z X-ALGVATSAQITAAVALVEAKQARSDI-Z X-ALGVATSAQITAAVALVEAKQARSDIE-Z X-ALGVATSAQITAAVALVEAKQARSDIEK-Z X-ALGVATSAQITAAVALVEAKQARSDIEKL-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLK-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKE-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKEA-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAI-Z X-ALGVATSAQITAAVALVEAKQARSDIEKLKEAIR-Z

25 The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited
to lipid-fatty acid conjugates, polyethylene glycol,
or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

## TABLE XXII HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG AMINO TRUNCATIONS

```
X-IRD-Z
                                   X-AIRD-Z
5
                                  X-EAIRD-Z
                                 X-KEAIRD-Z
                                X-LKEAIRD-Z
                              X-KLKEAIRD-Z
                             X-EKLKEAIRD-Z
                            X-IEKLKEAIRD-Z
                           X-DIEKLKEAIRD-Z
                          X-SDIEKLKEAIRD-Z
10
                         X-RSDIEKLKEAIRD-Z
                        X-ARSDIEKLKEAIRD-Z
                       X-QARSDIEKLKEAIRD-Z
                      X-KQARSDIEKLKEAIRD-Z
                     X-AKQARSDIEKLKEAIRD-Z
                    X-EAKQARSDIEKLKEAIRD-Z
                   X-VEAKQARSDIEKLKEAIRD-Z
15
                  X-LVEAKQARSDIEKLKEAIRD-Z
                 X-ALVEAKQARSDIEKLKEAIRD-Z
                X-VALVEAKQARSDIEKLKEAIRD-Z
               X-AVALVEAKQARSDIEKLKEAIRD-Z
              X-AAVALVEAKQARSDIEKLKEAIRD-Z
             X-TAAVALVEAKQARSDIEKLKEAIRD-Z
            X-ITAAVALVEAKQARSDIEKLKEAIRD-Z
           X-QITAAVALVEAKQARSDIEKLKEAIRD-Z
20
          X-AQITAAVALVEAKQARSDIEKLKEAIRD-Z
         X-SAQITAAVALVEAKQARSDIEKLKEAIRD-Z
        X-TSAOITAAVALVEAKQARSDIEKLKEAIRD-Z
       X-ATSAOITAAVALVEAKOARSDIEKLKEAIRD-Z
      X-VATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
     X-GVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
    X-LGVATSAQITAAVALVEAKQARSDIEKLKEAIRD-Z
```

The one letter amino acid code is used.

25

Additionally,
"X" may represent an amino group, a hydrophobic group,
including but not limited to carbobenzoxyl, dansyl, or
T-butyloxycarbonyl; an acetyl group; a 9fluorenylmethoxy-carbonyl (FMOC) group; a
macromolecular carrier group including but not limited

to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

PCT/US95/16733 WO 96/19495

#### TABLE XXIII REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

### Anti-Respiratory syncytial virus peptides

- X-TSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z
- X-SVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z
- X-VITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z
  - X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z
  - X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z
  - X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z
  - X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z
  - X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-Z
  - X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z
- X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z
- X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-Z
  - X-VNKIALLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
  - X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
  - X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
  - X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z
  - X-VAVSKVLHLEGEVNKIALLSTNKAVVSLSNGVS-Z
- X-AVSKVLHLEGEVNKIALLSTNKAVVSLSNGVSV-Z
- X-VSKVLHLEGEVNKIALLSTNKAVVSLSNGVSVL-Z
  - X-SKVLHLEGEVNKIALLSTNKAVVSLSNGVSVLT-Z
  - X-KVLHLEGEVNKIALLSTNKAVVSLSNGVSVLTS-Z
  - X-LEGEVNKIALLSTNKAVVSLSNGVSVLTSKVLD-Z
  - X-GEVNKIALLSTNKAVVSLSNGVSVLTSKVLDLK-Z

  - X-EVNKIALLSTNKAVVSLSNGVSVLTSKVLDLKN-Z X-VNKIALLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z
- X-NKIALLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
  - X-KIALLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
  - X-IALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
  - X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z

### Anti-human parainfluenza virus 3 peptides

- X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRSN-Z
  - X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRSNQ-Z
  - X-NNSVALDPIDISIELNKAKSDLEESKEWIRRSNQK-Z
  - X-NSVALDPIDISIELNKAKSDLEESKEWIRRSNQKL-Z
  - X-SVALDPIDISIELNKAKSDLEESKEWIRRSNQKLD-Z
  - X-VALDPIDISIELNKAKSDLEESKEWIRRSNQKLDS-Z
  - X-ALDPIDISIELNKAKSDLEESKEWIRRSNQKLDSI-Z
- X-LDPIDISIELNKAKSDLEESKEWIRRSNQKLDSIG-Z
  - X-DPIDISIELNKAKSDLEESKEWIRRSNQKLDSIGN-Z
  - X-PIDISIELNKAKSDLEESKEWIRRSNQKLDSIGNW-Z
  - X-IDISIELNKAKSDLEESKEWIRRSNQKLDSIGNWH-Z
  - X-DISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQ-Z
  - X-ISIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQS-Z
  - X-SIELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSS-Z
  - X-IELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSST-Z
- 35 X-ELNKAKSDLEESKEWIRRSNQKLDSIGNWHQSSTT-Z
- X-TAAVALVEAKQARSDIEKLKEAIRDTNKAVQSVQS-Z

```
X-AVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSSI-Z
X-LVEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNL-Z
X-VEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLI-Z
X-EAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVA-Z
X-AKQARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAI-Z
X-QARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIK-Z
X-QARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKS-Z
X-ARSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKS-Z
X-RSDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQ-Z
X-SDIEKLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQ-Z
X-KLKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVN-Z
X-LKEAIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
X-AIRDTNKAVQSVQSSIGNLIVAIKSVQDYVNK-Z
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### 10 Anti-simian immunodeficiency virus peptides

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X-WQEWERKVDFLEENITALLEEAQIQQEKNMYELQK-Z
X-QEWERKVDFLEENITALLEEAQIQQEKNMYELQKL-Z
X-EWERKVDFLEENITALLEEAQIQQEKNMYELQKLN-Z
X-WERKVDFLEENITALLEEAQIQQEKNMYELQKLNS-Z
X-ERKVDFLEENITALLEEAQIQQEKNMYELQKLNSWD-Z
X-RKVDFLEENITALLEEAQIQQEKNMYELQKLNSWDV-Z
X-VDFLEENITALLEEAQIQQEKNMYELQKLNSWDVF-Z
X-DFLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z
X-FLEENITALLEEAQIQQEKNMYELQKLNSWDVFG-Z
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#### Anti-measles virus peptides

X-LHRIDLGPPISLERLDVGTNLGNAIAKLEAKELL-Z
X-HRIDLGPPISLERLDVGTNLGNAIAKLEAKELLE-Z
X-RIDLGPPISLERLDVGTNLGNAIAKLEAKELLES-Z
X-IDLGPPISLERLDVGTNLGNAIAKLEAKELLESS-Z
X-DLGPPISLERLDVGTNLGNAIAKLEAKELLESSD-Z
X-LGPPISLERLDVGTNLGNAIAKLEAKELLESSDQ-Z
X-GPPISLERLDVGTNLGNAIAKLEAKELLESSDQI-Z
X-PPISLERLDVGTNLGNAIAKLEAKELLESSDQIL-Z
X-PISLERLDVGTNLGNAIAKLEAKELLESSDQILR-Z
X-SLERLDVGTNLGNAIAKLEAKELLESSDQILRSM-Z
X-LERLDVGTNLGNAIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

Additionally,
"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carb xyl group; an amido group; a T-butyloxycarbonyl group; a macr molecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

#### 5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. for example, Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques. Here, the nucleotide sequences encoding the peptides 10 of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, Sambrook, et al., 1989, Molecular Cloning, A Laboratory Manual, Vols. 1-3, Cold Spring Harbor 15 Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are non-peptide bonds. These alternative non-peptide 20 bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another embodiment of the invention, peptides comprising the 25 sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity of the peptides is enhanced. For example, hydrophobic 30 groups such as carbobenzoxyl, dansyl, or tbutyloxycarbonyl groups, may be added to the peptides! amino termini. Likewise, an acetyl group or a 9fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. (See "X" in Tables I to IV,

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above.) Additionally, the hydrophobic group, tbutyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the 15 peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may include, for example, lipid-fatty acid conjugates, 20 polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to the amino terminus of a peptide, with an additional 25 peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1, 35

bel w, and assays for antiviral activity are described in Section 5.5.2, bel w.

#### 5.5.1 ASSAYS FOR CELL FUSION EVENTS

Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides antifusogenic capabilities.

vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

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known to those of ordinary skill in the art, are used.

After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as crystal violet stain, may be used to facilitate the visualization of syncytial formation.

### 5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

The antiviral activity exhibited by the peptides of the invention may be measured, for example, by

asily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an 10 assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for 20 the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4+ cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4⁺ cells by cell-free HIV. Such an assay may comprise culturing an appropriate

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concentration (i.e., TCID₅₀) f virus and CD-4+ cells in the presence f the peptide t be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the present of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those 10 described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference 15 in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying nonretroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial 20 virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability. 30

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may

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Additionally, anti-RSV activity can be assayed in vivo via well known mouse mod ls. Fr exampl, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of 10⁴ to 10⁵ pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known. Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

5.6. USES OF THE PEPTIDES OF THE INVENTION

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The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral

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structure with a cell membrane. Among th intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

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These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not 15 limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

Non retroviral viruses whose transmission may be 20 inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides f the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective 10 in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the 15 antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4+ cells may be co-infected 20 with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose 25 retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identify of the viral isolate. DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific 35

peptide sequence is found. A diagnostic procedure as described, above, for DP178, may b used in conjunction with the DP107/DP178 analog of interest.

#### 5.5.1. SCREENING ASSAYS

As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the 15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described, 20 above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic compounds, natural products, and other sources of

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potentially effective materials may be screen d in a vari ty of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing, for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP107 peptide for a time sufficient to allow binding of the compound to the DP107 peptide;
  - (b) removing non-bound compounds; and
  - (c) determining the presence of the compound bound to the DP107 peptide,
  - thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

- (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;
  - (b) removing non-bound compounds; and

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(c) d termining the presence of the c mpound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

One method utilizing these types of approaches that may be pursued in the isolation of such DP107binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled, either directly or indirectly. In practice, 15 microtiter plates are conveniently utilized. anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

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In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of label immobilized on the surface indicates that

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compl xes were formed. Where the labeled comp nent is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for DP107 or DP178, whichever is appropriate for the given assay, or ab antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored complexes.

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By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107 25 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two peptides to interact and bind, thus forming a complex.

In ord r to test a compound for disruptive activity, th reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted 15 in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either 20 approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have

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been f rm d. The vari us formats are described briefly bel W.

In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with 10 a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the 25 binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled 30 anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alt rnatively, the reacti n can b conducted in a liquid phas in the pr sence or absence f the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

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In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for the their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41\Delta178 peptides and by assaying test

comp unds for the disruption of the c mplexes formed by thes two peptides by immun metrically visualizing DP178/M41\(\Delta\)178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41\(\Delta\)178 is a maltose binding fusion protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41A178 may be immobilized onto solid supports such as microtiter wells. A series of dilutions of a test compound may 10 then be added to each M41 $\Delta$ 178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room temperature for one hour, unbound DP-178 and test compound are removed from the wells and wells are then 15 incubated with the DP178/M41\Delta178-specific Fab-d antibody. After incubation and washing, unbound Fab-d is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be conducted. Test compounds showing an ability to 20 disrupt DP178/M41 $\Delta$ 178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41\Delta178 for the determination of binding constants of the ligand of inhibitory constants for competitors of DP178 binding.

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Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41\(\Delta\)178 is immobilized onto a solid support such as a microtiter well. DP178

binding to M41 $\Delta$ 178 is then quantitated by measuring the fraction of DP178 that is bound as ¹²⁵I-DP178 and calculating the total amount bound using a value for specific activity (dpm/ $\mu$ g peptide) determined for each labeled DP178 preparation. Specific binding to M41 $\Delta$ 178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).

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### 5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art. 15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may 20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal, 25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline 30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration of the peptides of the invention or other inhibitory

ag nts is pr f rred, techniques well known to th se f rdinary skill in the art may be utilized. F r example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adeno-20 associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley 30 Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure

to an HIV virus. Examples of such pr phylactic us of th peptides may include, but are n t limit d to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

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A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the  $LD_{50}$ (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with

r no toxicity. The dosage may vary within this rang dep nding upon the d sage form empl yed and the route of administration utilized. Fr any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the ICm (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels 15 in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

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The peptides may be formulated with a suitable adjuvant in order to enhance the immunological

r sponse. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydr xide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

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Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art.

Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 pl).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administrated dose in the management of the oncogenic disorder of interest

will vary with the severity f th condition t be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the 10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be 15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups, 20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated

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f r oral administration may be in the form f tablets, drag s, capsules, r solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active 10 compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, 15 such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain 20 suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

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add d, such as the cr ss-linked polyvinyl pyrr lidone, agar, or alginic acid or a salt there f such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

### 6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4⁺ cell-cell fusion and infection by cell free virus. In the fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1) shows that the antiviral activity of DP178 (SEQ ID:1)

is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-deriv d DP178 homol g is also found to block HIV-1-mediated syncytia formation.

#### 6.1. MATERIALS AND METHODS

#### 6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide 10 synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were 15 synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the 20 resin by treatment with trifluoracetic acid (TFA) (10ml),  $H_2O$  (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were 25 chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15µ spherical) with a linear gradient; H₂O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry 30 yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

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#### 6.1.2. <u>VIRUS</u>

The HIV-1_{LAI} virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2 µm filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25µl of 10 serial diluted virus was added to 75µl AA5 cells at a concentration of 2 x 105/ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post 15 infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497). 20 The titer of the HIV-1_{LAI} and HIV-1_{MN} stocks used for these studies, as measured on the AA5 cell line, was approximately 1.4  $\times$  10⁶ and 3.8  $\times$  10⁴ TCID₅₀/ml, respectively.

### 6.1.3. CELL FUSION ASSAY

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Approximately 7 x 104 Molt cells were incubated with 1 x 104 CEM cells chronically infected with the HIV-1_{LAI} virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of 100µl culture medium as previously described 30 (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10µl and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the ntire well in a single field.

### 6.1.4. CELL FREE VIRUS INFECTION ASSAY

synthetic peptides were incubated at 37°C with either 247 TCID₅₀ (for experiment depicted in FIG. 2), or 62 TCID₅₀ (for experiment depicted in FIG.3) units of HIV-1_{LAI} virus or 25 TCID₅₀ units of HIV-2_{NHZ} and CEM CD4⁺ cells at peptide concentrations of 0, 0.04, 0.4, 4.0, and 40µg/ml for 7 days. The resulting reverse transcriptase (RT) activity in counts per minute was determined using the assay described, below, in Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J. Hyg. 27: 493-497 for an explanation of TCID₅₀ calculations.

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#### 6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was adapted from Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). Supernatants from virus/cell cultures are adjusted to 1% Triton-X100. A 10µl sample of supernatant was added to 50µl of RT cocktail in a 96-well U-bottom microtitre plate and the samples incubated at 37°C for 90 min. The RT cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM MgCl₂, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01), 0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-radioactive dTTP, and 10µCi/ml ³²P-dTTP (Amersham, cat. No. PB.10167).

After the incubation period,  $40\mu l$  of reaction mixture was applied to a Schleicher and Schuell (S+S) NA45 membrane (or DE81 paper) saturated in 2 x SSC buffer (0.3M NaCl and 0.003M sodium citrate) held in a S+S Minifold over one sheet of GB003 (S+S) filter

paper, with partial vacuum appli d. Each well of the minifold was washed f ur tim s with 200µl 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

### 6.2. RESULTS

6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

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The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells 15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between  $10\mu g/ml$  and 12.5ng/ml were tested for blockade of the 20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1LAI, HIV-1MN, HIV-1gp, or HIV-1sp2 virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection 25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For  ${\rm HIV}_{\rm LAI}$ inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study 30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of  $40\mu g/ml$  (FIG. 4). These observations 35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not relat d to non-specific peptid /protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1_{SF2} isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) 20 failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as  $10\mu g/ml$ . This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 25 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1mediated cell fusion, but the peptide's inability to inhibit HIV-2 medicated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

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### 6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested f r its ability to block CD-4+ CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an 5 experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1LAI isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) 10 represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. et al., 1992, Proc. Natl. Acad, Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each 15 concentration (0, 0.04, 0.4, 4, and  $40\mu g/ml$ ) of peptide was incubated with 247 TCID₅₀ units of HIV-1_{LAI} virus and CEM cells. After 7 days of culture, cellfree supernatant was tested for the presence of RT activity as a measure of successful infection. 20 results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC50=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ: ID:8) and DP-118 (SEQ 25 ID:10), had over 60-fold higher IC50 concentrations of approximately  $5\mu g/ml$ .

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1_{IAI} or HIV-2_{NIHZ}. 62 TCID₅₀

30 HIV-1_{IAI} or 25 GCID₅₀ HIV-2_{NIHZ} were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC50 of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC50 for HIV-35 2_{NIHZ}, thus making DP178 (SEQ ID:1) two logs more potent

as a HIV-1 inhibitor than a HIV-2 inhibit r. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEO ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

### 7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

15 Approximately 3.8x10⁵ CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40μg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

#### 7.2. RESULTS

25 Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

The results of the cyt toxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects n cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested  $(40\mu g/ml)$  do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the 10 Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

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TABLE XXIV

% Viability
at time (hours)

5	<u>Peptide</u>	Peptide Concentration ug/ml	0	24	48	72
	DP178 (SEQ ID:1)	40	98	97	95	97
	-	10	98	97	98	98
10		2.5	98	93	96	96
	DP116 (SEQ ID:9)	40	98	95	98	97
15	-	10	98	95	93	98
		2.5	98	96	98	99
20	No Peptide		98	97	99	98

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107
Soluble recombinant forms of gp41 used in the
example described below provide evidence that the
DP178 peptide associates with a distal site on gp41
whose interactive structure is influenced by the DP107
leucine zipper motif. A single mutation disrupting
the coiled-coil structure of the leucine zipper domain
transformed the soluble recombinant gp41 protein from
an inactive to an active inhibitor of HIV-1 fusion.
This transformation may result from liberation of the
potent DP178 domain from a molecular clasp with the
leucine zipper, DP107, determinant. The results also
indicate that the anti-HIV activity of various gp41
derivativ s (p ptid s and recombinant proteins) may be

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due t their ability to form c mplexes with viral gp41 and interfere with its fusogenic process.

### 8.1. MATERIALS AND METHODS

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### 8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of 10 gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give M41. The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 15 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 20 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41 $\Delta$ 107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'-

- 25 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41 $\Delta$ 178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the
- 30 Xmn I site of pMal-p2. Primer A and 5'-ATAGCTTCTAGATTAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M41-
- 35 PA178. All inserted sequences and mutated residues

wer checked by restriction enzyme analysis and confirmed by DNA sequencing.

### 8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

- The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide 10 gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold, 15 or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed 20 protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.
  - 25 8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY
    Cell fusion assays were performed as previously
    described (Matthews et al., 1987, Proc. Natl. Acad.
    Sci. USA 84: 5424-5481). CEM cells (7 X 10⁴) were
    incubated with HIV-1_{HB} chronically infected CEM cells
    30 (10⁴) in 96-well flat-bottomed half-area plates
    (Costar) in 100 μl culture medium. Peptide and fusion
    proteins at various concentrations in 10 μl culture
    medium were incubated with the cell mixtures at 37°C
    for 24 hours. Multinucleated syncytia were estimated
    35 with microscopic examination. Both M41 and M41-P did

n t sh w cytot xicity at the concentrations t sted and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41\Delta178 or M41-P\Delta178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

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### 8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41 $\Delta$ 178 or M41-P $\Delta$ 178 (5  $\mu$ g/ml) in 0.1M NaHCO₃, pH 8.6, were coated on 96 wells 15 Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) 20 were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room 25 temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. 30 peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H2O2 were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H₂SO₄ after incubation at room temperature for 10 minutes. The optical density of the stopped reaction 35 mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

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#### 8.2. RESULTS

### 8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF GD41

As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic 10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because 15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (i.e., the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely 20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind 25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant 30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HTV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix 35 motif, i.e., DP107 or DP178, of the M41 fusion protein

liminated reactivity with Fab-d. These results indicate that both helical regions, separat d by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

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### 8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, <u>supra</u>, synthetic peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as high as 50 µM (Table XXV, below).

TABLE XXV								
		LEUCINE ZIPPER OF ANTI-HIV MOTIF						

20		DP107	DP178	<u>M41</u>	<u>M41-P</u>	<u>Μ41-ΡΔ178</u>
	Cell fusion (IC ₅₀ )	1 μΜ	1 nM	>50 µM	83 nM	> 50 μM
25	Fab-D binding (k _D )	-	-	3.5x10°	2.5x10*	•
	HIV infectivity (IC ₂₀ )	1 μΜ	80 nM	> 16 μM	66 nM	>8 µM

The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

^{- =} No detectable binding of Fab-d to the fusion proteins.

³⁵Antiviral Infectivity Assays. 20  $\mu$ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20  $\mu$ l of the indicated

concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20 µl of CEM4 cells at 6 x 10³ cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO₂ incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID₃₀) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

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Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1_{ma} infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PΔ178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41\Delta178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PΔ178, was not active in similar competition experiments (FIG. The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

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th DP178 r gi n, making it unavailable for anti-viral activity.

A specific association between thes two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the 5 pp178 peptide or the fusion protein M41 $\Delta$ 178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-P∆178, failed to reconstitute the epitope in similar mixing experiments.

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### EXAMPLE: METHOD FOR COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES

A number of known coiled-coil sequences have been 15 well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D 20 tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form 25 di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes 30 c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs 35 were tailored to the DP107 and DP178 sequences by

deducing the m st likely possibilities for heptad
p sitioning f the amino acids of HIV-1 Bru DP-107,
which is kn wn to have coiled-coil structure, and HIV1 Bru DP178, which is still structurally undefined.
The analysis of each of the sequences is contained in
FIG. 12. For example, the motif for GCN4 was designed
as follows:

- The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
  - 3. The PESEARCH motif would, therefore, be written as follows:

[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-

15 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-

[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-

[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

position either L, M, N, or V must occur; at positions
B and C (the next two positions) accept everything
except C, F, G, I, M, P, T, or W; at the D position
either L, M, N, or V must occur; at positions E, F,
and G (the next 3 positions) accept everything except
C, F, G, I, M, P, T, or W." This statement is
contained four times in a 28-mer motif and five times
in a 35-mer motif. The basic motif key then would be:
[LMNV]-{CFGIMPTW}. The motif keys for the remaining
well described coiled-coil sequences are summarized in
FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and als includes motif d signs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also 10 possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the 15 other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is [ILMNQTV] {CFIMPT}. Notice that now only two basic 25 hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. 30 It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

Hybridizations can be p rform d n any c mbination f two or m re motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

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A special set of motifs was designed based on the fact that DP-178 is located only approximately ten 20 amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper 30 motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped r glycopr t in sequences (library file PVIRUSE1).

Tables V through XIV c ntain lists of prot in sequ nce names and motif hit locations for all the motifs searched.

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### 10. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107 AND DP178-LIKE SEQUENCES IN HUMAN IMMUNODEFICIENCY VIRUS

FIG. 20 represents search results for HIV-1 BRU 10 isolate gp41 (PC/Gene protein sequence PENV_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 15 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, 20 for which the key is found in FIG. 17 ({CDGHP} {CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable 25 additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTIS hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies 30 the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV HV1BR. The proline-leucine zipper motifs also gave 35 several hits in HIV-1 BRU including 503-525 which is

at the v ry C-t rminus of gp120, just upstream f the cleavage site (P7LZIPC and P12LZIPC); and 735-768 in the cytoplasmic d main of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X under the same sequence name as mentioned above. Notice that the only area of HIV-1 BRU which is predicted by the Lupas algorithm to contain a coiled-coil region, is from amino acids 635-670. This begins eight amino acids N-terminal to the start and ends eight amino acids N-terminal to the end of DP178. DP107, despite the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using the Lupas method.

# 11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN RESPIRATORY SYNCYTIAL VIRUS

FIG. 21 represents search results for Human Respiratory Syncytial Virus (RSV; Strain A2) fusion glycoprotein F1 (PC/Gene protein sequence name PVGLF 20 HRSVA). Motif 107x178x4 finds three hits including amino acids 152-202, 213-243, and 488-515. arrangement of these hits is similar to what is found in HIV-1 except that the motif finds two regions with similarities to DP-178, one just downstream of what 25 would be called the DP107 region or amino acids 213-243, and one just upstream of the transmembrane region (also similar to DP178) or amino acids 488-515. Motif ALLMOTIS also finds three areas including amino acids 116-202, 267-302, and 506-549. The proline-leucine 30 zipper motifs also gave several hits including amino acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC), and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC). Notice that the PLZIP motifs also identify regions which share location similarities with DP-178 of HIV-35 1.

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41 (AGM3 isolate; PC/Gene protein sequence name 5 PENV_SIVAG) are shown in FIG. 22. Motif 107x178x4 finds three hits including amino acids 566-593, 597-624, and 703-730. The first two hits only have three amino acids between them and could probably be combined into one hit from 566-624 which would 10 represent a DP107-like hit. Amino acids 703 to 730 would then represent a DP178-like hit. ALLMOTI5 also finds three hits including amino acids 556-628 (DP107like), 651-699 (DP178-like), and 808-852 which represents the transmembrane spanning region. SIV 15 also has one region from 655-692 with a high propensity to form a coiled coil as predicted by the Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs find the same region. SIV does not have any PLZIP

motif hits in gp41.

The identification of DP178/DP107 analogs for a second SIV isolate (MM251) is demonstrated in the Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178 LIKE SEQUENCES IN CANINE DISTEMPER VIRUS

fusion glycoprotein F1 (PC/Gene Protein sequence name PVGLF_CDVO) has regions similar to Human RSV which are predicted to be DP107-like and DP178-like (FIG. 23).

Motif 107x178x4 highlights one area just C-terminal to the fusion peptide at amino acids 252-293. Amino acids 252-286 are also predicted to be coiled coil using the Lupas algorithm. Almost 100 amino acids C-terminal to the first region is a DP178-like area at residu s 340-367. ALLMOTI5 highlights three areas of

interest including: amino acids 228-297, which completely verlaps both the Lupas predicti n and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

## 14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

PIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTI5 finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

## 30 15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEOUENCES IN HUMAN PARAINFLUENZA VIRUS

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Both motifs 107x178x4 and ALLMOTI5 exhibit
DP107-like hits in the same region, 115-182 and 117182 respectively, of Human Parainfluenza Virus (strain
NIH 47885; PC/Gene protein s quence name PVGLF_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits near rethe transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

## 16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES OF INFLUENZA A VIRUS

rIG. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68) at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTI5 at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTI5 predicted the greatest portion of the 88 residue stretch.

## 17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated

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that several f the identified peptides exhibit pot nt antiviral capability. Additionally, it is shown that several of these peptides xhibit a substantial helical character.

### 17.1 MATERIALS AND METHODS

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Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from  $A_{200}$ using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented 30 at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected 35 cells, cultures of acutely infected Hep2 cells were

washed with DPBS (Dulbecco's Phosphate Buffered Saline w/ calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (lmg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD450/690 was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG.

27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;

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2) peptid s T-120 t T-141 and T-576, as sh wn in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and

3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100μg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC₁₀ data for each peptide represents the average of several experiments conducted utilizing that peptide.

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### 17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV
DP178/DP107-like peptides exhibited a detectable level
of antiviral activity. Peptides from the RSV
DP178/DP107-like F2 region (FIG. 27A-B), for example,
T-142 to T-145 and T-334 purfied peptides, exhibited
detectable levels of antiviral activity, as evidenced
by their IC₅₀ values. Further, a number of RSV F1
DP107-like peptides (FIG. 27C-D) exhibited a sizable
level of antiviral activity as purified peptides,
including, for example, peptides T-124 to T-127, T-

131, T-135 and T-137 t T-139, as demonstrat d by their 1 w IC $_{50}$  values. In additi n, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

The results summarized in FIG. 28A-B demonstrate
that a number of DP178-like purified peptides exhibit
a range of potent anti-viral activity. These peptides
include, for example, T-67, T-104, T-105 and T-107 to
T-119, as listed in FIG. 28A, and T-665 to T-669 and
T-671 to T-673, as listed in FIG. 28B. In addition,
some of the DP178-like peptides exhibited some level
of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV antiviral compounds.

## 18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS TYPE 3 DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

- In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.

  25 Additionally, circular dichroism (CD) structural
- analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

### 18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses
35 consisted of circular dichroism (CD) studies. The CD

spectra w re measur d in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at appr ximately 10mM concentrations, using a 1 cm pathlength c ll n a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from  $A_{210}$  using Edlehoch's method (1967, Biochemistry  $\underline{6}$ :1948).

Anti-HPIV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of Hep2 cells chronically infected with HPIV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

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Uninfected confluent monolayers of CV-1W cells

were grown in microtiter wells in 3% EMEM (Eagle

Minimum Essential Medium w/o L-glutamine [Bio

Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes

at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented

at 3%, antibiotics/antimycotics (Gibco BRL Life

Technologies Cat. No. 15040-017) added at 1%, and

glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected CV-1W cells, then adding peptides (at the

dilutions describ d below) in 3% EMEM, and 500 chr nically HPIV3-infected Hep2 c lls per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately  $50\mu l$  0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, avove, in Section 17.1.

Peptides: The peptides characterized in the
study presented herein were:

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- Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- Peptides 189 to 210, as shown in FIG. 30A, and T269, T-626, T-383 and T-577 to T-579, as shown in
  FIG. 30B. These peptides are primarily derived
  from the DP178 region of the HPIV3 F1 fusion
  protein (represented by HPF3 178, as shown in
  FIG. 30A). Peptide T-626 contains two mutated
  amino acid resides (represented by a shaded
  background). Additionally, peptide T-577
  represents F1 amino acids 65-100, T-578
  represents F1 amino acids 207-242 and T-579
  represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial
dilutions ranging from 500μg/ml to approximately

500ng/ml. For each f the assays, a w ll containing no peptide was also used.

### 18.2 RESULTS

The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

As shown in FIG. 29A-B, a number of the HPIV3

DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low IC50 values. In fact, peptides 201 to 205 exhibit IC50 values in the nanogram/ml range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-HPIV3 antiviral compounds.

19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

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FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were

located at amino acid residues 156-215 and 277-289.

The peptide regions found by ALLMOTI5 were located at

amino acid residues 156-219 and 245-286. Both motifs, ther f re, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm.

Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

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20. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN EPSTEIN-BARR VIRUS

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB_EBV) glycoprotein gp110 precursor (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

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FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a homodimer.

Search results domonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found between the known DNA binding and dimerization regions of the protein. Specifically, this region is located

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at amin acid residues 193-220, as sh wn in FIG. 33. The Lupas program pr dicted no coiled-c il regions.

#### COMPUTER-ASSISTED IDENTIFICATION OF **EXAMPLE:** 21. DP178/DP107 ANALOGS IN MEASLES VIRUS

FIG. 34 illustrates the motif search results for 5 the fusion protein F1 of measles virus, strain Edmonston (PC Gene® protein sequence PVGLF_MEASE), successfully identifying DP178/DP107 analogs.

The 107x178x4 motif identifies a single region at 10 amino acid residues 228-262. The ALLMOTI5 search motif identifies three regions, including amino acid residues 116-184, 228-269 and 452-500. Three regions containing proline residues followed by a leucine zipper-like sequence were found beginning at proline 15 residues 214, 286 and 451.

The Lupas program identified two regions it predicted had potential for coiled-coil structure, which include amino acid residues 141-172 and 444-483.

#### COMPUTER-ASSISTED IDENTIFICATION OF EXAMPLE: 22. 20 DP178/DP107 ANALOGS IN HEPATITIS B VIRUS

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FIG. 35 depicts the results of a PZIP motif search conducted on the Hepatitis B virus subtype AYW. Two regions of interest within the major surface antigen precursor S protein were identified. first lies just C-terminal to the proposed fusion peptide of the major surface antigen (Hbs) which is found at amino acid residues 174-191. The second region is located at amino acid residues 233-267. Lupas program predicts no coiled-coil repeat regions. 30

In order to test the potential anti-HBV antiviral activity of these D178/DP107 analog regions, peptides derived from area around the analog regions are synthesized, as shown in FIG. 52A-B. These peptides represent one amino acid peptide "walks" through the

putative DP178/DP107 anal g regi ns. The peptides ar synth sized according to standard Fm c chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Follwing complete synthesis, the peptide aminoterminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested
by utilizing standard assays to determine the test
peptide concentration required to cause an acceptable
(e.g., 90%) decrease in the amount of viral progeny
formed by cells exposed to an HBV viral inoculum.
Candidate antivial peptides are further characterized
in model systems such as wood chuck tissue culture and
animal sytems, prior to testing on humans.

## 23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure a amino acids 424-459.

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24. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN BACTERIAL PROTEINS

The results presented herein demonstrate th identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

FIG. 37 depicts the search motif results for the Pseudomonas aeruginosa fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTIS. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTIS.

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Pseudomonas gonorrhoeae fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 39 depicts the search motif results for the Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 40 depicts the search motif results for the Staphylococcus aureus toxic shock syndrome Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

r gion located at amino acid residues 102-148 w re identified by the ALLMOTI5 search motif. No c iled-c il regions were predict d by the Lupas pr gram.

FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTIS motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5 motif, with the first residing at amino acid residues

55-115, and the s cond residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

# 5 25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS WITHIN VARIOUS HUMAN PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

conducted on the human lupus KU autoantigen protein prot. The ALLMOTIS motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

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> POTENTIAL MEASLES VIRUS DP178/DP107 26. EXAMPLE: ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

#### 26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A280 using Edlehoch's method (1967, Biochemistry 6:1948).

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Anti-MeV antiviral activity syncytial reduction assay: The assay utilized herein tested the ability 25 of the peptides to disrupt the ability of Vero cells acutely infected with MeV (i.e., cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum

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[FBS; which had been heat inactivated for 30 minut s at 56°C; Bi Whittaker Cat. No. 14-501F) supplement d at 10%, antibiotics/antimyc tics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E). Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope. 25

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Anti-MeV antiviral activity plague reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as described above.

The antiviral assay was c nducted by, first, rem ving all media from the wells containing uninfected Vero cells, then adding peptid s (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

on day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

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Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from  $100\mu g/ml$  to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

#### 26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC₅₀ values for such peptides were d termined, as shown in FIG. 47, and ranged from  $1.35\mu g/ml$  (T-257B1/C1) to  $0.072\mu g/ml$  (T-265B1). None of th DP178-like peptides showed, by CD analysis, a detectable level of helicity.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

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### 27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides

15 identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral capability.

#### 27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis, A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk through the DP178-like region of the SIV TM protein.

Each peptide was tested at 2-fold serial dilutions ranging from  $100\mu g/ml$  to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

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#### 27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-SIV antiviral compounds.

28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP178 PEPTIDE TRUNCATIONS AND MUTATIONS

The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

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#### 28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1.

Assays utilized HIV-1/IIIb and/or HIV-2 NIHZ isolates.

Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

Peptides: The peptides characterized in the
study presented herein were:

1) FIGS. 49A-C present peptides derived from
the region around and containing the DP178
region of the HIV-1 BRU isolate.
Specifically, this region spanned from gp41
amino acid residue 615 to amino acid residue
717. The peptides listed contain
truncations of this region and/or mutations

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which vary from the DP178 sequence amino acid sequ nc. Further, c rtain of the peptides hav had amino- and/ r carb xy-terminal groups either added or removed, as indicated in the figures; and

2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

#### 28.2 RESULTS

Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

exhibited a high level of antiviral activity, as evidenced by their low IC₅₀ values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50 represents a test peptide which contains a point mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that

none of the peptides tested on the HIV-2 NIHZ isolate demonstrated appreciable antti-HIV-2 antiviral activity.

Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ( $IC_{50}>400\mu g/ml$ ) whereas the carboxy terminal peptide showed potent antiviral

activity ( $IC_{50}=3\mu g/ml$ ). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

Truncations of the DP107 peptide (referred to in IG. 50 as T21) were also produced and tested, as shown in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by their low IC50 values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

## 29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

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In the Example presented herein, peptides derived
from the Epstein-Barr (EBV) DP-178/DP107 analog region
of the Zebra protein identified, above, in the Example
presented in Section 20 are described and tested for
anti-EBV activity. It is demonstrated that among
these peptides are ones which exhibit potential antiviral activity.

#### 29.1 MATERIALS AND METHODS

Electrophoretic Mobility Shift Assays (EMSA): Briefly, an EBV Zebra protein was synth sized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10 10,000 to 20,000 c.p.m. of a 32P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-15 shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-20 bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

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#### 29.2 RESULTS

Th EBV Zebra pr tein transcription fact r contains a DP178/DP107 anal g region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

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The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays 15 described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the 20 DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of 25 the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects

f th inv ntion, and functionally equivalent methods and comp nents are within the sc pe of the invention. Indeed, various modificati ns f the invention, in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

#### WHAT IS CLAIMED IS:

 An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.

2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.

- 3. The peptide of Claim 2 in which the virus is 10 HIV-1 or HIV-2.
  - 4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
- 5. The peptide of Claim 2 in which the virus is a human parainfluenza virus.
- 6. The peptide of Claim 2 in which the virus is an influenza virus.
  - 7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
- 8. The peptide of Claim 2 wherein the virus is an Epstein-Barr virus.
  - 9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
- 10. The method of Claim 9 wherein the virus is
  HIV-1 or HIV-2.

11. The method f Claim 9 wherein the virus is a respiratory syncytial virus.

- 12. The method of Claim 9 wherein the virus is a human parainfluenza virus.
  - 13. The method of Claim 9 wherein the virus is an influenza virus.
- 14. The method of Claim 9 in which the virus is a hepatitis B virus.
  - 15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

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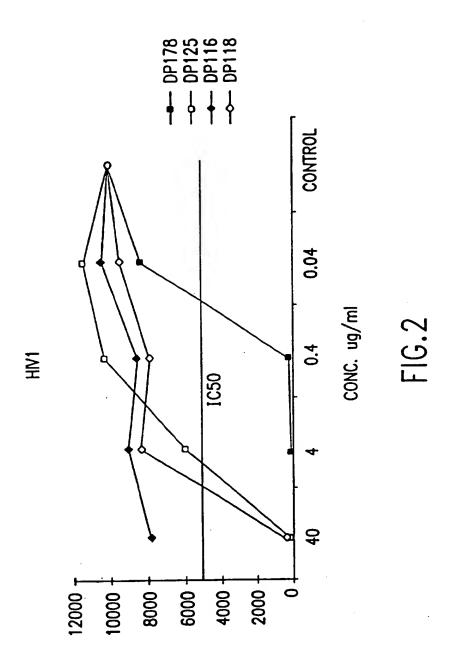
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### 7872-020 (SHEET | OF 63)

I DARTI AVERYI KI	DP116 (SEO 10.9)
CGGNNLLRATEAQQHLLQLTVMGTKQLQARTLAVERYLKI	DP125 (SEQ 10:8)
QQLLDVVKRQQEMLRLTVWGTKNLQARVTAIEKYLKDQ	DP118 (SEQ ID:10)
SSESFTLLEGMNNMKLQLAEGMLEQINEKHYLEDIS	0P180 (SEQ 10:2)
LEANISOSLEQAQIQQEKNMYELQKLNSWDVFTNWL	HIV2NIHZ (SEQ ID:7)
LEANISKSLEQAQIQQEKNMYELQKLNSWDIFGNWF	HIV2ROD (SEQ 10:6)
YTSL IYSLLEKSQTQQEKNEQELLELDKWASLWNWF	HIV1MN (SEQ ID:5)
YTG11YNLLEESQNQQEKNEQELLELDKWANLWNWF	HIV1RF (SEQ ID:4)
YTNTIYNLLEESQNQQEKNEQELLELDKWASLWNWF	HIV1SF2 (DP-185; SEQ ID:3)
YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF	HIV1LAI (DP-178; SEQ ID:1)

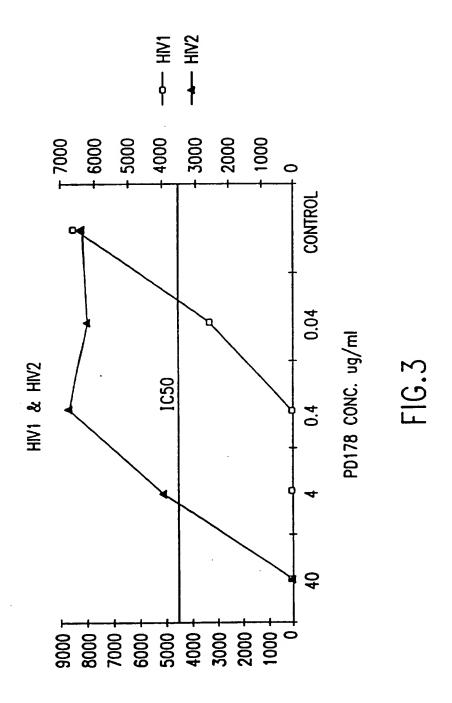
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### 7872-020 (SHEET 2 OF 63)



REVERSE TRANSCRIPTASE UNITS

### 7872-020 (SHEET 3 OF 63)



### 7872-020 (SHEET 4 OF 63)

		<u>•</u>			in μg/ml (micrograms/ml)				
0P178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
Syncylia				•	•	0	0	0	67
HIVILAL	0	0	0	0	0	0	-	ND	34
HIVIM	0	0	0	0	0	ND	ND	ND ND	65
HIVIRF	0	0	0	0	0	NO	ND	=	58
HIV1SF2	0	0	0	0	0	NĐ	ND	ND	30
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
Syncylia									63
HIVILAL	0	0	54	69	80	75	79	82	67
HIVIMN	0	0	30	36	ND	ND	ND	ND	34
HIVIRF	0	0	67	63	ND	ND	ND	ND	65
HIVISF2	0	0	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Contro
Syncylia									
HIVILAL	75	МD	ND	ND	МD	ND	ON	ND	67
HIVIMN	35	ND	ND	ND	ND	ND	ND	ND	34
HIVIRF	81	ND	ND	ND	ND	ND	П	ND	65
HIVISF2	81	ND	ND	ND	ND	ND	ND	ND	58

FIG.4A

DP180	40	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylia HIVILAI	50	>45	>45	>45	>45	>45	>45	>45	. 58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
Syncylio HIVILAI	0	0	0	0	0	0	0	ND	60

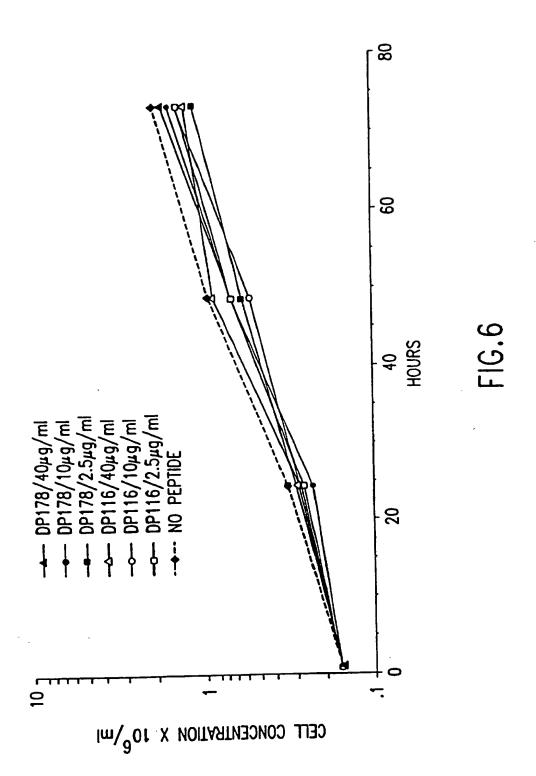
FIG.4B

## 7872-020 (SHEET 5 OF 63)

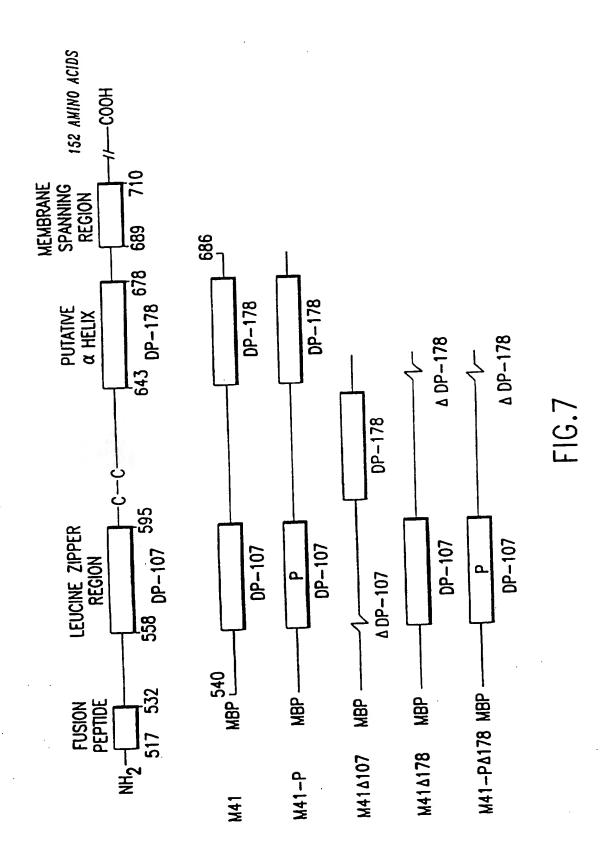
				HIVI	_					
	Number	oſ	Syncyl	o/well:	concer	itration	in ng/ml	(nanograms/ml)		
DP178	20	10	5	2.5_	1.25	0.625	0.3125	Control		
Syncylio HIV1	0	0	0	0	0	14	20	48		
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control		
Syncylia HIV1	ND	48	ND	ND	ND	ND	ND	ND		
				HIVZ	2					
Number of Syncytia/well: concentration in μg/ml (micrograms/										
DP178	20	10	5_	2.5	1.25	0.625	0.3125	Control		
Syncylio HIV2	50	54	55	57	63	77	78	76		
DP116	20	10	) 5	2.5	1.25	0.625	0.3125	Control		
Syncylio HIV2	ND	58	3 ND	ND	ND	ND	ND	ND		

FIG.5

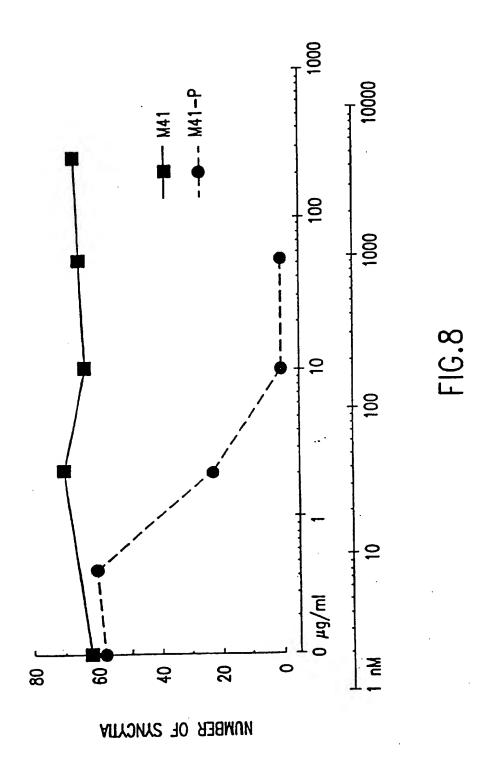
### 7872-020 (SHEET 6 OF 63)



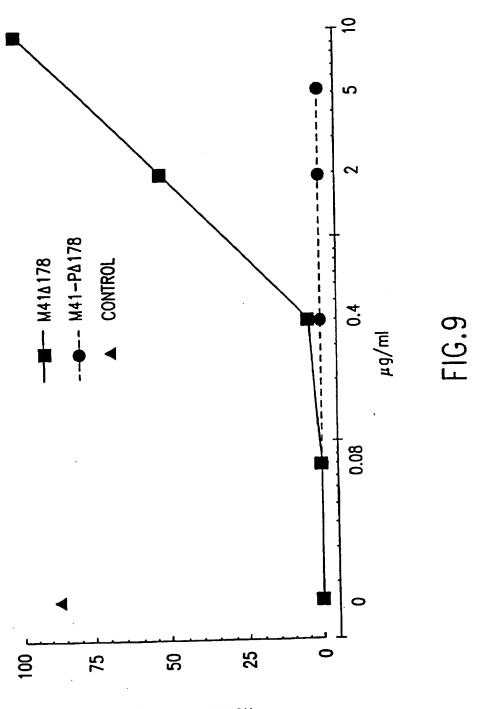
### 7872-020 (SHEET 7 OF 63)



## 7872-020 (SHEET & OF 63)

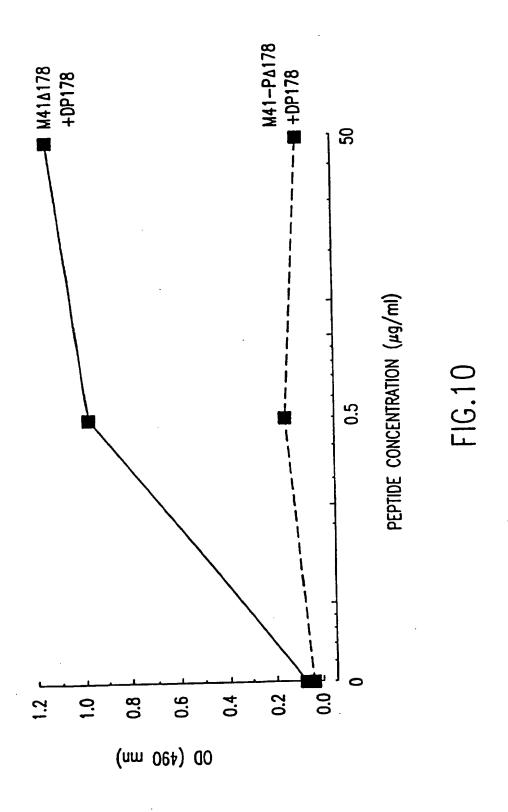


### 7872-020 (SHEET 9 OF 63)

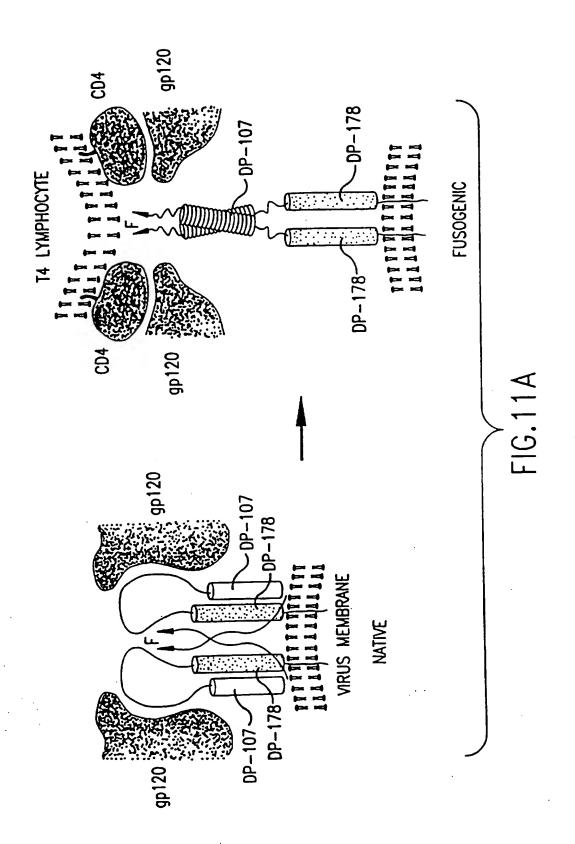


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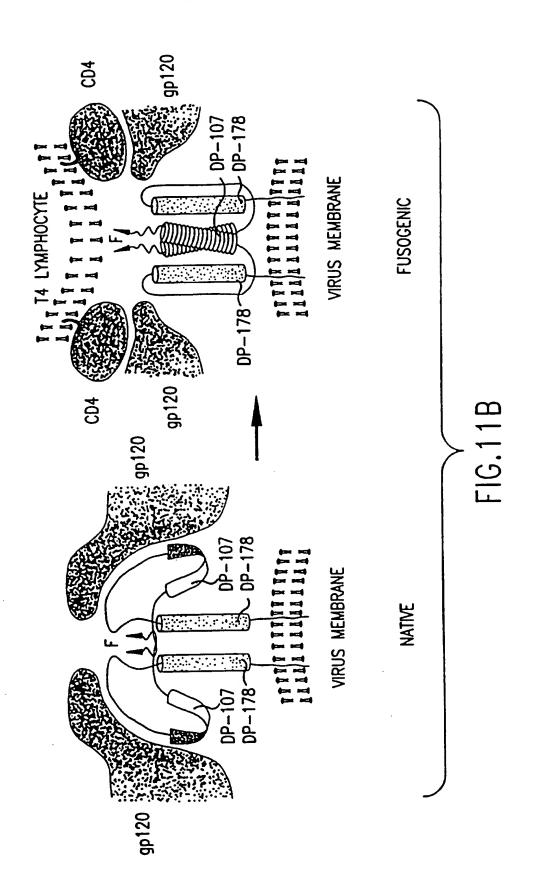
### 7872-020 (SHEET 10 OF 63)



## 7872-020 (SHEET II OF 63)



### 7872-020 (SHEET 12 OF 63)



7872-020 (SHEET 13 OF 63)

WOLLIS.		[LMNV] {CFGIMPTW} [IKLT] {CFGHIMPRWY} [AILNV] {CDFGHILPWYY} [ELR] {ACFGMPWYY} [FILTV] {ACFLMPTWW}
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	Sequence	GCN4 (gcn4 yeast) C-FOS (fos_human) C-JUN (tap1_human) C-AYC (myo_human) FLU LOOP 36

FIG. 12

7872-020 (SHEET 14 OF 63)

Motils			[EKLNOV] {COFKAPSVY} [EKLNOV] {CFKAPS} [EKLNOV] {CFKAPS}	[EKLOY] {ACFGAPRYMY} [EKLOMY] {CFGAPRYY} [EFKLOMY] {CFGAPRYY}	[EILNOSY] {ACFGMPRVMY} {EILNOSMY] {CFGMPRVY} {EFILNOSMY] {CFGMPRVY}
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FIG. 13

7872-020 (SHEET 15 OF 63)

	Hybrid Motil		[ILMOTV] {CF IMPT} [ILMOTV] {CF IMPT} [ILMOTV] {CF IMPT}	[EKLMNOV] {CFMP} [EKLMNOV] {CFMP}
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FIG. 14

7872-020 (SHEET 16 OF 63)

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FIG. 15

7872-020 (SHEET 17 OF 63)

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OP-107 (env_hv1bru)L2=0	NE NE	LRA RA	<u> </u>	ᇂ	<u>0</u> 11	<u>&gt;</u> 	— ပ ≆	× 0	V 0		. بد ۷ ح	ן    -	2 2 2	[EKLINGY] (CENTS)		
DP-178 (env_hv1bru)Y1=A   Y   T S L   1 H S L   1 E	¥ 1 S	<u> </u>	<u></u>	<u></u>	2 0	O E	0 X	۰ رب د سا	<u>.</u>	¥ .	N N N	Z (	ON O CITIC ON THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE	[EFRICATIO] [CEMPANI]	(CC 1K1 NOSTWAY) (CEL	ā
OP-178 (env_hv1bru)Y1=0		S <u>.</u> ≻	=	=	<u> </u>	0 Z 0	ר א ר	ر بر <u>ح</u>	<u>.</u>	 	E 2 2		E .	לכי ובתכאוון לכי מיי ועיין	ובו וערועסו נווו ) לפיי	- :
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FIG. 16

		7872	-020	(SHEET	18 0	F 63)
Hybrid Molil		[EFIKLIANDIVARY] {GFIJP}	[EF1LINORSTWY] {GFLIP}	[efklmowm] {grap}	[efikliakosvay] {cfiap}	
Parent Wolif		(LLOTV) (COFTAPST) [EFRLOWT] (GFGAPRYY)	[LHAV] {CFCINPTN! [ILOTV] {CDFINPST} [EFILNOSNY] {CFGNPRVY}	[LIAN] {GGIIAPTW] [EKLNOV] {GFKAPS} [EFKLOMY] {GGAAPRVY]	[LIAN] (CFCIMPTH) [EKLNOV] (CFOAPS) [EFILNOSHY] (CFOAPRYY)	
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		n4 yeast) env_hvibru)L1=0 env_hvibru)Y1=A	GCN4 (gand yeast) DP-107 (env_hvibru)L1=D DP-178 (env_hvibru)Y1=D	GCN4 (gcn4 yeast) DP-107 (env_hv1bru)L2=D DP-178 (env_hv1bru)Y1=A	GCN4 (gcn4 yeast) OP-107 (env_hv1bru)L2=0 OP-178 (env_hv1bru)Y1=0	
	Sequence	8 9 9	88 1-9 1-19	8 2 2 1 2	8 8 8	

FIG. 17

	78	72	2-	02	20		(8	SH	ΙE	E٦	Γ	19	OF	63)
Hybrid Molif										AEF IX	= facety form			
Parent Wolif		[LIMN] {CFC INPTH}	[1101V] (COF 114PST)	[EKLNOV] (CFNAPS)	[EFKLOHY] [CFGLIPRVY]	[EFILNOSIM] {CFCLLPRVM]	[IKLT] (CFGHIMPRWMY)	(AILIN) (COFCHILPMIY)	(ELR) {ACFGLPWITY]	[FILTV] {ACFLIAPTWH}				
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	Seguence	(DN4 (acn4 yeast)	DP-107 (env hylbrull	DP-107 (Pay hy)hru)1	P-178 (env hylbru) Y	DP-178 (env hv1bru)Y1=0	C-FOS (fos human)	C-JUN (top! human)	C-LYC (myo human)	FLU 100P 36				

### 7872-020 (SHEET 20 OF 63)

<del>-</del>16.19

#### 7872-020 (SHEET 21 OF 63)

Peptide

**4107x178x4 4** 

*.....FLGFLG A AGSTMGARSM TLTVQARQ *LL SGIVOQO DP107-NNL

#### LRAIEAOOHL LOLTYWGIKO LOARILAYER YLKDO-DP107 OLLGAY I WGC

**★107x178x4**★

**♥ALLMOTI5♥** 

*LVS Coilcd-Coil*

SGKLICT TAVP *WNASWS NKSLEQIWNN MTWM *E *WDREINN DP178-

#### YTSLIHSL IEESONOOEK NEOELLELDK* WASLWNWF-DP178 М

+Transmembrane Region +

TNWLWYIK + + IF IMIYGGLYGL RIVEAVLSIY NRVRQGYS + PL

+P23LZIPC+

SFQTHLPTPR GPDR +PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRSL+ CL

**♥ALLMOTI5♥** 

+107x178x4+

F *SYHRLRDLL LIVTRIVELL GRRGW *EALKY WWNLLOYWSO

ELKNSAVSLL NAT A ALAVAEG TDRVIEVVQG A CRAIRITIPR

RIRQGLERIL L

#### 7872-020 (SHEET 22 OF 63)

**Fusion** 

**VALLMOTISY** 

Peptide

4107x178x44

v....FLGFL

LGVGSAIAS GVA * YSKYLHL EGEVNICIKSA

+P1&12LZIPC+

LLSTNKAVVS LSNGVSVLTS KVLDLKNYID KQ + V LL +PIVNKQ

4107x178x44

SC &SISNIETY I+ EFOOKNNRLLETTREFSYNAG & VITTYVSTMLTNSELLSL

+P1&12LZIPC+

**♥ALLMOTI5♥** 

INDM →PI →TNDQ KKLMSNNVQI V→ RQQSYSI+ MS IIKEEVLAYV

VQ▼ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

+P7, 12, & 23LZIPC+

4107x178x44

**VALLMOTISY** 

EPIINFYDPLVF +PSDE +FDASISOVNEKINOSLAF *I+ RKSDELL+

◆ Transmembrane Region ◆

HNYNA + GK STIN + IMITTI IIVIIVILLIS LIAVGLLLY + C+

KARSTPVTLS KDQLSGINNI AFSN

#### 7872-020 (SHEET 23 OF 63)

Fusion

Peptide FLGELG

**♥ALLMOTI5♥ ♦107x178x4**◆

♥AAGTA MGAAA ◆TALTYOSOHLLAGILQQQKNLLAAY

4107x178x44

EAQ → QQM →LKLTIWGYKNLNARYTALEKYLEDOARLN → AWG → CA

*LVS Coilcd-Coil*

**♥ALLMOTI5♥ ♦107x178x4♦** 

WKQVCHTTVP WQWNNRTPDW VNNMT *WLE *WERQISYLEGNTT

4107x178x44

TOLEEARAOEEKNLD* AYOKLSS* WSDFWSW* FDF *SKWLN +ILK

◆ Transmembrane Region ◆ IGFLDYLGIIGLRLLYTY + YS + CIARVRQGYS PLSPQIHIHP WKGQPDNAEG

PGEGGDKRKN SSEPWQKESG TAEWKSNWCK RLTNWCSISS IWLYNS

**♥ALLMOTI5♥** 

♥CLTL LVIILRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL♥

ACRSAYRA IINSPRRVRQ GLEGILN

FIG. 22

#### 7872-020 (SHEET 24 OF 63)

Fusion +107x178x4 ↑

Peptide VALLMOTI5 V *LYS Coiled-Coil *

FAG VYL AGVALGVATA AQITAGIALHQ + *SNLNAQAIQ

SLRTSLEOSNIKAIEEIREATOETVIA* VOGVODY* VNNEL* VP

**♦ALLMOTI5♦** 

+P6 & 12LZIPC+

AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD +PISA + EISIQALIYAL

GGEIHKILEKLGYSGSD ↑ MIAILESRGIKTKI ▼ THVDLPGKF IILSISY

*PI & 12LZIPC*
*PTLSEVKGVIVHRLEAV* SYNIGSQEWYTTVPRYIATNGYLISNFDESSCVFVS

ESAICSQNSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTIINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYP

+P12 & 23LZIPC+

DMVYEGKVAL G +PAISLD +RL+DYGTNLGNALKKLDDAKYLI+

+ Transmembrane Region +
+ Transmembrane Region +
+ FGSLL SYPILSCTAL ALLLLLYCC +

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

#### 7872-020 (SHEET 25 OF 63)

Fusion ▼∧LLMOTI5▼

TIEAVHEYTDGLSQLAYA* VG KM* QQFVNDQFNNTAQELDCIKITQQV

♥ALLMOTI5♥

GVELNLYLTELTTV FGPQITSPAL ▼TQLTIQALYNAGGNMDYLLTKLGVG

+P1 & 12LZIPC+
NNOLSSLIGSGLIT GN → +PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET

LSVST TKGFASALVP KVVTQVGSVI EELDTSYCIE TDLDLYCTIU VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGIISQ

VALLMOTI5

*107x178x4

NYGEAVSLID RHSCN

*VLSLD GITLRLSGEF DATYQKNISI LDSQVIVTG

*LVS Coiled-Coil*
*N LDISTELGNV NNSISNALDK LEESNSKLDK VNVKLTSTSA + LTT* YIA

membrane Region ◆
LTAISLVCGIJ.SLV ◆ LACYLMY + KQKAQQKTLLWLGNNTLGQMRATTKM

#### 7872-020 (SHEET 26 OF 63)

Fusion

**YALLMOTISY** 

Peptide

*107x178x4* *LVS Coiled-Coil*

....FFGGV

**★IG ▼TIALG *YATSAQITAAVALYEAKQARSDIEKLKE** 

AIRDTNKAVOSVOSSIGNLIVAIKSVO* DYVNKE** IVPSIARLGCEAAG

**∀**ALLMOTI5**∀** 

**↑107x178x4↑** 

LQLGIALTQH *YSELTNIFGDNIGSLOEKGIKLQGIASLYRTNITEY*

+P5 & 12LZIPC+

IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL +PLLTRLLNTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITI-KECNTIGINGMLFNTNKEGTLAFYTP

**∀ALLMOTI5∀** 

4107x178x44

+P6 & 23LZIPC+

NDITLNNSVALD +PIDI +SIELN YKAKSDLEESKEWI+ RRSNOKL+

+ Transmembrane Region +

DSIGNWHOSSTT +IIIV+ LIMIILFIINVT II+ IIAVKYY+ R

IQKINIKVDQN DKPYVLTNK

## 7872-020 (SHEET 27 OF 63)

Fusion
Peptide
-----GLEGAI AGFIENGWEGMIDGWYGFRHQNSEGTG

4107x178x44

♥ALLMOTI5♥

*LVS Coiled-Coil*

*Q *AADLKST *QAAIDOINGKLNRVIEKTNEKTHOIEKEFSEVEGRIO

DLEKYVEDTKIDL* WSYNAELLVALENOHTI* DLT▼ DSEMNKLFEKTR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

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7872-020 (SHEET 28 OF 63)

F16, 27A

7872-020 (SHEET 29 OF 63)

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7872-020 (SHEET 30 OF 63)

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-IF. 30 B

# 7872-020 (SHEET 38 OF 63)

## LLDVVKROOELLRLTVWGTKNLOTRVTAIEKYLKDOAOL ↑NAWG ▼ CAF

**VALLMOTI5 ▼***LVS Predicted Coiled -Coil

RQVCHTTVPWPNASLTPDW *NND ▼TWQEWERKVDFLEENITALLEEAQIQQ

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWP WQIEYIHF

#### 7872-020 (SHEET 39 OF 63)

MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSFPFRVCELSSHGDLFRFSSD

**★107x178x4★** 

IQCPSFGTRENHTEGLLMVFKDNIIPYSF *KYRSYTKIYTNILIYNGWYADSVTNRHE*
EKFSVDSY ETDQMDTIYQ CYNAVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR
YASQTELYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN
KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW
QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD
RYTKGQEAIT YFITSGGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG
STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA
RAWCLEQKRQ NMVLRELTKI NPTTVMSSIY GKAVAAKRLG DVISVSQCVP VNQATVTLRK
SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

*107x178x4*
EIHVYNDYHH FKTIELDGIA TLQTFISLNT *SLIENIDFASLELYSRDEQRASNVFD *LE*

*LVS Predicted Coiled Coil* TM Potential
GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

÷P12LZIPC÷

TM Potential

LVSTVGGLFSSLVSGFISF FK N *PFGGMLILVLVAGVVILVISL* TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQKR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

# 7872-020 (SHEET 40 OF 63)

MMDPNSTSED VKFTPDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQGQ

*
LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@ <u>\$107x178x4</u> +Dimerization+
@KRY KNRVASRKCRAK <u>\$FK@Q</u> +<u>LLOHYREVAAAKSSENDRLRLLLKQ</u>

MCPSLDVD+ SI IPRTPDVLHE DLLNF

#### 7872-020 (SHEET 41 OF 63)

Fusion

 *LVS Coiled-Coil*

FAG

♥VVLAGAALGVATAAQITAGIALHQSML*NSQAIDNLRASLETTN

QAIEAIRQAGQEMI*LAVQGVQDYINN ▼ ELIPSMNQLSCDLIGQKLGLKLLRYYT

*P23LZIPC*

*****P6,12LZIPC***** 

<u> 107x178x4</u> ↑

**▼ALLMOTI5▼** 

EILSLFGPSLRD +PISA * VEISIQALSYALGGDINKV+ LEKLGYSGGDL+

÷P1,12LZIPC÷

LGILES ↑ RGIKARI ▼ THVDTESYFIVLSIAY +PTLSEIKGVIVHRLEGV+ SY

NIGSQEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

**P23LZIPC**

→P12LZIPC →

**▼**ALLMOTI5 **▼** 

*LVS Coiled-Coil*

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP ♣P ♥IS*LERLDVGTNLGN

◆Transmembrane Region ◆

AIAKLEDAKELL + ESSDOI + L + RSMK + GLSSTSIVYILI ▼ AVCLGGLIGIP

<u>ALICCC</u> ◆ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL

#### 7872-020 (SHEET 42 OF 63)

Pre S1 and Pre S2
MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRIGDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

**♣P12 & 23LZIPC♣** 

MENITSG FLG +PLL VLQAGFFLLTRILTI+ PQSLDSWWTSLNFLGGTTVCLG

*P12 & 23LZIPC*
QNSQSPTSNHSPTSCPPTC *PGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQGML*
PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKF

◆ <u>Transmembrane Region</u> ◆
LWEWASARFSWLS ◆ <u>LLVPFVOWFVGLSPTVWLSVI</u> ◆ WMMWYWGPSL

- ♦ Transmembrane Region ♦
- +YSILSPFLPLLPIFFCLWVYI+

## 7872-020 (SHEET 43 OF 63)

Fusion ▼ALLMOTI5▼ <u>↑107x178x4</u>↑

Peptide *LVS Coiled Coil

AIQLIPLFVG LGI ▼TTAVSTGAAGLGVS ↑IT *QYTKLSHQLISDV

OAISSTIQDLQDQVDSLAEVVLQ* NRRGLDLLTAE A QGGI ♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region
RLEQEDSGGSYLTLT......?????????????????????.......

FIG 36

# 7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

- **↑107x178x4↑**
- **♥**ALLMOTI5♥
- **↑ YODYTARTOVTRAVSEVSALKTAAESAILEGKEIVSSA ↑ T**

PK DTQYDIGFT

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **♠♥ESTLLDGSGKSQIQVTDNQDGTVELVATLGKSSGS**♠AIKGAVITVSR♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

# 7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

- 4107x178x44
- ♥ALLMOTI5♥
- **▲♥KDNTSAGVASSSSIKGKYVKEVKVENGVVTAT**◆

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

## 7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

- **↑107x178x4↑**
- ♥ALLMOTI5♥
- **♦♥SWKNVDKENNFTLKNEQTTADYATNVNI**

QLMESNGTKAISVVGKETE*

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

#### 7872-020 (SHEET 47 OF 63)

MNKKLLMNFF IVSPLLLATT ATDFTPVP

- 4107x178x44
- **♥ALLMOTI5♥**
- **↑ VLSSNQIIKTAKASTNDNIKDLLDWYSSGSDTFTNS ↑ V**

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

- **↑107x178x4↑**
- **♦DLNTKRTKKSOHTSEGTYIHFOISGYT♦**

N TEKLPTPIEL PLKVKVHGKD SPLKYG

- · *P12LZIPC÷
  - *PKFDKKQLAISTLDFEIRHQLTQI *

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

F19. 40

#### 7872-020 (SHEET 48 OF 63)

**♥ALLMOTI5♥** 

MKKTAFILLL FIALTLTTSP L ♥VNG

**↑107x178x4↑** 

- *LVS Predicted Coiled-Coil*
- *S & EKSEEINEKDLRKKSELORNALSNLROIY* YYNEKAITENKESDD &

OFLENTLL♥ FKG FFTGHPW

- **↑107x178x4 ↑**
- **♦YNDLLVDLGSKDATNKYKGKKVDLYGAY♦**

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEEKKVP INLWIDGKQTTV

- *P12LZIPC*
- *PIDKVKTSKKEVTVQELDL* QARHYLHGK FGLYNSDSFGGKVQ

#P12LZIPC#
RGLIVF HSSEGSTVSY DLFDAQGQY #P DTLLRIYRDN KTINSENLHI#

DLYLYTT

## 7872-020 (SHEET 4 OF 63)

**♥ALLMOTI5♥** 

MKKTAFTLLL FIALTLTTSP L

**♥VNGS** 

**↑107x178x4↑** 

**♦EKSEEINEKDLRKKSELOGTALGNLKQIYYYNEKAKTENKESHD ♦** Q**▼** 

FLQHTILFKG FFTDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKKVPINLWLDGKQNTV

**♥**ALLMOTI5**♥** 

*P12LZIPC*

**♣P ♥L ♠ETVKTNKKNVTVQELDLQARRYL**♣ QEKYNLYN♠

SDVFDGKVQR♥ GLIVF HTSTE

*P23LZIPC*

*PSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHI* DIYLYTS

F1G. 42

## 7872-020 (SHEET 50 OF 63)

#### MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

- **♥ALLMOTI5♥**
- **♥QMNINLYDHARGTQTGFVRYDDGYV**
- 4107x178x44
- **♦STSLSLRSAHLAGOYILSGYSLTIYIVI ♦** ANMFNVNDVISVY **♥**

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

**CGDSSRTITG DTCNE** 

- **♥ALLMOTI5♥**
- **▼ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL ▼**

#### 7872-020 (SHEET 51 OF 63)

MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM
GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLVQPA
LVSSVAPSQT RAPHPFGVPA PSAGAYSRAG VVKTMTGGRA

*LVS Predicted Coiled-Coil*
QSIGRRGKVE QLSPEEEEKR RIRRE *RNKMA AAK

#### **★107x178x4★**

- **♥ALLMOTI5♥**
- ◆CRNRRREL ◆TDTLQAETDQLEDEKSALQTEIANLLKEKEKL◆

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

## 7872-020 (SHEET 52 OF 63)

SGWESYYKTEGDEEAEEQEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCIQSVYISKIISSDRDLLAVVFYGTEKDKNS
VNFKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR
TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

**↑107x178x4↑** 

**♥ALLMOTI5♥** 

*LVS Predicted Coiled-Coil*

**♥LRVH *FEE &SSKLEDLLRKVRAKETRKRALSRLKLKLNKDIV* ISV** 

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTKTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS DSFENPVLQQHFRNLEALALDLME

*P12LZIPC*

*PEQAVDLTLPKVEAMNKRL* GSLVDEFKELVYPPDYNPEGKVTKR
KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG
LKKQELLEALTKHFQD

#### 7872-020 (SHEET 53 OF 63)

#### **GGGALSPQHSAVTQGSIIKNKEGMDAKS**

- **↑107x178x4↑**
- ♥ALLMOTI5♥
- ▼▲LTAWSRTLVTFKDVFVDFTREEWKLLDT▲ AQQIVYRNV

  MLENYKNLVSLGYQLT♥ KPDVILRLEKGEEPWLVEREIHQETHPD

  SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR

  DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT

  HTGEEPYECKECGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH

  SSRLIRHQRTHTGHKPYECPECGKSFRQSTHLILHQRTHVRVRPYECN

  ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSRSSHLYSHQRTH

  TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN

  DLIKHQRIHVGAETYKCNQCGIIFSQNS
- +P23LZIPC+
- *PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI * RENAY

7872-020 (SHEET 54 OF 63)

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## 7872-020 (SHEET 62 OF 63)

Domain I: 174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

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C-1-1-7-1-4-1-1-1-1-1-0-4-0-0-W-1-7-V-C-7-1-1-P-0-9-8-1-8-T-0-P-C-X-T-C-M L-C-L-I-P-L-L-V-L-L-L-D-Y-Q-A-L-P-V-C-P-L-I-P-G-8-3-T-8-T-G-P-C-R-T-L-L-C-L-I-Y-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G-8-8-T-9-T-G-P-C-R-T L_L_L-C-L-I.P-L-L-V-L-L-Y-Q-Q-H-L-P-V-C-P-L-I-P-Q-8-3-T-5-T-G-P-C-R F-I-1-1-1-C-C-L-I-P-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G-8-9-T-8-7-G-P L-P-I-L-L-L-C-L-I-P-L-L-V-L-L-D-Y-Q-G-N-L-P-V-C-P-L-I-P-G-8-8-T-9-T-0 ₽-L-₽-1-L-L-L-C-L-1-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P-L-1-P-Q-9-8-T-S-T I-F-L-F-I-L-L-L-L-C-L-I-P-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-G-8-8-8-F-I-I-F-L-F-L-L-L-L-L-C-L-I-P-L-L-V-L-L-D-Y-Q-G-N-L-P-V-C-P+L-I-P-Q-S-S-T R.R.F-I-1-F-L-7-1-1-L-L-L-C-L-1-F-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P-Q L-R-R-F-I-I-F-L-L-L-L-L-L-L-L-L-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C-P-L-I-P M-C-L-R-R-F-I-I-I-F-L-F-I-L-L-L-I-F-L-L-V-L-L-D-Y-Q-G-M-L-P-V-C-P R.W-M-C-L-R-R-R-I-I-F-L-F-I-L-L-L-L-I-F-L-L-V-L-L-D-Y-Q-G-H-L-P-V-C T-R-H-M-C-L-R-R-B-1-1-F-L-F-L-L-C-L-1-F-L-L-V-L-L-D-Y-Q-Q-M-L-P-V G-T-R-W-M-C-L-R-R-P-I-I-P-I-L-L-L-L-C-L-I-P-L-L-V-L-L-D-Y-Q-G-W-L-P

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#### INTERNATIONAL SEARCH REPORT

International application No. PCT/US95/16733

US CL :	SSIFICATION OF SUBJECT MATTER  COTK 7/04,14/025, 14/16; C12N 9/94, 9/96, 9/98, 9/  530/324; 424/184.1  o International Patent Classification (IPC) or to both n		
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	530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1,		
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C. DOC	UMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where app	propriate, of the relevant passages	Relevant to claim No.
x	PROCEEDINGS OF THE NATIONAL OF THE UNITED STATES OF AMER		1-3, 9, and 10
Υ	21, issued November 1992, Wild e Inhibitor of Human Immunodefic	t al, "A Synthetic Peptide	4-8 and 11-15
!	Correlation Between Solution Struct pages 10537-41, see entire document	ture and Viral Inhibition",	
	pages 10557-41, see entire docum	10111.	
	her documents are listed in the continuation of Box C.	See patent family annex.	
	pocial categories of cited documents:	"T" have document published after the im	creational filing date or priority
.V. 9	comment defining the general state of the art which is not considered to be of particular relevance	principle or theory underlying the in	ventice
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#### INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/16733

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
K	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	1-3, 9 and 10 4-8 and 11-15
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X  Y	JOURNAL OF VIROLOGY, Volume 67, Number 5, issued May 1993, Lazinski et al, "Relating Structure to Function in the Hepatitis Delta Virus Antigen", pages 2672-80, see pages 2672-73 and 2678.	1 and 7  9 and 14
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